

Db 557 TCTGCCAAGACAAACAGGCGCCGTTACGGGAGCTTATCGCTACATGCTATACCAT 616
 QY 1993 GGTGCTTTGATACAGCCGCGCTTGTATGAAGCGTTGCTGACCGCTGTAGAGCCAG 2052
 Db 617 GGTGCTTTGATACAGCCGCGCTTGTATGAAGCGTTGCTGACCGCTGTAGAGCCAG 676
 QY 2053 ACCTGAGCGCTTCTCTCTTTGCGAGAGCTTCATGAGAGTTCAGAGTATAGAGCAT 2112
 Db 677 ACCTGAGAGCTTCTCTCTTTGCGAGAGCTTCATGAGAGTTCAGAGTATAGAGCAT 736
 QY 2113 GCGGCTTCGAGGCTTCCACATTAAGCCGCTACACCCCGAGAGCGTGTATCTGATGGCC 2172
 Db 737 GCGGCTTCGAGGCTTCCACATTAAGCCGCTACACCCCGAGAGCGTGTATCTGATGGCC 796
 QY 2173 GACTTCTTGAACCGGTGCAAGACCCAGATCACTGGGTGATATATCTGAGACAGG 2232
 Db 797 GACTTCTTGAACCGGTGCAAGACCCAGATCACTGGGTGATATATCTGAGACAGG 856
 QY 2233 CTGAGCGCATATAGAGAGTACATGAGAGTATCTGAGAGAGTGTATGACACTG 2292
 Db 857 CTGAGCGCATATAGAGAGTACATGAGAGTATCTGAGAGAGTGTATGACACTG 916
 QY 2293 GCGGCGGCTCTACGCTTCTGAGAGTACGTTGAGAGCTGAGAGCGTGTAGAGCGGC 2352
 Db 917 GCGGCGGCTCTACGCTTCTGAGAGTACGTTGAGAGCTGAGAGCGTGTAGAGCGGC 976
 QY 2353 TACCTTGAGATGTTTACATCTGAGAGTCCGCGAGCTGCGAGACCGTGGCGCTTGA 2412
 Db 977 TACCTTGAGATGTTTACATCTGAGAGTCCGCGAGCTGCGAGACCGTGGCGCTTGA 1036
 QY 2413 ATTGACCAACCGCATGAGTCTGCGGCACTGCGACCTGCGTGAAGTGTACAGACTGA 2472
 Db 1037 ATTGACCAACCGCATGAGTCTGCGGCACTGCGACCTGCGTGAAGTGTACAGACTGA 1096
 QY 2473 ACCTGAGAGCCTTCAATATTAGCGCGGCGAGACCGGATTAATATGTCCGAG 2532
 Db 1097 ACCTGAGAGCCTTCAATATTAGCGCGGCGAGACCGGATTAATATGTCCGAG 1156
 QY 2533 CTGAACTGGTTTTT 2546
 Db 1157 CTGAACTGGTTTTT 1170

RESULT 6

US-09-237-183A-1015
 ; Sequence 1015, Application US/09237183A
 ; Publication No. US20030135870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheikh, No. US20030135870A1dine
 ; APPLICANT: Fisher, Dane K.
 ; APPLICANT: Liu, Jindong
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
 ; FILE REFERENCE: 38-21(15089)B
 ; CURRENT APPLICATION NUMBER: US/09/237,183A
 ; PRIOR FILING DATE: 1999-01-26
 ; PRIOR APPLICATION NUMBER: US 60/067,000
 ; NUMBER OF SEQ ID NOS: 2814
 ; SEQ ID NO 1015
 ; LENGTH: 428
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; US-09-237-183A-1015

Query Match 10.1%; Score 278; DB 10; Length 428;
 Best Local Similarity 99.7%; Pred. No. 5.1e-133;
 Matches 328; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2218 ATATCTGAGAGCGGCTGCAAGCATATAGAGAGTACACATGAGATATATCTGAGAG 2277
 Db 63 ATATCTGAGAGCGGCTGCAAGCATATAGAGAGTACACATGAGATATATCTGAGAG 122

QY 2278 AGGTGATGACACTGAGCGCGGCTCTACGCTTCTGAGAGTACGTTGCAAGCTGAGAG 2337
 Db 123 AGGTGATGACACTGAGCGCGGCTCTACGCTTCTGAGAGTACGTTGCAAGCTGAGAG 182
 QY 2338 CTGAGAGAGCGGCTACCTTGAAGTCTTCAATATCTGAGAGTTCGAGAGTGAAG 2397
 Db 183 CTGAGAGAGCGGCTACCTTGAAGTCTTCAATATCTGAGAGTTCGAGAGTGAAG 242
 QY 2398 ACCGCGCGCTTGAATGACCAACCGAGTACCTTGGCACTGCGAAGCTGAGACT 2457
 Db 243 ACCGCGCGCTTGAATGACCAACCGAGTACCTTGGCACTGCGAAGCTGAGACT 302
 QY 2458 TGTACAGAGCTGAACCTGAAGACCTTCAATATTTAGCGCGGCGAGAGCTGAGCA 2517
 Db 303 TGTACAGAGCTGAACCTGAAGACCTTCAATATTTAGCGCGGCGAGAGCTGAGCA 362
 QY 2518 TAAATGTGCGGAGCTGAACCTGTTTTT 2546
 Db 363 TAAATGTGCGGAGCTGAACCTGTTTTT 391

RESULT 7

US-09-237-183A-533
 ; Sequence 533, Application US/09237183A
 ; Publication No. US20030135870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cheikh, No. US20030135870A1dine
 ; APPLICANT: Fisher, Dane K.
 ; APPLICANT: Liu, Jindong
 ; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
 ; FILE REFERENCE: 38-21(15089)B
 ; CURRENT APPLICATION NUMBER: US/09/237,183A
 ; PRIOR FILING DATE: 1999-01-26
 ; PRIOR APPLICATION NUMBER: US 60/067,000
 ; NUMBER OF SEQ ID NOS: 2814
 ; SEQ ID NO 533
 ; LENGTH: 303
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; US-09-237-183A-533

Query Match 9.2%; Score 255; DB 10; Length 303;
 Best Local Similarity 100.0%; Pred. No. 4.3e-121;
 Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1761 GCTGATGAGAGCTTGTCTAAGTGCCTTAAGCTGAGAGAGCTGTGAACCTTGTGCTG 1820
 Db 1 GCTGATGAGAGCTTGTCTAAGTGCCTTAAGCTGAGAGAGCTGTGAACCTTGTGCTG 60
 QY 1821 TGGCGGGTACATGATGTGCAAGATCCAGAGAGAGAGAGATGAGAGAG 1880
 Db 61 TGGCGGGTACATGATGTGCAAGATCCAGAGAGAGAGAGATGAGAGAG 120
 QY 1881 GATGATGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1940
 Db 121 GATGATGAGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 1941 GACAAAG 2000
 Db 181 GACAAAG 240
 QY 2001 GGTACAGCGGCTT 2015
 Db 241 GGTACAGCGGCTT 255

RESULT 8

US-10-080-114A-13
 ; Sequence 13, Application US/10080114A
 ; Publication No. US20030005482A1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2004, 06:46:08 ; Search time 976.542 Seconds
(without alignments)
12830.798 Million cell updates/sec

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Perfect score: 2757
Sequence: 1 atgtctgcccgaagctga.....aaaaaaaaagggcgccgc 2757

Scoring table: OLIGO_NUC
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Searched: 2953838 seqs, 2272363821 residues

Word size : 50

Total number of hits satisfying chosen parameters: 19

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Post-processing: Listing first 45 summaries

Database :

1: Published Applications_NA.*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2757	100.0	2757	15	US-10-080-114a-11	Sequence 11, Appl
2	2571	93.3	2737	15	US-10-080-114a-1	Sequence 1, Appl
3	990	35.9	1874	13	US-10-425-114-6561	Sequence 6561, Ap
4	963	34.9	2275	13	US-10-425-114-6036	Sequence 6036, Ap
5	695	25.2	1340	13	US-10-425-114-5285	Sequence 5285, Ap
6	278	10.1	428	10	US-09-237-183A-1015	Sequence 1015, Ap
7	255	9.2	303	10	US-09-237-183A-533	Sequence 533, Ap
8	246	8.9	347	15	US-10-080-114a-13	Sequence 53, Appl
9	209	7.6	283	10	US-09-237-183A-526	Sequence 526, Appl
10	159	5.8	285	10	US-09-237-183A-513	Sequence 513, Appl
11	158	5.7	297	10	US-09-237-183A-516	Sequence 516, Appl
12	150	5.4	150	10	US-09-237-183A-527	Sequence 527, Appl
13	143	5.2	411	10	US-09-237-183A-1018	Sequence 1018, Appl
14	134	4.9	235	10	US-09-237-183A-528	Sequence 528, Appl

ALIGNMENTS

RESULT 1									
US-10-080-114a-11									
; Sequence 11, Application US/10080114A									
; Publication No. US20030005482A1									
; GENERAL INFORMATION:									
; APPLICANT: Dhuaga, Kanwarpal S.									
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes									
; TITLE OF INVENTION: to Improve Stalk and Grain Quality									
; FILE REFERENCE: 1301P									
; CURRENT APPLICATION NUMBER: US/10/080,114A									
; PRIOR FILING DATE: 2002-04-30									
; PRIOR APPLICATION NUMBER: US 60/270,777									
; NUMBER OF SEQ ID NOS: 13									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 11									
; LENGTH: 2757									
; TYPE: DNA									
; ORGANISM: Zea mays									
; FEATURE:									
; NAME/KEY: CDS									
; LOCATION: (1)...(2430)									
; FEATURE:									
; NAME/KEY: source									
; LOCATION: (1)...(39)									
; OTHER INFORMATION: Sorghum pronguinum									
; FEATURE:									
; NAME/KEY: source									
; LOCATION: (40)...(2757)									
; OTHER INFORMATION: Zea mays									
US-10-080-114a-11									
Query Match									
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;									
Matches 2757; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ATGCTTCCCGGAGCTGAAACCGGACGAGCATCCGGACCGCGTGAAGACACCTCTC	60						
DB	1	ATGCTTCCCGGAGCTGAAACCGGACGAGCATCCGGACCGCGTGAAGACACCTCTC	60						
QY	61	CACGCGACCGCAACGAGCTGTGCTCTCTTCCAAATCTGAAACAGGGAAGGAC	120						
DB	61	CACGCGACCGCAACGAGCTGTGCTCTCTTCCAAATCTGAAACAGGGAAGGAC	120						
QY	121	ATCTTGAGCGCGACCAATCTGAGCGCTGACGAGGTCGAGGCTCCGGGATCCGC	180						
DB	121	ATCTTGAGCGCGACCAATCTGAGCGCTGACGAGGTCGAGGCTCCGGGATCCGC	180						
QY	181	GGCTTCGCGGAGGAGACCTTCTCTGAGCTCTCCGCTCCGCGAAGAGGATCTGTG	240						
DB	181	GGCTTCGCGGAGGAGACCTTCTCTGAGCTCTCCGCTCCGCGAAGAGGATCTGTG	240						
QY	241	CGCGCTTGTGTGTCATGCGGTGCGCGCGCGCGCGGAGGATTTGGAGATAGTCCGCTC	300						
DB	241	CGCGCTTGTGTGTCATGCGGTGCGCGCGCGCGCGGAGGATTTGGAGATAGTCCGCTC	300						
QY	301	AACGTTACGAGCTCAAGCTGAGAGTCAAGTCTGAGGATCTCCGCTTCAAGAG	360						
DB	301	AACGTTACGAGCTCAAGCTGAGAGTCAAGTCTGAGGATCTCCGCTTCAAGAG	360						
QY	361	GAGCTTGTGACGCGACGACCAATGATCTTCAAGCTTGAAGCTTGAAGCGCTTC	420						
DB	361	GAGCTTGTGACGCGACGACCAATGATCTTCAAGCTTGAAGCTTGAAGCGCTTC	420						

421 AATGCTCAGTCCACGCGCAATCGGTCACTCATATGAGAAAGGTGCAATTCC 480
421 AATGCTCAGTCCACGCGCAATCGGTCACTCATATGAGAAAGGTGCAATTCC 480
481 AACCGACATCTGCTCAATCATATGTTCCGCAACAGGATTCCTGAGCCCTGTGAT 540
481 AACCGACATCTGCTCAATCATATGTTCCGCAACAGGATTCCTGAGCCCTGTGAT 540
541 TTCCCTCCGTGCGCACCGGCAACAGGCGCATGTTATGATGCTTAATGATGATACAAAG 600
541 TTCCCTCCGTGCGCACCGGCAACAGGCGCATGTTATGATGCTTAATGATGATACAAAG 600
601 TTGCGGAGGCTTCAGTCTGCTGACCAAAAGCTGAGAGACCTTGTCAAAAGCTCCCTGCT 660
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661 GACACACCATCTCAAAATTTGCTTATTAATTTCAAGAGTGGGCGCTGGAGAAAGGTTGG 720
661 GACACACCATCTCAAAATTTGCTTATTAATTTCAAGAGTGGGCGCTGGAGAAAGGTTGG 720
721 GGTGATACAGCAGCAGATGTTTGGAAAAGATCCATCCCTCTTGAACATCAATCAGAGG 780
721 GGTGATACAGCAGCAGATGTTTGGAAAAGATCCATCCCTCTTGAACATCAATCAGAGG 780
781 CCAAGCCCATCTACCCCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTTGT 840
781 CCAAGCCCATCTACCCCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTTGT 840
841 GTGATATCCCTCATGATTAATTTGGTCAAGCTAATGATTAAGGCTGCCAGACACAGGA 900
841 GTGATATCCCTCATGATTAATTTGGTCAAGCTAATGATTAAGGCTGCCAGACACAGGA 900
901 GAGCAGATGCTTATTAATCTGAGACCAAGTCCGTCGACCTGAGAAATGAGATGCTCCGT 960
901 GAGCAGATGCTTATTAATCTGAGACCAAGTCCGTCGACCTGAGAAATGAGATGCTCCGT 960
961 TTAAGAAACAAAGGCTGATGTTTCCCAAGATTTCTCATGTTTACTCGGCTGATACCA 1020
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1021 GATGCAAAAGAAATCATGATCAATCGCGCTTGGAGAAATTAAGTGAACAAGCATACT 1080
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1081 TACATTAATGAGAGTCCCTTCAAGAAATGAAATGAGATCTTAAGAAATGAGATCAAGA 1140
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1141 TTTGATGTTGCGCATATCTGAGAAACATTTGCTGAGATGCTGCTGTAATTCGCT 1200
1141 TTTGATGTTGCGCATATCTGAGAAACATTTGCTGAGATGCTGCTGTAATTCGCT 1200
1201 GAATTAACAAGTATCTCCACAATTTGATTAATGAGAAATTAAGTGAACAAGCATACT 1260
1201 GAATTAACAAGTATCTCCACAATTTGATTAATGAGAAATTAAGTGAACAAGCATACT 1260
1261 TATGTCATCTTCAACAAGTGAATTAACCATGAGATTAACCATGAGATTAACCATGAG 1320
1261 TATGTCATCTTCAACAAGTGAATTAACCATGAGATTAACCATGAGATTAACCATGAG 1320
1321 ACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAAATTAACCATGAG 1380
1321 ACTAAGTATCCAGATTCAGACATATTTTGAAGAAATTTGATGAGAAATTAACCATGAG 1380
1381 TCCGATTCATGCTGATTAATTTGATTAATGAGAAATTAAGTGAACAAGCATACT 1440
1381 TCCGATTCATGCTGATTAATTTGATTAATGAGAAATTAAGTGAACAAGCATACT 1440
1441 TACCAAGAAATTTGCTGAGAAACAAATTAAGTGAACAAGCATACTGCTGCTT 1500
1441 TACCAAGAAATTTGCTGAGAAACAAATTAAGTGAACAAGCATACTGCTGCTT 1500

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1501 ACTGTCCTGCTGCTGACCGAGTGTCCATGAGATGATGCTTGTGATCCAAAGTTCAAT 1560
1561 AATGTCCTCTCTGAGAGTGAACATGTCATATTAATTTTCAATACAGAGAGGCAAGGCA 1620
1561 AATGTCCTCTCTGAGAGTGAACATGTCATATTAATTTTCAATACAGAGAGGCAAGGCA 1620
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1681 CACATTTGGCATCTGATGACCGGTCGAAAGCCCATCTCTTCTTCAATGCGAAATCTGAC 1740
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1741 AAGGTAAGAAATATTAACAGGAGTGTGTAAGCTTTTGTGTAAGTGGCTTAAGTGAAGGAG 1800
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1801 CTTGTAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
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1981 GCTGATACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
1981 GCTGATACCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
2041 GTTGAAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2041 GTTGAAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2100
2101 ATCATTAAGCATGAGGCTCTGAGGCTTCTGAGACCGGCTTGTATGAGCGTGGCTGACCGCT 2160
2101 ATCATTAAGCATGAGGCTCTGAGGCTTCTGAGACCGGCTTGTATGAGCGTGGCTGACCGCT 2160
2161 AATCTGATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2161 AATCTGATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220
2221 TCTGAGCAGGCTGAGGCTGAGGCTATTAAGGATGATGATGATGATGATGATGATGATGATGAT 2280
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2281 TTTGATGACATGAGGCTGAGGCTTCTGAGACCGGCTTGTATGAGCGTGGCTGACCGCT 2340
2281 TTTGATGACATGAGGCTGAGGCTTCTGAGACCGGCTTGTATGAGCGTGGCTGACCGCT 2340
2341 GAGCAGAGGCTGATCTTGAATGTTCTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 2400
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2401 GTGCGCTGCTGCAATTAACCAACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2460
2401 GTGCGCTGCTGCAATTAACCAACCGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2460
2461 TACCAAGTGAATCTGAGGATCTTCAATTAATTTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2520
2461 TACCAAGTGAATCTGAGGATCTTCAATTAATTTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 2520
2521 AATGTCCTGAGGCTGATGCTGCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2580
2521 AATGTCCTGAGGCTGATGCTGCTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2580
2581 TGAAGGCAAGTGGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640

[illegible]

```

RESULT 2
US-10-080-114A-1
: Sequence 1, Application US/10080114A
: Publication No. US20030005482A1
: GENERAL INFORMATION:
: APPLICANT: Dugga, Kanwarpal S.
: TITLE OF INVENTION: to Improve Stalk and Grain Quality
: FILE REFERENCE: 1301P
: CURRENT APPLICATION NUMBER: US/10/080,114A
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/270,777
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 2737
: TYPE: DNA
: ORGANISM: Zea mays
US-10-080-114A-1

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Query Match	Similarity	93.3%	Score 2571	DB 15	Length 2737
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					Gaps
					0
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Db	167	GCCGAGGAGACCCCTTCTCGACGCTCTCGGCTCCGGCAGAGAGCGCATCGTCCGCGCG	226		
QY	247	TTTCGTGGCCCATGCGCGGTGGCCCGCCCGGAGATTGTGGAGATAGTCCGCGCTCAACGTT	306		
Db	227	TTTCGTGGCCCATGCGCGGTGGCCCGCCCGGAGATTGTGGAGATAGTCCGCGCTCAACGTT	286		
QY	307	CACGAGCTCAGGTGAGAGAGCTCAACGTCGTGAGATCCTCGCTTCAAGAGAGACTT	366		
Db	287	CACGAGCTCAGGTGAGAGAGCTCAACGTCGTGAGATCCTCGCTTCAAGAGAGAGCTT	346		
QY	367	GTGCAAGGCAACACATAGATCCCACTTCTCGAGCTTGACCTCGAGCCGTTCAATGTC	426		
Db	347	GTGCAAGGCAACACATAGATCCCACTTCTCGAGCTTGACCTCGAGCCGTTCAATGTC	406		
QY	427	TCAGTCCCAAGCCCAATCGTCAATCATCTATTGGAAACGATGTGCACTTCTCAACGCA	486		
Db	407	TCAGTCCCAAGCCCAATCGTCAATCATCTATTGGAAACGATGTGCACTTCTCAACGCA	466		
QY	487	CACCTGTCTCTCAATCATGTTTCGGCAACAGGAGATGTTGGAGCCCTGTGGATTTCCGC	546		
Db	467	CACCTGTCTCTCAATCATGTTTCGGCAACAGGAGATGTTGGAGCCCTGTGGATTTCCGC	526		
QY	547	CGTGGCAACCGGCAACAGGGGCAATGTTAGATGCTTAAATGATAGAAATACAAAGCTTGGGG	606		
Db	527	CGTGGCAACCGGCAACAGGGGCAATGTTAGATGCTTAAATGATAGAAATACAAAGCTTGGGG	586		
QY	607	AGGCTTCAAGTCTGTGCTGACCAAGAGTGAAGACATTGTCAAAAGTCTCTGCTGACACA	666		
Db	587	AGGCTTCAAGTCTGTGCTGACCAAGAGTGAAGACATTGTCAAAAGTCTCTGCTGACACA	646		
QY	667	CCATATCTCAATTTGCTTATAATTTCAAGATGGGGGCTGGAGAAAGGTGGGGGTGAT	726		
Db	647	CCATATCTCAATTTGCTTATAATTTCAAGATGGGGGCTGGAGAAAGGTGGGGGTGAT	706		

QY	727	ACAGCAGACATGTTTGGAAATGATTCATCTCTCTTGACATCACTTACGCGCCAGAC	786
Db	707	ACAGCAGACATGTTTGGAAATGATTCATCTCTCTTGACATCACTTACGCGCCAGAC	766
QY	787	CCATCTACCCCTAGAGAAATCTTGGCGAGGATCCCATGATTTTAACTGTTGTGAGTA	846
Db	767	CCATCTACCCCTAGAGAAATCTTGGCGAGGATCCCATGATTTTAACTGTTGTGAGTA	826
QY	847	TCCCTCTATGAGATACCTTGGTCAAGCTTAATGATTTAGGCTTGGCAGACACAGAGGACAG	906
Db	827	TCCCTCTATGAGATACCTTGGTCAAGCTTAATGATTTAGGCTTGGCAGACACAGAGGACAG	886
QY	907	ATCGCTATATATCTAGACCAAGTCCGTGCACTAGAAAATGATGTTCTCCGTTTAAAG	966
Db	887	ATCGCTATATATCTAGACCAAGTCCGTGCACTAGAAAATGATGTTCTCCGTTTAAAG	946
QY	967	AAACAGAGGCTGATGTTTCCCAAGATTTCTCATTTCTAGCTGGCTGATPACAGATGCA	1026
Db	947	AAACAGAGGCTGATGTTTCCCAAGATTTCTCATTTCTAGCTGGCTGATPACAGATGCA	1006
QY	1027	AAAGAAACATCATGSCATCAACGGCTTGAGAGAAATTAGTGAACACAGCATTACTTACATA	1086
Db	1007	AAAGAAACATCATGSCATCAACGGCTTGAGAGAAATTAGTGAACACAGCATTACTTACATA	1066
QY	1087	TTACAGATTCCTTCAAGAAATGAAATGGGATCTTAAAGAAATGAGATATCAAGATTGAT	1146
Db	1067	TTACAGATTCCTTCAAGAAATGAAATGGGATCTTAAAGAAATGAGATATCAAGATTGAT	1126
QY	1147	GTGAGGCAATCTCTGAAAACATTTGCTGAGATCTCTGGTGAATTTGCTGCTGAATTA	1206
Db	1127	GTGAGGCAATCTCTGAAAACATTTGCTGAGATCTCTGGTGAATTTGCTGCTGAATTA	1186
QY	1287	CAAGTACTCCAGACTTCATATATTTGAAACTCAAGTATGGAATCTTGCGCTCATTTG	1286
Db	1187	CAAGTACTCCAGACTTCATATATTTGAAACTCAAGTATGGAATCTTGCGCTCATTTG	1246
QY	1287	CTATCTTACAGATGGGAATTACCCAGCTGCAACTTGGCTCATGCTCTGAAAAACATCAAG	1326
Db	1247	CTATCTTACAGATGGGAATTACCCAGCTGCAACTTGGCTCATGCTCTGAAAAACATCAAG	1306
QY	1327	TATCCAGATTCACATATTTTGGAAATTTGCATGAGAATGACATTTTCTCTGCGAG	1386
Db	1307	TATCCAGATTCACATATTTTGGAAATTTGCATGAGAATGACATTTTCTCTGCGAG	1366
QY	1387	TTCACTGCTGATATATATTTGCTATGACATGCTGATTTTATCATCACACGACATACAA	1446
Db	1367	TTCACTGCTGATATATATTTGCTATGACATGCTGATTTTATCATCACACGACATACAA	1426
QY	1447	GAAATTTGTTGAGAGAAAAATACGTTGAGACAGTATGAGATCATCTGCTTTACTGTG	1506
Db	1427	GAAATTTGTTGAGAGAAAAATACGTTGAGACAGTATGAGATCATCTGCTTTACTGTG	1486
QY	1587	CTGAGTCTGATACGAGTTGTCATGAGATGAGTGTTCGATCCAAAGTTCAATATATGTC	1566
Db	1487	CTGAGTCTGATACGAGTTGTCATGAGATGAGTGTTCGATCCAAAGTTCAATATATGTC	1546
QY	1567	TCTCTGAGAGTGAACATGTCATATTAATCTTCAATACACGAGAGGCCAAGCATCAAC	1626
Db	1547	TCTCTGAGAGTGAACATGTCATATTAATCTTCAATACACGAGAGGCCAAGCATCAAC	1606
QY	1627	TCTCTTCAATGTTCAATCGAAATTTGATTTATGACCCGAGCAAAAACATGAAACATTT	1686
Db	1607	TCTCTTCAATGTTCAATCGAAATTTGATTTATGACCCGAGCAAAAACATGAAACATTT	1666
QY	1687	GAGCATCTGATGACCGGTCAAGGCTCATCTTTCTCATAGSAAACCTGACAGAGCTG	1746
Db	1667	GAGCATCTGATGACCGGTCAAGGCTCATCTTTCTCATAGSAAACCTGACAGAGCTG	1726
QY	1747	AAGAATATACAGGAGCTGATCGAAGCTTTTCTATAGTGCCTTAAGCTGAGAGGACTGGTA	1806
Db	1727	AAGAATATACAGGAGCTGATCGAAGCTTTTCTATAGTGCCTTAAGCTGAGAGGACTGGTA	1786
QY	1807	AACCTTGTGTCGTTCCGGGTCAATGATGTCAACAAGTCCAAAGACAGGAGAGACATTC	1866

Db	781	TTGGGCAATCGTTGCTATCTTTCACAGATGGAAATTACCAATGCAACATTCCTATGCTCT	840
Qy	1314	GGAAAGACATAGATATCCAGATTTCAGACATATTTTGGAGAAATTCGATGAGATGACCA	1373
Db	841	GGAAAGACATAGATATCCAGATTCAGACATATTTTGGAGAAATTCGATGAGATGACCA	900
Qy	1374	TTTCTCCTGCACTGTCATGCTGATATATATTTGCTATGAGAAATAGCTGATTTTATCATAC	1433
Db	901	TTTCTCCTGCACTGTCATGCTGATATATATTTGCTATGAGAAATAGCTGATTTTATCATAC	960
Qy	1434	CAGCACATACCAAGAAATTTCTGGAGCAAAATACTGTTGACAGATGAGAGTCATAC	1493
Db	961	CAGCACATACCAAGAAATTCCTGGAGCAAAATACTGTTGACAGATGAGAGTCATAC	1020
Qy	1494	TGCTTTACTCTGCTGCTGATCTGTAACGAGTTTTCATGGAGTGAATCTTTCATCCAA	1553
Db	1021	TGCTTTACTCTGCTGCTGATCTGTAACGAGTTTTCATGGAGTGAATCTTTCATCCAA	1080
Qy	1554	GTTCATATATGTCCTCTCTGAGAGTCACATGTCATATATCTTTCACATACCGAGAGGC	1613
Db	1081	GTTCATATATGTCCTCTCTGAGAGTCACATGTCATATATCTTTCACATACCGAGAGGC	1140
Qy	1614	CAAGCAGCTCACCTCTCTTCATGCTTCATATGAAATTTGATTTATGACCCGAGACAAA	1673
Db	1141	CAAGCAGCTCACCTCTCTTCATGCTTCATATGAAATTTGATTTATGACCCGAGACAAA	1200
Qy	1674	CGATGAACACATTTGGGACATCGAGATGACCGGTCAAAGCCCATCTCTTCTCCATGGCAG	1733
Db	1201	CGATGAACACATTTGGGACATCTGATGACCGGTCAAAGCCCATCTCTTCTCCATGGCAG	1260
Qy	1734	ACTGACACAGGCTGAAAGAACATTAACAGGCTGCTGGTGAAGCTTTTGCTAAGTCGCTAAGCT	1793
Db	1261	ACTGACACAGGCTGAAAGAACATTAACAGGCTGCTGGTGAAGCTTTTGCTAAGTCGCTAAGCT	1320
Qy	1794	GAGGAGCTGGTAAACCTTGTCTGCTGTTGTCGGGTTACAAATGATTCAAACATGCCAAGA	1853
Db	1321	GAGGAGCTGGTAAACCTTGTCTGCTGTTGTCGGGTTACAAATGATTCAAACATGCCAAGA	1380
Qy	1854	CAGGAAAGATATCCGCGAGATAGAGAAAGATCATGAATCATCAAGACCCACAACTTGTT	1913
Db	1381	CAGGAAAGATATCCGCGAGATAGAGAAAGATCATGAATCATCAAGACCCACAACTTGTT	1440
Qy	1914	CGGCGATGTTCCGCTGGATCTCTGCCACAGACAAACAGGCCCCGTAAACGGCGAGCTCTATCG	1973
Db	1441	CGGCGATGTTCCGCTGGATCTCTGCCACAGACAAACAGGCCCCGTAAACGGCGAGCTCTATCG	1500
Qy	1974	CTATCATGCTGATATCCCATGGATGCTTTGTATCAGCCGCGCTGTATGATGAAGGTTTCGGCT	2033
Db	1501	CTATCATGCTGATATCCCATGGATGCTTTGTATCAGCCGCGCTGTATGATGAAGGTTTCGGCT	1560
Qy	2034	CACCGTCGTTGAGGCCATGACCTGTGGGCTTCTCATTTTGGCGAGCGCTCCATGGAGGTC	2093
Db	1561	CACCGTCGTTGAGGCCATGACCTGTGGGCTTCTCATTTTGGCGAGCGCTCCATGGAGG66CC	1620
Qy	2094	AGCTGAGATCATAGAGCATGGGCTCTCGGCGTTCCATATACCCGTATCCACCCCGAACA	2153
Db	1621	AGCTGAGATCATAGAGCATGGGCTCTCGGCGTTCCATATACCCGTATCCACCCCGAACA	1680
Qy	2154	GGCTGTATATCTGATGAGGCCGCACTTTTGACCCGCTGCAAGACAGACCCAGATCATGCGCT	2213
Db	1681	GGCTGTATATCTGATGAGGCCGCACTTTTGAGAGGCTGCAAGACAGACCCAGATCATGCGCT	1740
Qy	2214	GATATATCTGGAGCAGGCGCTGACGCGCATATATGAGAAATGACACATGGAATATATCTC	2273
Db	1741	GATATATCTGGAGCAGGCGCTGACGCGCATATATGAGAAATGACACATGGAATATATCTC	1800
Qy	2274	AGAGAGGTTGATGACATCTGGCCCGGCGGTCTACCGCTTCTGGAAGTACGTGTGGAAGCTGGA	2333
Db	1801	AGAGAGGTTGATGACATCTGGCCCGGCGGTCTACCGCTTCTGGAAGTACGTGTGGAAGCTGGA	1860
Qy	2334	GAGGCTGAGACGAGGCGCTACCTTGAATGTTCTTACATCTGAAGTTTCGGAGCTGGC	2393

Db	1861	GAGGCTGGAGACGAGCGCTACTTGGATGTTCACACTACTGAAGTTCCGGAGCTGC	1920
Qy	2394	GAAGACGTGCC	2405
Db	1921	GAAGACGTGCC	1932
 RESULT 5 US-10-425-114-5285			
; Sequence 5285, Application US/10425114			
; Publication No. US2004003488A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jindong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kowalic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaska, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCE: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 5285			
; LENGTH: 1340			
; TYPE: DNA			
; ORGANISM: Zea mays			
; FEATURE:			
; OTHER INFORMATION: Clone ID: 700454567_FLI			
US-10-425-114-5285			
 Query Match 25.2%; Score 695; DB 13; Length 1340;			
Best Local Similarity 39.2%; Pred. No. 0;			
Matches 1145; Conservative 0; Mismatches 9; Indels 0; Gaps 0;			
Qy	1393	GGTGATTATATGTCATATGACAAATGCTGATTTTATCATCACCAGCACTATCCAGAAT	1452
Db	17	GGTAGATATATGTCATATGACAAATGCTGATTTTATCATCACCAGCACTATCCAGAAT	76
Qy	1453	GCTGAGAACAAAATACTGTTGACANMNTGAGATCATACCTGCTTA	1512
Db	77	GCTGAGAACAAAATACTGTTGACAGTATGAGATCATACCTGCTTA	136
Qy	1513	CTGTACCGAGTCTCCATGGAGATCATGCTCTTCATCCAAAGTCAATATAGCTCTCC	1572
Db	137	CTGTACCGAGTCTCCATGGAGATCATGCTCTTCATCCAAAGTCAATATAGCTCTCC	196
Qy	1573	GGAGCTGACATGTCATATACCTTCCATACATACGAGAGGCCAAGGACTCACCTCTCT	1632
Db	197	GGAGCTGACATGTCATATACCTTCCATACATACGAGAGGCCAAGGACTCACCTCTCT	256
Qy	1633	CATGCTCATCGAAATTTGATTATATGACCCGAGCAAAACGATGACATTTGGGAT	1692
Db	257	CATGCTCATCGAAATTTGATTATATGACCCGAGCAAAACGATGACATTTGGGAT	316
Qy	1693	CTGGATGACCCGGTCAAAAGCCCATCTCTCCATGGCAGAGATCCACAGGGTGAAGAC	1752
Db	317	CTGGATGACCCGGTCAAAAGCCCATCTCTCTCCATGGCAGAGATCCACAGGGTGAAGAC	376
Qy	1753	ATTAACAAGGCTGCTCGAAGCTTTTGCTAAAGTGCGCTAAAGCTGAAGAGCTGTAAACCTT	1812
Db	377	ATTAACAAGGCTGCTCGAAGCTTTTGCTAAAGTGCGCTAAAGCTGAAGAGCTGTAAACCTT	436
Qy	1813	GTGTGCTTTGCCGGGTACATATGATGTCCAAACATCCAAAGACAGGGAGAAGATGCGGAG	1872
Db	437	GTGTGCTTTGCCGGGTACATATGATGTCCAAACATCCAAAGACAGGGAGAAGATGCGGAG	496
Qy	1873	ATAGAAGAATGATGAATCATCAAGAGCCCAACAATTTGTTCCGGGAGTTCCGCTGATC	1932
Db	497	ATAGAAGAATGATGAATCATCAAGAGCCCAACAATTTGTTCCGGGAGTTCCGCTGATC	556
Qy	1933	TCTGCCAGACAAACAGGCCCCGTAAACGGCGAGCTTATGCTACATCGCTGATACCCAT	1992

GENERAL INFORMATION:
APPLICANT: Dhingra, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080,114A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/270,777
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 347
TYPE: DNA
ORGANISM: Sorghum proproquum
US-10-080-114a-13

Query Match 8.9%; Score 246; DB 15; Length 347;
Best Local Similarity 100.0%; Pred. No. 2e-116;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTCTCCCGGAGCTGAAACCGCAAGCATCCGGGACCGGCTCGAGACACCTTC 60
DB 102 ATGCTCTCCCGGAGCTGAAACCGCAAGCATCCGGGACCGGCTCGAGACACCTTC 161
QY 61 CACGCGACCGCAACGAGCTGTCGCCCTCTCTCAAGTACGTGAACAAAGGGAGAGGC 120
DB 162 CACGCGACCGCAACGAGCTGTCGCCCTCTCTCAAGTACGTGAACAAAGGGAGAGGC 221
QY 121 ATCTCGAGCGCGCAACCATCTCTGAGCGCTCGACGAGTCCAGGGCTCCGGGCTCCG 180
DB 222 ATCTCGAGCGCGCAACCATCTCTGAGCGCTCGACGAGTCCAGGGCTCCGGGCTCCG 281
QY 181 GCGCTCGCGCGAGGACCTTCTCTGAGCTCTCGGCTCCGGCGAGAGGCGATCTGCTG 240
DB 282 GCGCTCGCGCGAGGACCTTCTCTGAGCTCTCGGCTCCGGCGAGAGGCGATCTGCTG 341
QY 241 CCGCGCG 246
DB 342 CCGCGCG 347

RESULT 9
US-09-237-183A-526
Sequence 526, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
TITLE OF INVENTION: Sucrose Pathway
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 526
LENGTH: 283
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-526

Query Match 7.6%; Score 209; DB 10; Length 283;
Best Local Similarity 100.0%; Pred. No. 3e-97;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 1608
DB 9 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 68
QY 1609 AAGGCAAGGAGCTCACTCTCTTCAATGAGTCAATGAAAAATTGATTTATAGACCGGAG 1668

DB 69 AAGGCAAGGAGCTCACTCTCTTCAATGAGTCAATGAAAAATTGATTTATAGACCGGAG 128
QY 1669 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 1728
DB 129 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 188
QY 1729 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 1757
DB 189 CCAAGTCAATATAGTCTCTCTGAGCTGACATGTCATATACCTTCCACATACCGAG 217

RESULT 10
US-09-237-183A-513
Sequence 513, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
TITLE OF INVENTION: Sucrose Pathway
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 513
LENGTH: 285
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-513

Query Match 5.8%; Score 159; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.5e-71;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1857 GGAAGATCCGCGAGATGAGAGATGATGATCACTATCAAGACCCCACTTGTTCG 1916
DB 1 GGAAGATCCGCGAGATGAGAGATGATGATCACTATCAAGACCCCACTTGTTCG 60
QY 1917 GCAAGTCCGCTGATCTCTGCGCCAGACAAAGGGCCCGGTAAAGGCTTATGCTA 1976
DB 61 GCAAGTCCGCTGATCTCTGCGCCAGACAAAGGGCCCGGTAAAGGCTTATGCTA 120
QY 1977 CATGCTGATACCATGATGCTTTCGACAGCCGACCTT 2015
DB 121 CATGCTGATACCATGATGCTTTCGACAGCCGACCTT 159

RESULT 11
US-09-237-183A-516
Sequence 516, Application US/09237183A
Publication No. US20030135870A1
GENERAL INFORMATION:
APPLICANT: Cheikh, No. US20030135870A1dine
APPLICANT: Fisher, Dane K.
APPLICANT: Liu, Jindong
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
TITLE OF INVENTION: Sucrose Pathway
FILE REFERENCE: 38-21(15089)B
CURRENT APPLICATION NUMBER: US/09/237,183A
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: US 60/067,000
PRIOR FILING DATE: 1997-11-24
NUMBER OF SEQ ID NOS: 2814
SEQ ID NO 516
LENGTH: 297
TYPE: DNA
ORGANISM: Zea mays
US-09-237-183A-516

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Query Match          5.7%; Score 158; DB 10; Length 297;
Best Local Similarity 99.2%; Pred. No. 8, 2e-71;
Matches 258; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1122 TAAGAAATGATATCAAGATTGATGTGGCCATATCTGGAAACATTGCTGAGATGC 1181
DB 2 TAAGAAATGATATCAAGATTGATGTGGCCATATCTGGAAACATTGCTGAGATGC 61

QY 1182 TGCTGTGTAATTCGTGCGTAATTAAGAGTACTCCAGACTTCATATTTGAAATCAAG 1241
DB 62 TGCTGTGTAATTCGTGCGTAATTAAGAGTACTCCAGACTTCATATTTGAAATCAAG 121

QY 1242 TGATGAATATCTTGTGGGCTCATGCTATCTTACAAAGATGGAAATTTACCAAGTCAACAT 1301
DB 122 TGATGAATATCTTGTGGGCTCATGCTATCTTACAAAGATGGAAATTTACCAAGTCAACAT 181

QY 1302 TGCTCATGCTCTGGAAGAAAGACTTAAGTATCCAGATTGACATATTTTGGAAATTTGCA 1361
DB 182 TGCTCATGCTCTGGAAGAAAGACTTAAGTATCCAGATTGACATATTTTGGAAATTTGCA 241

QY 1362 TGAGAAATGACATTTCTCTCT 1381
DB 242 TGAGAAATGACATTTCTCTCT 261

RESULT 12
US-09-237-183A-527
; Sequence 527, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; TITLE OF INVENTION: Sucrose Pathway
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 527
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-527

Query Match          5.4%; Score 150; DB 10; Length 150;
Best Local Similarity 100.0%; Pred. No. 1, 2e-66;
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1517 ACCGAGTTCGATCGGATGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCGAG 1576
DB 1 ACCGAGTTCGATCGGATGATGCTTCGATCCAAAGTTCAATATAGTCTCTCCGAG 60

QY 1577 CTGACATGTCATATCTTCCATATCCGAGGAGCCAGCACTCTCTCTCAAG 1636
DB 61 CTGACATGTCATATCTTCCATATCCGAGGAGCCAGCACTCTCTCTCTCAAG 126

QY 1637 GTTCAATCGAAATTTGATTTATGACCCCG 1666
DB 121 GTTCAATCGAAATTTGATTTATGACCCCG 150

RESULT 13
US-09-237-183A-1018
; Sequence 1018, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The

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; TITLE OF INVENTION: Sucrose Pathway
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 1018
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(411)
; OTHER INFORMATION: unsure at all n locations
US-09-237-183A-1018

Query Match          5.2%; Score 143; DB 10; Length 411;
Best Local Similarity 100.0%; Pred. No. 4, 8e-63;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1759 GGGCTGATCGAAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAACTTGTCTC 1818
DB 88 GGGCTGATCGAAGCTTTTGTCTAAGTCGGCTAAGCTGAGGAGCTGTAACTTGTCTC 147

QY 1819 GTTCCGGGATCAATGATGTCAACAGTCCAGACAGGGAAGATCGGGAGATGAG 1878
DB 148 GTTCCGGGATCAATGATGTCAACAGTCCAGACAGGGAAGATCGGGAGATGAG 207

QY 1879 AAGATGATGATCACTCAATCAAGAC 1901
DB 208 AAGATGATGATCACTCAATCAAGAC 230

RESULT 14
US-09-237-183A-528
; Sequence 528, Application US/09237183A
; Publication No. US20030135870A1
; GENERAL INFORMATION:
; APPLICANT: Cheikh, No. US20030135870A1dine
; APPLICANT: Fisher, Dane K.
; APPLICANT: Liu, Jindong
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
; TITLE OF INVENTION: Sucrose Pathway
; FILE REFERENCE: 38-21(15089)B
; CURRENT APPLICATION NUMBER: US/09/237,183A
; CURRENT FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: US 60/067,000
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 2814
; SEQ ID NO 528
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Zea mays
US-09-237-183A-528

Query Match          4.9%; Score 134; DB 10; Length 255;
Best Local Similarity 100.0%; Pred. No. 2, 3e-58;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 ATGATAGAAATCAAAAGCTTGGGAGGCTTCAAGTCTGCTGACCAAGCTGAGAGCACT 643
DB 110 ATGATAGAAATCAAAAGCTTGGGAGGCTTCAAGTCTGCTGACCAAGCTGAGAGCACT 169

QY 644 TGTCAAAGCTCCCTGCTGACACACCATATCTCAATTTGCTATATAATTTCAAGAGTGG 703
DB 170 TGTCAAAGCTCCCTGCTGACACACCATATCTCAATTTGCTATATAATTTCAAGAGTGG 229

QY 704 GCTTGGAAGAAAGCT 717
DB 230 GCTTGGAAGAAAGCT 243

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1 RESULT 15
2 US-09-237-183A-524
3 : Sequence 524, Application US/09237183A
4 : Publication No. US20030135870A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Cheikh, No. US20030135870A1dine
7 : APPLICANT: Fisher, Dane K.
8 : APPLICANT: Liu, Jingdong
9 : TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With The
10 : TITLE OF INVENTION: Sucrose Pathway
11 : PTE REFERENCE: 38-21(15089)B
12 : CURRENT APPLICATION NUMBER: US/09/237,183A
13 : CURRENT FILING DATE: 1999-01-26
14 : PRIOR APPLICATION NUMBER: US 60/067,000
15 : PRIOR FILING DATE: 1997-11-24
16 : NUMBER OF SEQ ID NOS: 2814
17 : SEQ ID NO 524
18 : LENGTH: 181
19 : TYPE: DNA
20 : ORGANISM: Zea mays
21 US-09-237-183A-524

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	Query Match	4.7%	Score 130;	DB 10;	length 181;
	Best Local Similarity	99.4%	Pred. No. 2.7e-56;		
	Matches 180;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1408	ATGAACAATGCTGATTATTCATCATCCAGCACATACACAGAAATTTGCTGGAAGCAAAAT	1467		
Db	1	ATGAACAATGCTGATTATTCATCATCCAGCACATACACAGAAATTTGCTGGAAGCAAAAT	60		
QY	1468	ACTGTGGACAGTATGAGAGTCATCTGCTTACTGCTGCTGTGCTGACCGAGTTGTC	15277		
Db	61	ACTGTGGACAGTATGAGAGTCATCTGCTTACTGCTGCTGTGCTGACCGAGTTGTC	120		
QY	1528	CATGGGATCGATGTCCTTGCATGCCAAAGTTCAATATAGTCTCTCTGAGCTGACATGTCC	1587		
Db	121	CATGGGATCGATGTCCTTGCATGCCAAAGTTCAATATAGTCTCTCTGAGCTGACATGTCC	180		
QY	1588	A 1588			
Db	181	A 181			

Search completed: May 26, 2004, 13:23:01
Job time : 978.542 secs

INDIVIDUAL ISOLATE: Saccharosynhase
IMMEDIATE SOURCE:
LIBRARY: phage lambda zap
FEATURE:
NAME/KEY: CDS
LOCATION: 3..2303
US-08-553-436A-7

Query Match 43.0% Score 1177.8; DB 2; Length 2563;
Bseq Local Similarity 70.9% Pred. No. 2.2e-295;
Matches 1592; Conservative 0; Mismatches 647; Indels 6; Gaps 2;

164 CTAGCCGAGGAGCCCTTCTGAGCTCTCCGCTCCGCGCAGAGGCGATCGTCCG 223
21 CTAGCCGAGGAGCCCTTCTGAGCTCTCCGCTCCGCGCAGAGGCGATCGTCCG 80
224 CCGTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 283
81 CCGTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 140
284 GTTCACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 343
141 GTTCACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 200
344 CTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 403
201 CTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 260
404 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 463
261 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 320
464 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 523
321 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 380
524 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 583
381 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 440
584 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 643
441 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 500
644 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 703
703 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 763
501 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 560
704 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 763
561 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 623
764 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 823
823 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 883
681 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 740
884 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 943
741 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 803
944 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1003
801 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 860
1004 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1063
861 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 920
1064 GTTCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1123

921 ATCTGAGAGGTTCTTTCGATCAGAGGAGGATCTCCGGAATGATATCTGATT 980
1124 GATGATGAGGATATCTGAGGAGGATCTTCTGAGAGGATCTCTGAGGATCT 1183
981 GATGATGAGGATATCTGAGGAGGATCTTCTGAGAGGATCTCTGAGGATCT 1040
1184 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1243
1041 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1100
1244 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1303
1101 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1160
1304 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1363
1161 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1220
1364 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1423
1221 TTAAGGATCTCTGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCTGAG 1280
1424 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1483
1281 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1340
1484 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1543
1341 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1400
1544 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1600
1401 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1460
1601 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1660
1461 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1520
1521 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1580
1721 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1780
1581 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1640
1781 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1840
1641 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1700
1841 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1900
1701 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1760
1901 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1960
1761 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1820
1961 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 2020
1821 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1880
2021 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 2080
1881 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 1940
2081 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 2140
1941 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 2000
2141 TTAAGGATCTCTGAGGAGGATCTTCTGAGGAGGATCTTCTGAGGATCTCT 2200

2001 AA---AATGACTGAATTCCTTTGTCAGAGTGCAGAGAGATCCAACTACTGACCTAAATTC 2057
 2201 TCTGAGAGAGGCTGACAGGCGCATATACAGAGTACACATGGAAGATATCTACAGAGAG 2260
 2058 TCTGAGAGAGGCTTACTAAGATCAAGAGATATACCTGCGCAAAAGATTTCTGAAAG 2117
 2261 TTGATGACACTGCGCGGGCTTACGCTTCTGGAAGTACGTGTGGAAGCTGAGAGGCTG 2320
 2118 TTAAAGATATGAGAGAGGCTGTATGTTCTGAAATATGCTCTAAACTAGAGAGAGA 2177
 2321 GAGAGAGGCGCTACCTTGAAGTGTCTTCACTACTGAAAGTCCGCGAGCTGCGAAGACC 2380
 2178 GAGACACACCTTATCTTGAAGTGTCTCAATTTGAAGTCCGATCTGCGCACTT 2237
 2381 GTCGCGCTTGAATGACCAACGC 2405
 2238 GTCCGCTGCGCAACGATGAGAGC 2262

RESULT 2

US-09-598-401C-57
 / Sequence 57, Application US/09598401C
 / Patent No. 6596925
 / GENERAL INFORMATION:
 / APPLICANT: Perera, J. Ranjan
 / APPLICANT: Bagleton, Clare
 / APPLICANT: Rice, Stephen J.
 / TITLE OF INVENTION: Compositions and Methods for the
 / FILE REFERENCE: 11000.10362
 / CURRENT FILING DATE: 2000-06-20
 / PRIOR FILING DATE: 1999-07-30
 / PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,539
 / NUMBER OF SEQ ID NOS: 120
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 57
 / LENGTH: 3103
 / TYPE: DNA
 / ORGANISM: Eucalyptus grandis
 / US-09-598-401C-57

Query Match 41.0%; Score 1123; DB 4; Length 3103;
 Best Local Similarity 67.0%; Pred. No. 4e-281;
 Matches 1610; Conservative 0; Mismatches 790; Indels 3; Gaps 1;

5 ACCCAAGCGCTCCGCGAGCGCTGAGAGACACCTCCAGCGCGACGCAAGAGCTGCTC 64
 471 AGCCAGAGCTTGGAGAGCTTGGAGAGACCTCTCTGCTCAACGCAACGATATGTC 530
 65 GCGCTCTCTCAAGTACGTGAACAAAGGAGGAGCTCTGCAAGCGGACCAATCTC 124
 531 GCGTCTCTTCAAGGCTTGAAGCCAAAGGCAAGGACATCTTGAAGCGGCAACGATTTT 530
 125 GAGCGCTGAGAGAGCTTCAAGGCTCCGCGGCGCGCTAGCCAGAGGAGACCTTCTC 184
 591 GCTGATTTGAGGCTCTCTGAGAGAGAGCAAGCAAGCTTCTTGAAGGAGCTTTGAT 650
 185 GACGCTCTCGCTCCGCGAGAGAGGAGTGTCTGCGCGCTTCTGCTGCTGCTGCTGCT 244
 651 GAAGTCTTCAATCTCACTCAAGAGAGGAGTGTCTGCTGCTGCTGCTGCTGCTGCT 710
 245 GCGCGCGCGCGAGGAGTGTGAGAGTACGTCTGCGCTCAAGTCTCAAGAGCTTCAAGCT 304
 711 GGTCCAAAGCGCGGCGCTGTGAGAGCAATCGTGTGAACGTTCATGAGGCTTGTCTGAG 770
 305 CAGCTCAAGCTCTGAGAGTACCTCCGCTTCAAGAGAGGAGCTTGTGCAAGCGGCAAGAT 364
 771 CAATGAGAGGTGTGAGTATCTGCACTTCAAGAGAGAGCTTGTGTATGAGAGCTTGAAT 830

365 GATCCCTAGCTTCTGAGCTTGAATTTGAGCGCTTCAATGTCTAGTCCAGCGCCCAAT 424
 831 GGTAACTTGTCTGAGCTTGAATTTGAGCGCTTCAATGTCTAGTCCAGCGCCCAAT 890
 425 CGGTATATCTATTTGAGAAAGGCTGTGAGCTTCTCAAGCGAGCTTGTCTCAATCAT 484
 891 CTTTCCAGCTTATTTGAGAGAGGCTGTGAGCTTCTCAAGCGAGCTTGTCTCAATCAT 950
 485 TTCCGCAAGAGAGTGTGAGAGCGCTTGTGAGTGTCTTCCGCGCGCAACCGCAAG 544
 951 TTCCATGAGAGAGAGAGCTTGAACCTCTGCTTGAATTTCTCAAGCGAGCTTCAAG 1010
 545 GCGCATGTATATGCTTATATATATATATATATATATATATATATATATATATAT 604
 1011 GCGAAGAGATATGCTTATATATATATATATATATATATATATATATATATATAT 1070
 605 ACCAAGCTGAGAGAGCTTGTCAAGCTTCCGCTGAGCAACATATCTCAATTTGCT 664
 1071 AGAAGAGAGAGAGATCTGAGCTTCTGCTTGAACCGAGAGCGCTTGTCTCAATTTG 1130
 665 TATTAATTTCAAGAGTGTGAGCGCTGAGAGAGGTTGAGGAGTATACAGAGAGATTTT 724
 1131 CAAAGTTCAGAGAGATTCGAGCTGAGCGGCTGAGAGAGCGCTTGTCTCAATTTG 1190
 725 GAATATATCTATCTTCTTGAACATCTTCAAGCGCGAGAGCGCTTGTCTCAATTTG 784
 1191 GAGATATCTAGCTTCTTGTGATCTCTTGAAGCTTGTGAGAGCTTGTGAGAGCTTGT 1250
 785 TTCTGAGAGAGATTCGAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 844
 1251 TTCTGAGAGAGATTCGAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1310
 845 GGTCAAGCTAT 904
 1311 GCTCAAGAGAGATTCGAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1370
 905 CAAAGTCTGAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 964
 1371 CAAAGTCTGAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1430
 965 TCCCAAGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1524
 1431 ACTCTGAGATTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1490
 1491 CAGAGCTTGAAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1550
 1085 AATGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1144
 1551 AATGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1610
 1145 ACATTTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1204
 1611 AGATCACTAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1670
 1205 ATATATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1264
 1671 ATCATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1730
 1265 ATATCCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1324
 1731 GTTACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1790
 1325 TTTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1384
 1791 TACTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1850
 1385 GCTATGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1444
 1851 GCGATGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1910

QY 832 TCATGATCTTGTCAAGCTAATGATAGCTTGCAGACACAGAGACAGATCGT 891
 DB 1084 CCAGGTTGGTTCGACACAGAGAGGGGTTTAGTCTGTCAGATACGTGTGTAAGTCT 1143
 QY 892 CTATATATCTGACCAAGTCCGTGCTACCTAGAAAATGAGATG-----GTCTCCGTTT 942
 DB 1144 GTACGTCCTTGACCAAGCTAAGATTTAGAAAAGCAATGCAAGAGATCCATCTATGTC 1203
 QY 943 AAGAAACAAAGGCTTGATGTTTCCCAAGATTCATGTTTACCTGCTGATACAG 1002
 DB 1204 AGGTTTAGAGGTAATTAAGTCAGCCCAAGGTAAATTCCTACCCGCTGTGATTCCTAA 1263
 QY 1003 TGCAAAGAGACATCATGCAATCAGCGCTTGAGAGATTAAGTAAACAGACATCTTA 1062
 DB 1264 TAGTGACGAAAGCTTTGTACCAAGGTTTGAAGAAAGTCTACGGTAACAGAAAGCGCTG 1323
 QY 1063 CATATTACAGTTCCTTCAGAAATGAAAATGGGATATCTTA--AGAAATGATATCAAG 1119
 DB 1324 GATTTTGGCTGTAACCTGCGGAGGTTTAACTCCCAAGATGACGACAGAACTGATTTCTCG 1383
 QY 1120 ATTGTATGTGTGCCATATCTGAAAATTTGCTGAGAGTGTGCTGTGTAATTTGCTGC 1179
 DB 1384 ATTCGAGTTTGGCTTATCTAGAAACCTTTCATGACTCAGAAAAGAAATTTGTTGCG 1443
 QY 1180 TGAATTACAAAGTACTCCAGACTTCAATTGGAATCTACAGTGAATGAAATCTTGTCG 1239
 DB 1444 AGAATTCAGAGGTAGACACAGCTTAAATCGGGTAATTAATCACTGACGGAATCTGATGTC 1503
 QY 1240 GTCAATGCTATCTTACAGAGTGGGAATTTACCCAGTGCACATGCTCATCTCTGAAAA 1299
 DB 1504 TTTTCTGTTGACGCAAGCGAGTAAAGTTTACCCTAATGCAACATGCTCATCTTATGAAAA 1563
 QY 1300 GACTAATGATCCAGATTCAGACATTTTGGAGAAATTTGATGAGAAAGTACATTTCTC 1359
 DB 1564 ATCCAAATCTTGTATGTAACCTCTAATGCAAGATTTGGAGAAAATTAATCACTTTCTC 1623
 QY 1360 CTGCGAGTCTCACTGTGATATTAATTTGCTATGAAATGCTGATTTTATCACTACACAGAC 1419
 DB 1624 TTTTCAATTCACGCGTATTTAATGATAGAAATGCTGTAATCTGCTATGACGACAC 1683
 QY 1420 ATACCAAGAAATGCTGGAACAAAATCTGTTGACAGTATGAGAGTCACTGCTT 1479
 DB 1684 CTATCAAGAAATGTTGGCACACACAGACAGTATAGGCAATGAGTCTTCAAAATGCTT 1743
 QY 1480 TACTGCGCTGTCTGACGAGTGTTCACAGGATGATGTCTTCATCCAAAGTTCA 1539
 DB 1744 TACCATGCGGAACTGTATCATGTGTCAAGGCAATGAAATTTATTTAGCCCAATTTAA 1803
 QY 1540 TATAGTCTCTCTGAGCTGACATGTCCATATATCTTTCACATACCGAGAAAGCCAAAGC 1599
 DB 1804 CGTTGTAACCCCTGCTGTGATGAAATGAAATTCCTACTTCCCTACACAAATCTCAAAACAG 1863
 QY 1600 ACTACCTCTCTTCATGTTCAATGCAAAATTTGATTTATGACCCGAGCAAAACGATGA 1659
 DB 1864 AATAGAAAGGATGCGCATGCGCTAGAGAAATGCTGTTTAACTCTAAGATTTCTAGCCA 1923
 QY 1660 AACCATTTGGCATCTGATGATGACCGGTCAAGGCCATCTCTTTCATGAGCAAGATCTGA 1719
 DB 1924 AATCTTCGCAATCTGACGACCCCAATATAGCGTCTCATTTTCTCAATTTGGCGCATTTGA 1983
 QY 1720 CAGGTTGAGAAACATACAGAGGCTGTGCAAGCTTTTGTCAATAGTCCGTAAAGCTGAGGGA 1779
 DB 1984 CCGAATTAATAAACTCAAGAGTTTGGCAAGATGCTTTGTGCAAGTCAAGAAATTTGACAGA 2043
 QY 1780 GCTGTGAACCTTGTCTGTTGCGGGTACATGATGATCAAGAGTCCAAAGTCAAGAGCA 1839
 DB 2044 ACCTTGCACTTATTTATTTAGTTGCAAGGTAGCTGCGATTCGAAGAAATTCAGAAATTAACA 2103
 QY 1840 AGAGATGCGGAGATAGAGAAATGATGCAATGCAATCATCAAGACCAACATCTGTGCGGCA 1899
 DB 2104 AGAAGAGAGCAAAATCTGCAACTTTTACCGGATTTATGAGCAATACAACTGCTGACGCA 2163

QY 1900 GTTCCGCTGATCTTCCGACAGCAACAGAGCCCGTAAAGGAGCTTATGCTACAT 1959
 DB 2164 AATTCGCTGATGATGATGCTGTATTCACAAAATGATCTCGGTGAATTTATGCTCAT 2223
 QY 1960 CGCTGAATACCATGATGCTGTGATACAGCGGCTTGATGAAAGCTTCCGCTCAAGCT 2019
 DB 2224 TTGCGATGCGCAAGCAATTTTGTACGACAGCATTTTGAAGCTTTGGGTTGACAT 2283
 QY 2020 CGTTGAGGCCATGACCTGTGAGGCTTCTTACTTTTCGACAGCTTCATGAGAGTCCAGCTGA 2079
 DB 2284 CCGAGATGATGATTTCCGATTTCCCAATTTGCTACCAATTTGCGGAGCCATTTGA 2343
 QY 2080 GATCATAGACATGCGCTCTGCGGCTTCCATTTGACCCGTAACACCCCAAGAGGCTGT 2139
 DB 2344 GATTTATCAGATATGATATGATGCTCTTCACTTAACTCATCATCTATGAAAGAAACAGC 2403
 QY 2140 TATCTGATGCGGACTCTTCTGACCGGTGCAAGCAAGCCAGATCATCTGGTGAATAT 2199
 DB 2404 CACAAAATCTTGAATTTGCTACCAATGCAACAAATCTTAACTATTTGAAACATAT 2463
 QY 2200 ATCTGAGCAGGCTGCAAGCATATACGAAGTACACATGAAATATCTAGAGAG 2259
 DB 2464 TTCCGAGAAAGCATTTGACAGAGTATATAGTACATACCTGGAATATACACAACTAA 2523
 QY 2260 GTTGATGACACTGCGCGGCTTACGCTTTCTGGAAGTACGTGTGCAAGCTCGAGAGCT 2319
 DB 2524 GCTGTAACTCTTACCTGCGATTTACCGCTTCTGAAATTTACTCTGAAAGAAAAACGCA 2583
 QY 2320 GGAAGCAGAGGCGCTACCTTGA 2341
 DB 2584 AGATTTATTTAGCTTACCTTGA 2605

RESULT 4

US-09-313-294A-1862
 : Sequence 1862, Application US/09313294A
 : Patent No. 6476212
 : GENERAL INFORMATION:
 : APPLICANT: Laljudi, Raghunath V.
 : APPLICANT: Ico, Laura Y.
 : APPLICANT: Sherman, Bradley K.
 : TITLE OR INVENTION: POLYNUTRIENTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 : FILE REFERENCE: PL-0017 US
 : CURRENT APPLICATION NUMBER: US/09/313,294A
 : NUMBER OF SEQ ID NOS: 7600
 : SOFTWARE: PERL Program
 : SEQ ID NO 1862
 : LENGTH: 265
 : TYPE: DNA
 : ORGANISM: Zea mays
 : FEATURE:
 : NAME/KEY: misc feature
 : OTHER INFORMATION: Incyte ID No. 6476212 700551647H1
 : US-09-313-294A-1862

Query Match 8.4%; Score 229.2; DB 4; Length 265;

Best Local Similarity 95.3%; Pred. No. 6.9e-50;

Matches 257; Conservative 0; Mismatches 8; Indels 3; Gaps 2;

QY 454 GTTCTTCAACCGACATCTTCTTCAATCATGTTCCGCAAGGAGTTGCTTGGAGCCCT 513
 DB 1 GTTCTTCAACCGACATCTTCTTCAATCATGTTCCGCAAGGAGTTGCTTGGAGCCCT 60
 QY 514 GTTGATTTCTCTGCTGACACCGGCAAGAGGAGATTTATGATGATGAT 573
 DB 61 GCTGATTTCTCTGCTGACACCGGCAAGAGGAGATTTATGATGAT 119
 QY 574 ACAAGCTTGGAGGCTTGAATGCTTGTCTTCAACAAAGCTTGAAGCACTTGTCAAAGCT 633
 DB 120 ACAAGCTTGGAGGCTTGAATGCTTGTCTTCAACAAAGCTTGAAGCACTTGTCAAAGCT 179
 QY 634 CCTGCTGACACCATCTACAAATTTGCTTATTAATTTCAAGAGTGGGCTGTGAGAA 693

RESULT 6
US-09-598-401C-56
Sequence 56, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Perera, J. Ranjan
APPLICANT: Eagleton, Clare
APPLICANT: Rice, Stephen J.
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Expression
FILE REFERENCE: 11000.1036C2
CURRENT APPLICATION NUMBER: US/09/598,401C
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: PCT/N200/00018
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 532
TYPE: DNA
ORGANISM: Pinus radiata
US-09-598-401C-56

Query Match 4.9%; Score 134; DB 4; Length 532;
Best Local Similarity 61.4%; Pred. No. 56-25; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 5 ACCACGGCTCCGCGAGCGCTCCGAGACACCTCTCCAGCGCAGCGAGCGCTCCG 64
DB 182 AGCCACAGCTTCCGAGAGCTTGGACAGACACCTCTCTCCAGCGCAGCGATATG 241
QY 65 GCGCTCTCTGCTCACTAGTGAACAAAGGAGGATCTCTGACCGCAGCGATCTCTC 124
DB 242 GCTCTCTCTTCAAGGCTTGAAGCAAGGAGGATCTCTGACCGCAGCGATATG 301
QY 125 GACGGCTTCGAGAGGCTCCGAGCGCTCCGAGCGCGCGCTGAGCGAGCGATCTCTC 184
DB 302 GCTGAGTTGAGCGCATCTCTGAGAGAGCAAGCAAGCTTCTATGCGCGCTTGG 361
QY 185 GACGCTCTCCGCTCCGCGAGAGCGATCTCTGCGCGCTCTGAGCGCGATCTCTC 244
DB 362 GAGCTCTCTAAATTCATCAGAGAGGATCTGCTGCGCTCTGAGCGCGATCTCTC 421
QY 245 GCGCGCGCGCGAGGATCTGAGAGTACGCTCCGCTCAAGCTTCAAGCTCAGCGTGA 304
DB 422 CCGTCCAGAGCGCGCGCTGAGAGCGATCTCTGAGAGCGATCTCTGAG 481
QY 305 GAGCTCAGCTCTCGAGAGTACCTCCGCTTCAAGAGAGAGGCTTTCAGCG 354
DB 482 CAATGAGAGTCTGATGATCTGCACTTCAAGAGAGAGCTTCTATG 531

RESULT 7
US-09-313-294A-1221
Sequence 1221, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalagudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 1221
LENGTH: 272

TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700550572H1
US-09-313-294A-1221

Query Match 4.3%; Score 117.2; DB 4; Length 272;
Best Local Similarity 67.0%; Pred. No. 7.9e-21;
Matches 181; Conservative 0; Mismatches 88; Indels 1; Gaps 1;

QY 1446 ATACTGTGACAGATGAGAGTCACTACTGCTTACTCTGCTGCTGTAACCGATG 1505
DB 4 ACACCGTGGCGAGTACAGAGTCCACATCGCTTCACTTCTGCGCTTACCGGTG 63
QY 1506 TCCATGAGATGATGCTCTGATCCAAAGTTCAATATATGCTCTCTGAGCTGACATG 1565
DB 64 TCCATGAGATGATGCTCTGATCCAAAGTTCAATATATGCTCTCTGAGAGATG 123
QY 1566 CCATATCTTTCATATACCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1625
DB 124 GTGTTACTACCGGTATAGGA-AAAGACAGAGAGGAGGAGGAGGAGGAGGAGGAG 182
QY 1626 AAAATTGATTTATGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1685
DB 183 AGAGCTCATCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 242
QY 1686 CAAGGCGGATCTCTTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1715
DB 243 AGAGGCGGATCTCTTCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 272

RESULT 8
US-09-313-294A-1826
Sequence 1826, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalagudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 1826
LENGTH: 271
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700551585H1
US-09-313-294A-1826

Query Match 4.1%; Score 111.8; DB 4; Length 271;
Best Local Similarity 65.7%; Pred. No. 2e-19;
Matches 178; Conservative 0; Mismatches 92; Indels 1; Gaps 1;

QY 869 CAGACAGAGAGAGAGATCTCTATATAGTACAGGAGGAGGAGGAGGAGGAGGAGGAG 928
DB 2 CCGACAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 61
QY 929 ATGCTCTCCGTTAAAGAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 988
DB 62 ATGCTCTGAGATCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 121
QY 989 CGGCTGATACAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1048
DB 122 AGGTTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181
QY 1049 ACAGAGATCTTACATATATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1108

US-08-718-777-6

Query Match 3.3%; Score 89.8; DB 2; Length 3509;
Best Local Similarity 51.0%; Pred. No. 4.1e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1558 GAACACATTGGGCGATCTGATGACCGGCTCAAGGCCATCTCTTCTCCATGCGAAGACTC 1717
1543 GAAGTATGCGGTTCTCTGACCAACCTCTCAAGCCCATATCTGCGTTATCCAGACCA 1602
1718 GACAGGATGAAGACATTAACAGGCGCTGCGAGCTTTGCTAAGGCGCTAAGCTGAGG 1777
1603 GACCCGAAGAGAACATCACTACCTCTGCAAGCCTTTGAGAGTGTCTCCACTCAGG 1662
1778 GAGCTGTAACTTGTCTGCTGCTGCGGCTTCAATGATGTCACAACTGCAAGGACAG 1837
1663 GAACCTTGCAAACTTACTGATCATGSGTACAGAGATGACATGACGACATGCTGCT 1722
1838 GAAGAGATGCGGAGATGAGAGATGATGAACTCATCAAGACCCCAACTTGTTCGGG 1897
1723 GGCATATGCCAGTGTCTCTACCAACAGTTCTGAAGCTTATGACAAAGTATGATCTGACGG- 1781
1898 CAGTTCGCTGATCTCTGCCCCAGACAAAGGCGCCGTAACGCGGAGCTTATGCTGCTAC 1957
1782 --AAGCGTGGCGTTCCCTTAAGCATCAATCAGGCTGAGCGTCCCGAGATCTATCGCTC 1839
1958 ATGCTGATACCCATGCTGCTTGTGACAGCGCGCTTGTATGAAGCGTTGCTGCTAC 2017
1840 GCGGCCAAATGAAAGGCGCTCTTCATCAACCTGCTGCTGAGCGGTTTGTGCTCACC 1899
2018 GTGCTGAGGCGCATGACCTGTGGGCTTCTACTTGTGGCAGCTCCATGAGGCTCCAGCT 2077
1900 CTGATCGAGGCTGCGGACACAGGACTCCGATGATGCTGCTACCAAGATGTGTGCTCGGCTC 1959
2078 GAGATCATGAGAGATGAGCGCTCTGCGCTTCAATTGACCCGATACACC 2126
1960 GACATTACAAATGATTAAACAGGACTGCTGTTGACCCACACAGACC 2008

RESULT 11

US-09-078-862-2
Sequence 2, Application US/09078862
Patent No. 6091003

GENERAL INFORMATION:

APPLICANT: Nan, Guo-Jing

APPLICANT: Nagai, Chifumi

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC
TITLE OF INVENTION: TRANSFORMATION OF PINAPPLE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/078,862

FILING DATE: 14-MAY-1998

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.

REGISTRATION NUMBER: 32,937

REFERENCE/DOCKET NUMBER: US-03321

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3509 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-09-078-862-2

Query Match 3.3%; Score 89.8; DB 3; Length 3509;
Best Local Similarity 51.0%; Pred. No. 4.1e-13;
Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1658 GAACACATTGGGCGATCTGATGACCGGCTCAAGGCCATCTCTTCTCCATGCGAAGACTC 1717
1543 GAAGTATGCGGTTCTCTGACCAACCTCTCAAGCCCATATCTGCGTTATCCAGACCA 1602
1718 GACAGGATGAAGACATTAACAGGCGCTGCGAGCTTTTGTCTAAGTGGCTAAGCTGAGG 1777
1603 GACCCGAAGAGAACATCACTACCTCTGCAAGCCTTTGAGAGTGTCTCCACTCAGG 1662
1778 GAGCTGTAACTTGTCTGCTGCTGCGGCTTCAATGATGTCACAACTGCAAGGACAG 1837
1663 GAACCTTGCAAACTTACTGATCATGSGTACAGAGATGACATGACGACATGCTGCT 1722
1838 GAAGAGATGCGGAGATGAGAGATGATGAACTCATCAAGACCCCAACTTGTTCGGG 1897
1723 GGCATATGCCAGTGTCTCTACCAACAGTTCTGAAGCTTATGACAAAGTATGATCTGACGG- 1781
1898 CAGTTCGCTGATCTCTGCCCCAGACAAAGGCGCCGTAACGCGGAGCTTATGCTGCTAC 1957
1782 --AAGCGTGGCGTTCCCTTAAGCATCAATCAGGCTGAGCGTCCCGAGATCTATCGCTC 1839
1958 ATGCTGATACCCATGCTGCTTGTGACAGCGCGCTTGTATGAAGCGTTGCTGCTAC 2017
1840 GCGGCCAAATGAAAGGCGCTCTTCATCAACCTGCTGCTGAGCGGTTTGTGCTCACC 1899
2018 GTGCTGAGGCGCATGACCTGTGGGCTTCTACTTGTGGCAGCTCCATGAGGCTCCAGCT 2077
1900 CTGATCGAGGCTGCGGACACAGGACTCCGATGATGCTGCTACCAAGATGTGTGCTCGGCTC 1959
2078 GAGATCATGAGAGATGAGCGCTCTGCGCTTCAATTGACCCGATACACC 2126
1960 GACATTACAAATGATTAAACAGGACTGCTGTTGACCCACACAGACC 2008

RESULT 12

US-09-051-341-6
Sequence 6, Application US/09051341
Patent No. 6124528

GENERAL INFORMATION:

APPLICANT: Shewmaker, C. K.

TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rae-Yenter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/051,341

FILING DATE: 25-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/17351

FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
 FILING DATE: 27-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/372,200
 FILING DATE: 12-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara Rae-Venter, Ph.D.,
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.110.02US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)328-4400
 TELEFAX: (415)328-4477
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3509 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cdna to mRNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 112..3315
 US-03-051-341-6

Query Match 3.3%; Score 89.8; DB 3; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps -;

1568 GAACACATTGGGCATCTGATGACCGGTCGAAAGCCCATCTTCTTCATGCGAAGACTC 1717
 1543 GAAGTAGCGGTTCTCTACCAACCTTCAAGCCGATGATCTGGCGTTATCAAGACCA 1602
 1718 GACAGGGTGAAGAAATATTAACAGGGGCTGTGCGAAGCTTTTGAAGGCGCTAAGCGAGG 1777
 1603 GACCCGAAGAAACATACATACCTCTGCAAGGCTTTGAGAGTGTCTCACTCAGG 1662
 1778 GAGCTGTAAACCTTGTGCTGCTCCGCGGTACAAATGATGTCAACAGTCCAAAGACAG 1837
 1663 GAACCTGCAAACTTACTCTGATCATGAGGTACAGAGATGACATGACAGCATGTCTGCT 1722
 1838 GAAGAGATGCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1897
 1723 GGCATGCGCAGTGTCTCTACCAACAGTTCGAAAGCTGATGACAGATGATGATGATGATGAT 1731
 1898 CAGTTCGCGTATCTCTGCGCCAGCAACAGGCGCCGTAAGCGGAGCTTATGCTATC 1957
 1782 --AAGCGTGGCGTTCCTTAAGATACATACAGGCTGAGCTCCCGAGATCTATGCGCTC 1839
 1958 ATCGCTGATACCCATGCTGCTTCTGTAACGCGGCTTGTATGAAAGCGTTGCGTCTAC 2017
 1840 GGGGCCAAATGAAAGGGCGCTTCTCATCAACCTGCTCTGTTGAGCGTTTGGTCTCACC 1899
 2018 GTGTTGAGCCATGACCTGTGGGCTTCTCTTCTTTCGCAAGCTCCATGAGAGTCCAGCT 2077
 1900 CTGATCGAGGCTGCGGACACGAGCTCCGATAGTGTGCTAACAAAGATGTGTGTCGGTCT 1959
 2078 GAGATCATGAGAGATGAGCGCTCTCGGCTTCCACATGACCCGATACACC 2126
 1960 GACATTACAAATGATTAACAAACGAGCTGCTGTTGACCCACACAGACC 2008

RESULT 13

US-09-866-153-12
 Sequence 12, Application US/09866153
 Patent No. 6638766
 GENERAL INFORMATION:
 APPLICANT: Albert, Henrik H.
 APPLICANT: Wei, Hairong
 TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
 FILE REFERENCE: US-03648
 CURRENT APPLICATION NUMBER: US/09/866,153
 CURRENT FILING DATE: 2001-05-24
 PRIOR APPLICATION NUMBER: 09/270,976

PRIOR FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 12
 LENGTH: 3509
 TYPE: DNA
 ORGANISM: Zea mays
 US-09-866-153-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1568 GAACACATTGGGCATCTGATGACCGGTCGAAAGCCCATCTTCTTCATGCGAAGACTC 1717
 1543 GAAGTAGCGGTTCTCTACCAACCTTCAAGCCGATGATCTGGCGTTATCAAGACCA 1602
 1718 GACAGGGTGAAGAAATATTAACAGGGGCTGTGCGAAGCTTTTGAAGGCGCTAAGCGAGG 1777
 1603 GACCCGAAGAAACATACATACCTCTGCAAGGCTTTGAGAGTGTCTCACTCAGG 1662
 1778 GAGCTGTAAACCTTGTGCTGCTCCGCGGTACAAATGATGTCAACAGTCCAAAGACAG 1837
 1663 GAACCTGCAAACTTACTCTGATCATGAGGTACAGAGATGACATGACAGCATGTCTGCT 1722
 1838 GAAGAGATGCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1897
 1723 GGCATGCGCAGTGTCTCTACCAACAGTTCGAAAGCTGATGACAGATGATGATGATGATGAT 1781
 1898 CAGTTCGCGTATCTCTGCGCCAGCAACAGGCGCCGTAAGCGGAGCTTATGCTATC 1957
 1782 --AAGCGTGGCGTTCCTTAAGATACATACAGGCTGAGCTCCCGAGATCTATGCGCTC 1839
 1958 ATCGCTGATACCCATGCTGCTTCTGTAACGCGGCTTGTATGAAAGCGTTGCGTCTAC 2017
 1840 GGGGCCAAATGAAAGGGCGCTTCTCATCAACCTGCTCTGTTGAGCGTTTGGTCTCACC 1899
 2018 GTGTTGAGCCATGACCTGTGGGCTTCTCTTCTTTCGCAAGCTCCATGAGAGTCCAGCT 2077
 1900 CTGATCGAGGCTGCGGACACGAGCTCCGATAGTGTGCTAACAAAGATGTGTGTCGGTCT 1959
 2078 GAGATCATGAGAGATGAGCGCTCTCGGCTTCCACATGACCCGATACACC 2126
 1960 GACATTACAAATGATTAACAAACGAGCTGCTGTTGACCCACACAGACC 2008

RESULT 14

US-09-693-467A-12
 Sequence 12, Application US/09693467A
 Patent No. 6686513
 GENERAL INFORMATION:
 APPLICANT: Albert, Henrik H.
 APPLICANT: Wei, Hairong
 TITLE OF INVENTION: PLANT PROMOTER SEQUENCES AND METHODS OF USE THEREOF
 FILE REFERENCE: US-04331
 CURRENT APPLICATION NUMBER: US/09/693,467A
 CURRENT FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 09/270,976
 PRIOR FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 12
 LENGTH: 3509
 TYPE: DNA
 ORGANISM: Zea mays
 US-09-693-467A-12

Query Match 3.3%; Score 89.8; DB 4; Length 3509;
 Best Local Similarity 51.0%; Pred. No. 4.1e-13;
 Matches 239; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

1568 GAACACATTGGGCATCTGATGACCGGTCGAAAGCCCATCTTCTTCATGCGAAGACTC 1717

1543 GAAGTATGCGGTTCTGACCAACCCCTCAAGCCGATGCTGCGGTTATCAAGACCA 1602
 1718 GACAGGTAAGACATTAACAGGCGTGTGCAAGCTTTTGTAGTGCCTTAAGCTAGG 1777
 1603 GACCCGAAAGAACATCACTACCTCTGCAAGGCTTTGGAGAGTGTGTCCACTCAGG 1662
 1778 GAGCTGTAAACCTTCTGCTGCTGCGGCTTAACAATGATGTAACAAGTCCAGAGCAGG 1837
 1663 GAACCTGCAACCTTACTCTGATCAATGCTTAACAGAGATGATGACATGATGTCTGCT 1722
 1838 GAAGAGATGCGGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 1897
 1723 GGCATATGCAAGTGTCTTCAACAGTCTGATGATGATGATGATGATGATGATGATGATGATG 1781
 1898 CAGTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1957
 1782 --AAGCGTGGGCTTCCCTTAAGATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1839
 1958 ATGCGTATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2017
 1840 GGGGCAAAATGAGGGGCTTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
 2018 GTGCTTGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2077
 1900 CTGATCGAGGCTGCGGCAACAGGCTCCGATAGTGTGCTAACAAGATGATGATGATGATGATG 1959
 2078 GAGATATAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2126
 1960 GACATTAACAATGATTAACAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2008

RESULT 15

US-08-429-054A-12
 Sequence 12, Application US/08429054A

GENERAL INFORMATION:
 APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
 APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
 TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
 TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
 TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERMAN AND MUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,054A
 FILING DATE: 26-APR-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 842,337
 FILING DATE: 20-March-1992
 APPLICATION NUMBER: PCT/FR 91/00593
 FILING DATE: 18-July-1991
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: French 90402894.9
 FILING DATE: 20-July-1990
 CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 NAME: Charles A. Musserlian
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 146.1137
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000
 TELEFAX: (212) 661-9002
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3509
 TYPE: Nucleic acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: cDNA
 US-08-429-054A-12

Query Match 2.9%; Score 80.4; DB 2; Length 3509;
 Best Local Similarity 51.2%; Pred. No. 1.1e-10;
 Matches 214; Conservative 0; Mismatches 201; Indels 3; Gaps 1;

1543 GAAGTATGCGGTTCTGACCAACCCCTCAAGCCGATGCTGCGGTTATCAAGACCA 1602
 1718 GACAGGTAAGACATTAACAGGCGTGTGCAAGCTTTTGTAGTGCCTTAAGCTAGG 1777
 1603 GACCCGAAAGAACATCACTACCTCTGCAAGGCTTTGGAGAGTGTGTCCACTCAGG 1662
 1778 GAGCTGTAAACCTTCTGCTGCTGCGGCTTAACAATGATGTAACAAGTCCAGAGCAGG 1837
 1723 GGCATATGCAAGTGTCTTCAACAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1781
 1898 CAGTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1957
 1782 --AAGCGTGGGCTTCCCTTAAGATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1839
 1958 ATGCGTATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2017
 1840 GGGGCAAAATGAGGGGCTTCTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1899
 2018 GTGCTTGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2075
 1900 CTGATCGAGGCTGCGGCAACAGGCTCCGATAGTGTGCTAACAAGATGATGATGATGATGATG 1957

Search completed: May 25, 2004, 22:35:39
 Job time: 135.516 secs

GenCore version 5.1.6
(c) 1993 - 2004 Compu

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 pna/us10_PUBCOMB.seq.*

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10-114A-11	Sequence 11, Appl
11-6036	Sequence 6036, Ap
15-114-6561	Sequence 6561, Ap
15-114-15113	Sequence 15113, A
4-559-98889	Sequence 98889, A
5-114-5285	Sequence 5285, Ap
8-842A-2415	Sequence 2415, Ap
8-842A-2415	Sequence 2415, Ap
7-939-29	Sequence 29, Appl
7-939-27	Sequence 27, Appl
10-114A-6	Sequence 6, Appl
15-114-2283	Sequence 2283, Ap
11-26430	Sequence 26430, A

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-10-425-114-5316	Sequence 17596, Ap
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-10-424-599-115562	Sequence 115562, A
-10-425-114-6460	Sequence 6460, Ap
-10-424-599-11458	Sequence 11458, A
-10-425-114-1764	Sequence 31764, A
-10-360-114-A-4	Sequence 4, Appl1
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-10-289-757-3	Sequence 13, Appl
-10-393-840-139	Sequence 139, Appl
-10-137-036-57	Sequence 57, Appl
-10-288-757-133	Sequence 133, Appl
-10-289-757-12	Sequence 12, Appl
-10-289-757-15	Sequence 15, Appl
-10-289-757-1534	Sequence 134, Appl
-10-425-114-2574	Sequence 2574, Appl
-10-289-757-14	Sequence 14, Appl
-13-003-405-1	Sequence 1, Appl1
-10-260-238-25	Sequence 25, Appl
-09-938-842A-1620	Sequence 1620, Ap
-09-938-842A-1620	Sequence 1620, Ap
-10-425-114-35609	Sequence 35609, Ap
-10-425-114-9355	Sequence 9355, Ap
-10-425-114-35558	Sequence 35558, Ap
-10-425-114-8902	Sequence 8902, Ap
-10-425-114-10123	Sequence 10123, A

ALIGNMENTS

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0/080, 114
270, 777
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	Score 2737;	DB 15;	Length 2737;	
	Pred. 0.73;			
	Mismatches	0;	Indels	0;
			Gaps	0
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CCGCCTGACAGACACCTTCACGGCGACCGGCACGAGCT	60			
CCGCCTGACAGACACCTTCACGGCGACCGGCACGAGCT	60			
CGTGAACAAGGCGAATCTGACGCGCACCAAT	120			
CGTGAACAAGGCGAATCTGACGCGCACCAAT	120			
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CCAGGCGCTCCGCGGCGCGCGCTACCCGAGGACCCCT	180			
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181 CCTGACGTCCTCCGCTCCGCGAGAGAGGCGATCGTCGCGCCGCTTCGTCGCAATGCC 240
181 CCTGACGTCCTCCGCTCCGCGAGAGAGGCGATCGTCGCGCCGCTTCGTCGCAATGCC 240
QY 241 GGTGGCGCCGCGCCGCGAGGTTGGAGATACGTCGCGCTCAAGCTTCAAGAGCTAGCGCT 300
Db 241 GGTGGCGCCGCGCCGCGAGGTTGGAGATACGTCGCGCTCAAGCTTCAAGAGCTAGCGCT 300
QY 301 CGAGAGCTCAAGCTCTCGAGTACCTCCGCTTCAAGAGAGAGCTTGTGAGCGCGAGCA 360
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QY 361 CAATATCCCTAAGCTTCTCGAGCTTGAATCGAGCGCTTCAATGCTCAGTCCGCGCC 420
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QY 421 AATGCGTCATCATTTATTTGAAAGGTTGAGTTCCTCAACCGCACTTGTCCCAAT 480
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Db 481 CATGTCGCGCAACAGAGATTGCTTGAAGCCCTGTGATTTCTCCGTCGCGCGCA 540
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Db 541 CAAGGCGCATGTTATGATGCTTAAATGATTAAGATTAAGATTAAGATTAAGATTAAG 600
QY 601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGAGACACACCACTACCAAT 660
Db 601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGAGACACACCACTACCAAT 660
QY 661 TGTCTTAATTAATTTCAAGAGTGGAGCTGAGAGAGGTTGGAGTGAATACAGCAGAG 720
Db 661 TGTCTTAATTAATTTCAAGAGTGGAGCTGAGAGAGGTTGGAGTGAATACAGCAGAG 720
QY 721 TTTGGAATTAATTTCAAGAGTGGAGCTGAGAGAGGTTGGAGTGAATACAGCAGAG 780
Db 721 TTTGGAATTAATTTCAAGAGTGGAGCTGAGAGAGGTTGGAGTGAATACAGCAGAG 780
QY 781 GAATTTCTGGAGAGGATCCCAATTTTAACTGTTGATGATGATGATGATGATGATGAT 840
Db 781 GAATTTCTGGAGAGGATCCCAATTTTAACTGTTGATGATGATGATGATGATGATGAT 840
QY 841 CTTGGTCAAGCTAATGATTAAGCTTTCGACAGACAGAGAGAGAGATGCTATATACT 900
Db 841 CTTGGTCAAGCTAATGATTAAGCTTTCGACAGACAGAGAGAGAGATGCTATATACT 900
QY 901 GGACCAAGCTCGGACACTAGAAATGAGATGCTTCCGTTAAAGAAACAGAGGCTTGA 960
Db 901 GGACCAAGCTCGGACACTAGAAATGAGATGCTTCCGTTAAAGAAACAGAGGCTTGA 960
QY 961 TGTTCCTCCCAAGATTTCTCATTTGTTACTGCGCTGATACAGATGCAAAAGCAATCATG 1020
Db 961 TGTTCCTCCCAAGATTTCTCATTTGTTACTGCGCTGATACAGATGCAAAAGCAATCATG 1020
QY 1021 CAATCAGCGGCTTGAAGATTAAGTGAACACAGCAATCTTACATTTACAGATTCCTT 1080
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QY 1081 CAGAAATTAAGAAATGAGATTAAGTGAATGATTAAGATTAAGTGAATGATTAAGTGA 1140
Db 1081 CAGAAATTAAGAAATGAGATTAAGTGAATGATTAAGATTAAGTGAATGATTAAGTGA 1140
QY 1141 GGAATCATTTGCTGAGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 1200
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QY 1201 CTTGATTAATGGAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 CTTGATTAATGGAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 GGAATTAATGGAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1320

1261 GGAATTAATGGAATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 CATATTTTGAAGATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1380
Db 1321 CATATTTTGAAGATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 AATGCTATGAACAAATGCTATTTATATCAACAGACATACCAAGAAATTCGAGAG 1440
Db 1381 AATGCTATGAACAAATGCTATTTATATCAACAGACATACCAAGAAATTCGAGAG 1440
QY 1441 CAAAAATATGTTTGAAGATTAAGTGAATGATGATGATGATGATGATGATGATGATGAT 1500
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QY 1801 TGGCGGATTAATGATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 1860
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QY 2041 GCTTCTTACTTTCGAGAGCTTCATGAGAGTCAAGTGAATCAATGATGATGATGATGAT 2100
Db 2041 GCTTCTTACTTTCGAGAGCTTCATGAGAGTCAAGTGAATCAATGATGATGATGATGAT 2100
QY 2101 GGGCTTCCATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
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QY 2161 CGACCGGTCAGAGAGGCGGATCACTGAGGTTGAATATGATGATGATGATGATGATGATGAT 2220
Db 2161 CGACCGGTCAGAGAGGCGGATCACTGAGGTTGAATATGATGATGATGATGATGATGATGAT 2220
QY 2221 CATATACGAGAGTACATGAGAGTATATCAAGAGTGAATGATGATGATGATGATGATGAT 2280
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QY 2281 CTAAGCTTTTGAAGATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 2340
Db 2281 CTAAGCTTTTGAAGATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 2340
QY 2341 GATGTTTCAATATGAGAGTTCGAGAGTGGAGAGGCGGCTTGAATGATGATGATGATGAT 2400

Db 2341 GATGTTCACTAGAGTTCGCGAGCTCGGAGAACCGCTGCGCTTGCAATTGACCA 2400
QY 2401 ACCGAGTAGCTTGGCGCACTGCGACTGCGTAGCACTTGATACAGACTGAACCTGAAG 2460
Db 2401 ACCGAGTAGCTTGGCGCACTGCGACTGCGTAGCACTTGATACAGACTGAACCTGAAG 2460
QY 2461 GACCTTCACTAATTAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 2461 GACCTTCACTAATTAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2521 GTTTTAT 2580
Db 2521 GTTTTAT 2580
QY 2581 TTGTGTGTTCTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 2640
Db 2581 TTGTGTGTTCTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACTGTTACT 2640
QY 2641 GCAAGCCGAGCGACTGTTGAGAGTGTGTAATAATATATATATATATATATATATATAT 2700
Db 2641 GCAAGCCGAGCGACTGTTGAGAGTGTGTAATAATATATATATATATATATATATATAT 2700
QY 2701 AAA 2737
Db 2701 AAA 2737

RESULT 2
US-10-080-114A-11

Sequence 11, Application US/10080114A
Publication No. US20030005482A1
GENERAL INFORMATION:
APPLICANT: Dnuga, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080,114A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/270,777
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2757
TYPE: DNA
ORGANISM: Zea mays
FEATURES:
NAME/KEY: CDS
LOCATION: (1)...(2430)
FEATURE:
NAME/KEY: source
LOCATION: (1)...(39)
OTHER INFORMATION: Sorghum prounginum
FEATURE:
NAME/KEY: source
LOCATION: (40)...(2757)
OTHER INFORMATION: Zea mays
US-10-080-114A-11

Query Match 99.2% Score 2714; DB 15; Length 2757;
Best Local Similarity 99.8% Pred. No. 0;
Matches 2717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 16 CCGGCGACCGCTGAGAGACACCTCCACCGCGACCGCGACCGAGCTGTGCGCTCTCTGTC 75
Db 36 CCGGCGACCGCTGAGAGACACCTCCACCGCGACCGCGACCGAGCTGTGCGCTCTCTGTC 95
QY 76 CAAAGTACGTGAACAGAGGAG 135
Db 96 CAAAGTACGTGAACAGAGGAG 155
QY 136 CAAAGTACGTGAACAGAGGAG 195
Db 136 CAAAGTACGTGAACAGAGGAG 195

Db 156 CGAGGTTCAGAGGCTCCGGGGCTCCGGCGCTCCGGCGAGAGAGAGAGAGAGAGAGAGAGAG 215
QY 196 CTCGCGGAG 255
Db 216 CTCGCGGAG 275
QY 256 GGGAGTTTGGAGAGTACGTCCGCTCAACCTTCAACAGCTCAAGCTCAAGCTCAAGCTCAAG 315
Db 276 GGGAGTTTGGAGAGTACGTCCGCTCAACCTTCAACAGCTCAAGCTCAAGCTCAAGCTCAAG 335
QY 316 CTCGAGTACCTCCGCTCAAG 375
Db 336 CTCGAGTACCTCCGCTCAAG 395
QY 376 TCTCGAGCTTGAAGCTTCAAG 435
Db 396 TCTCGAGCTTGAAGCTTCAAG 455
QY 436 TATTGAAACGTTGAGAGTCTTCAACCGAGACTTGTCTCAATCATATGTTCCGCAAGAG 495
Db 456 TATTGAAACGTTGAGAGTCTTCAACCGAGACTTGTCTCAATCATATGTTCCGCAAGAG 515
QY 496 GATGCTTGGAGCCCGCTGTGAGATTCTCCGAGGCGAGAGAGAGAGAGAGAGAGAGAGAG 555
Db 516 GATGCTTGGAGCCCGCTGTGAGATTCTCCGAGGCGAGAGAGAGAGAGAGAGAGAGAGAG 575
QY 556 GATGCTTAAATGATAGATAAAG 615
Db 576 GATGCTTAAATGATAGATAAAG 635
QY 616 GAGGACTTGTCAAAGCTCCCTGCTGACACACACACACACACACACACACACACACACAC 675
Db 636 GAGGACTTGTCAAAGCTCCCTGCTGACACACACACACACACACACACACACACACACAC 695
QY 676 AGAGTGGGCGCTGAG 735
Db 696 AGAGTGGGCGCTGAG 755
QY 736 TCTCCTTCTAGACATATTCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795
Db 756 TCTCCTTCTAGACATATTCAGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815
QY 796 GATCCCGAGATTTTAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 855
Db 816 GATCCCGAGATTTTAAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 875
QY 856 TGTATTAGCTTCCAGAGACAG 915
Db 876 TGTATTAGCTTCCAGAGACAG 935
QY 916 ACTAGAAATGAGATGTTCTCCGTTTAAAGAAACAAAGGCTTGAATGTTTCCCAAGAT 975
Db 936 ACTAGAAATGAGATGTTCTCCGTTTAAAGAAACAAAGGCTTGAATGTTTCCCAAGAT 995
QY 976 TCTCATTGTTACCTCGGCTGATACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1035
Db 996 TCTCATTGTTACCTCGGCTGATACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1055
QY 1036 GAGAAATTAGAGAACAG 1095
Db 1056 GAGAAATTAGAGAACAG 1115
QY 1096 GATACCTTAAGAAATGATATCAAGATTTGATGATGATGATGATGATGATGATGATGATG 1155
Db 1116 GATACCTTAAGAAATGATATCAAGATTTGATGATGATGATGATGATGATGATGATGATG 1175
QY 1156 GATGCTGCTGAG 1215
Db 1176 GATGCTGCTGAG 1235
QY 1216 CTACAGTATGAGAAATCTTGGCGTCAATGCTATCTTACAGATGAGAGATTAACCAAGTG 1275
Db 1236 CTACAGTATGAGAAATCTTGGCGTCAATGCTATCTTACAGATGAGAGATTAACCAAGTG 1295

QY	1276	CAAAATGCTCAAGCTCTGGAAAAAGCTAAAGTATCGAGTTCCAGACATATTTTGGAAAGAA	1335
Db	1296	CAAAATGCTCAAGCTCTGGAAAAAGCTAAAGTATCGAGTTCCAGACATATTTTGGAAAGAA	1355
QY	1336	TTTTCGATGAGAAATGACCAATTTCTCTCCAGTTCACTGCTATATAATTTGCTATGAACAA	1395
Db	1356	TTTTCGATGAGAAATGACCAATTTCTCTCCAGTTCACTGCTATATAATTTGCTATGAACAA	1415
QY	1396	TGCTGATTTTATCATCACCAACATATCCAAAGAAATGCTCGAAGGAAAAATCTGTTGG	1455
Db	1416	TGCTGATTTTATCATCACCAACATATCCAAAGAAATGCTCGAAGGAAAAATCTGTTGG	1475
QY	1456	ACAGTATGAGAGTCATCTACTGCTTTACTCTGAGCTGCTGTACCGAGTTGCTCAAGGAT	1515
Db	1476	ACAGTATGAGAGTCATCTACTGCTTTACTCTGAGCTGCTGTACCGAGTTGCTCAAGGAT	1535
QY	1516	CGATGTTCTTGATCCAAAGTTCAATATATGTTCTCTCTGAGAGCTGACATGTCCATATCTT	1575
Db	1536	CGATGTTCTTGATCCAAAGTTCAATATATGTTCTCTCTGAGAGCTGACATGTCCATATCTT	1595
QY	1576	TTCCACATACCGAGAGAGGCGCAAGCGACATCACTCTCTTCATAGTTCAATCGAAATTTGAT	1635
Db	1596	TTCCACATACCGAGAGAGGCGCAAGCGACATCACTCTCTTCATAGTTCAATCGAAATTTGAT	1655
QY	1636	TTATGACCCCGAGCAAAACGATGAACAATTGAGCATCTGAGTATGCCGTCAAGCCCAT	1695
Db	1656	TTATGACCCCGAGCAAAACGATGAACAATTGAGCATCTGAGTATGCCGTCAAGCCCAT	1715
QY	1696	CCCTCTTCTTCCATGCGCAGACATCTCGACAGGGTGAABAACTATAACAGGCTGTGTCAGACTTT	1755
Db	1716	CCCTCTTCTTCCATGCGCAGACATCTCGACAGGGTGAABAACTATAACAGGCTGTGTCAGACTTT	1775
QY	1756	TGCTAAGTGGCCTAAGCTGAGGAGAGCTGGTAAACCTTGTCGTCTGCCCGGATCAATGA	1815
Db	1776	TGCTAAGTGGCCTAAGCTGAGGAGAGCTGGTAAACCTTGTCGTCTGCCCGGATCAATGA	1835
QY	1816	TGTCAAACAAGTCCAAAGACAGAGAAAGAGATCGCGAGATAGAGAAATGACATGAATCTCAT	1875
Db	1836	TGTCAAACAAGTCCAAAGACAGAGAAAGAGATCGCGAGATAGAGAAATGACATGAATCTCAT	1895
QY	1876	CAAGACCCCAACAATTGTTGGGGGAGTTCCGCTGGATCTCTGCCAGACAAACAGGGCCCG	1935
Db	1896	CAAGACCCCAACAATTGTTGGGGGAGTTCCGCTGGATCTCTGCCAGACAAACAGGGCCCG	1955
QY	1936	TAAAGCGAGCTCATCGCTACATCGCTGATACCCATAGTGTCTTTGTACAGCCGAGCCTT	1995
Db	1956	TAAAGCGAGCTCATCGCTACATCGCTGATACCCATAGTGTCTTTGTGTACAGCCGAGCCTT	2015
QY	1996	GTATGAACCGTTCCGCTCTCACCCGTCTTGAGGCAATGACCTGTGTGGCTTCTCTACTTTCCG	2055
Db	2016	GTATGAACCGTTCCGCTCTCACCCGTCTTGAGGCAATGACCTGTGTGGCTTCTCTACTTTCCG	2075
QY	2056	GAGCGTCCATGAGAGGTCCAGCTGAGATCATAGAGCATAGGCGTCTCGGCGCTTCCACATTGA	2115
Db	2076	GAGCGTCCATGAGAGGTCCAGCTGAGATCATAGAGCATAGGCGTCTCGGCGCTTCCACATTGA	2135
QY	2116	CCCGTACACCCTCGAAAGCGCTGTTAATCTGATGAGCCGACCTTCTTTCACCGGTGCAGACA	2175
Db	2136	CCCGTACACCCTCGAAAGCGCTGTTAATCTGATGAGCCGACCTTCTTTCACCGGTGCAGACA	2195
QY	2176	AGACCCAGATTCATCGGTGGATATATATCTGAGACAGGCGCTGAGGGCATATACGAAAGTA	2235
Db	2196	AGACCCAGATTCATCGGTGGATATATATCTGAGACAGGCGCTGAGGGCATATACGAAAGTA	2255
QY	2236	CACATGGAAGATATACTCAGAGAGGTTGATGACATCGGCGGAGGTCTAACGGTTTCTGGAA	2295
Db	2256	CACATGGAAGATATACTCAGAGAGGTTGATGACATCGGCGGAGGTCTAACGGTTTCTGGAA	2315
QY	2296	GTATGTTGTCCAGCTCTCAGAGAGCTTGAGACAGAGGCGCTAACCTGTAGATGTTCTCAATACT	2355
Db	2316	GTATGTTGTCCAGCTCTCAGAGAGCTTGAGACAGAGGCGCTAACCTGTAGATGTTCTCAATACT	2375

QY	2356	GAAGTTCCGGAGCTGGCGAAGACCGGCGCGTTGCATTTGACCAACCGAGAGAGCTTCG	2415
Db	2376	GAAGTTCCGGAGCTGGCGAAGACCGGCGCGTTGCATTTGACCAACCGAGAGAGCTTCG	2435
QY	2416	GCAACTCGACTCGTGGTGAACCTTGTTACAAAGCTGAACCTGAAAGACCTTCACTAAATT	2475
Db	2436	GCAACTCGACTCGTGGTGAACCTTGTTACAAAGCTGAACCTGAAAGACCTTCACTAAATT	2495
QY	2476	AGCGCGCGCAGACGGTNGCCATTAATAATGTGCGGAGCTGAACCTGTTTATTATTAAGTA	2535
Db	2496	AGCGCGCGCAGACGGTNGCCATTAATAATGTGCGGAGCTGAACCTGTTTATTATTAAGTA	2555
QY	2536	CATTAATGCGAGTATTAATAAATACTACTGCAAGCGAGTGGGTGCACTGTGTGTCGTAC	2595
Db	2556	CATTAATGCGAGTATTAATAAATACTACTGCAAGCGAGTGGGTGCACTGTGTGTCGTAC	2615
QY	2596	TGTTTACCTGATATTTGTCAAGCTGTGGCTGTCGCAATTTCTTTGCTGGCAAGCGCAGAC	2655
Db	2616	TGTTTACCTGATATTTGTCAAGCTGTGGCTGTCGCAATTTCTTTGCTGGCAAGCGCAGAC	2675
QY	2656	TGCTGAAGTGTCTGATAATAATCATCATTTCTGTGACCTGTGAATAAAAAAAAAAAAAA	2715
Db	2676	TGCTGAAGTGTCTGATAATAATCATCATTTCTGTGACCTGTGAATAAAAAAAAAAAAAA	2735
QY	2716	AAAAAAAAAAAAAAAAAGGCGCGCGCGC	2737
Db	2736	AAAAAAAAAAAAAAAAAGGCGCGCGCGC	2757

RESULT 3

US-10-425-114-6036

; Sequence 6036, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jindong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K

APPLICANT: Steven

APPLICANT: Tabacka, Tat

APPLICANT: Jaddabka, Jack E
APPLICANT: Cao Yongwei

APPLICANT: Cao, Yongwei

5 TITLE OF INVENTION: Nucleic Acid Molecules

TITLE OF INVENTION: Platcs and

FILE REFERENCE: 38-21 (53313

; CURRENT AP

CURRENT FILING

NUMBER OF SEQ ID NO

SEQ ID NO 6036

LENGTH: 2275

TYPE: DNA

US-10-425-114-6036

Query Match	80.0%	Score 2189.2	DB 13	Length 2275
Best Local Similarity	98.9%	Pred. No. 0		
Matches 2275	0	Mismatches 23	Indels 2	Gaps 2

QY	454	TTTCTCTCAACCGACATCTTCCCTCAATATATGTTCCGAAACAGGATTTGCTTGAGCCCT	5-3
Db	1	GTCTCTCAACCGACATCTTCTCAATATATTTCCGAAACAGGATTTGCTTGAGCCCT	60
QY	514	GTTGGATTTCTCCCTGGCCACCGGCACAAAGGGCATGTTATGATGCTTAATGATAGAT	573
Db	61	GCTGGATTTCTCCCTGGCCACCGGCACAAAGGGCATGTTATGATGCTTAATGATAGAT	120
QY	574	ACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACCAAACTGAGGAGCATTTGTCAAAAGCT	633
Db	121	ACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACCAAACTGAGGAGCATTTGTCAAAAGCT	180
QY	634	CCCTGCTGACACACATATCTCACAATTTTGCTTATTAATTTCAAGAGTGGGGCTCTGGAGAA	693
Db	181	CCCTGCTGACACACATATCTCACAATTTTGCTTATTAATTTCAAGAGTGGGGCTCTGGAGAA	240

QY 694 AGGTGGGGGTGATACAGCAGGACATGTTTGGAAATGATCCATCTCCTTCTAGACATCAT 753
 DB 241 AGGTGGGGGTGATACAGCAGGACATGTTTGGAAATGATCCATCTCCTTCTAGATATAT 300
 QY 754 TCAGGGCCAGAGCCCTTACCTTAGAGAAATCTTGGGGAGATGCCCTGATTTTAA 813
 DB 301 TCAGGGCCAGAGCCCTTACCTTAGAGAAATCTTGGGGAGATGCCCTGATTTTAA 360
 QY 814 CGTTGTTGATATCCCTCATGATATCTTGGTCAAGTATGATATAGCTTGCACA 873
 DB 361 CGTTGTTGATATCCCTCATGATATCTTGGTCAAGTATGATATAGCTTGCACA 420
 QY 874 CACAGAGACAGATGCTATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGCT 933
 DB 421 CACAGAGACAGATGCTATATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGCT 480
 QY 934 TCTCCGTTTAAAGAAACAAGGGCTTATTTTCCCAAGAAATCTCATCTTCTGCGCT 993
 DB 481 TCTCCGTTTAAAGAAACAAGGGCTTATTTTCCCAAGAAATCTCATCTTCTGCGCT 540
 QY 994 GATACCAATGCAAAAGAAACATCATCATCAGCGGCTTGAAGAAATAGTGAACACA 1053
 DB 541 GATACCAATGCAAAAGAAACATCATCATCAGCGGCTTGAAGAAATAGTGAACACA 600
 QY 1054 GCATACTTACATTTACAGATTCCTTCAAGAAATGAAATGGATTTAGAAATGGAT 1113
 DB 601 GCATACTTACATTTACAGATTCCTTCAAGAAATGAAATGGATTTAGAAATGGAT 660
 QY 1114 ATCAAGATTTGATGTCGTCGCAATCTGAAACATTTGCGAGAGATGCTGCTGTAAT 1173
 DB 661 ATCAAGATTTGATGTCGTCGCAATCTGAAACATTTGCGAGAGATGCTGCTGTAAT 720
 QY 1174 TCTGCTGATTTACAGAGTCTCAGACTTCATATTTGAAACTAGAGTGAATATCT 1233
 DB 721 TCTGCTGATTTACAGAGTCTCAGACTTCATATTTGAAACTAGAGTGAATATCT 780
 QY 1234 TGTGGCGTATTTGCTATCTTACAGATGGAAATTTCCAGTCAATGCTCATGCTCT 1293
 DB 781 TGTGGCGTATTTGCTATCTTACAGATGGAAATTTCCAGTCAATGCTCATGCTCT 840
 QY 1294 GAAAAAGACTAAGTATTCAGATTCAGACATTTTGGAAATTTGATGAGAAATAGCA 1353
 DB 841 GAAAAAGACTAAGTATTCAGATTCAGACATTTTGGAAATTTGATGAGAAATAGCA 900
 QY 1354 TTCTCTGTCAGATTCAGTCTGATATTAATGCTATGAAACATGCTGATTTATCATCAC 1413
 DB 901 TTCTCTGTCAGATTCAGTCTGATATTAATGCTATGAAACATGCTGATTTATCATCAC 960
 QY 1414 CAGACATACCAAGAAATTTGCTGGAAGCAAAATACCTTTGACAGTATGAGTCTATAC 1473
 DB 961 CAGACATACCAAGAAATTTGCTGGAAGCAAAATACCTTTGACAGTATGAGTCTATAC 1020
 QY 1474 TGTCTTACTCTGCGCTGCTGTCAGAGAGTGTCCATGGATGATGCTTCCATCCAAA 1533
 DB 1021 TGTCTTACTCTGCGCTGCTGTCAGAGAGTGTCCATGGATGATGCTTCCATCCAAA 1080
 QY 1534 GTTCATATATAGTCTCTCTGAGACTGATGTCATATATCTTCCATACATACCGAAGAGC 1593
 DB 1081 GTTCATATATAGTCTCTCTGAGACTGATGTCATATATCTTCCATACATACCGAAGAGC 1140
 QY 1594 CAAAGCACTACCTCTCTTATGTTTCAATCGAAATTTGATTTATGACCCGAGCAAAA 1653
 DB 1141 CAAAGCACTACCTCTCTTATGTTTCAATCGAAATTTGATTTATGACCCGAGCAAAA 1200
 QY 1654 CGATGAACACATTTGGGATCTGATGACCGGTCAAAAGCCCATCTCTTCCATGGCAAG 1713
 DB 1201 CGATGAACACATTTGGGATCTGATGACCGGTCAAAAGCCCATCTCTTCCATGGCAAG 1260
 QY 1714 ACTCGACAGGGTGAAGAACATAA CAGGGCTGTGTAAGCTTTTGTAGTGCCTAAGCT 1773
 DB 1261 ACTCGACAGGGTGAAGAACATAA CAGGGCTGTGTAAGCTTTTGTAGTGCCTAAGCT 1320

QY 1774 GAGGAGAGCTGTAAACCTTGTGTGCTGTCGCGGGTACATAGATGTCAACAAGTCCAAAGCA 1833
 DB 1321 GAGGAGAGCTGTAAACCTTGTGTGCTGTCGCGGGTACATAGATGTCAACAAGTCCAAAGCA 1380
 QY 1834 CAGGAAAGATGCGCGAGATAGAGAGATGATGAACTCATCAAGACCAACCACTTGT 1893
 DB 1381 CAGGAAAGATGCGCGAGATAGAGAGATGATGAACTCATCAAGACCAACCACTTGT 1440
 QY 1894 CCGGCAAGTTCGCTGATCTCTGCGCAACAACAGGGCCGTTAACCGCGAGCTCTATCG 1953
 DB 1441 CCGGCAAGTTCGCTGATCTCTGCGCAACAACAGGGCCGTTAACCGCGAGCTCTATCG 1500
 QY 1954 CTACATGCTGATACCCATGATGCTTCTGTCACAGCGGCTTGTATGAAAGCTTGTCT 2013
 DB 1501 CTACATGCTGATACCCATGATGCTTCTGTCACAGCGGCTTGTATGAAAGCTTGTCT 1560
 QY 2014 CACGCTGTTGAGGCCATGACCTGTGGGCTTCCATCTTTCGCGAGCGCTCCATGAGAGTCC 2073
 DB 1561 CACGCTGTTGAGGCCATGACCTGTGGGCTTCCATCTTTCGCGAGCGCTCCATGAGAGTCC 1620
 QY 2074 AGCTGAGATCATAGAGATGAGCTGTGCGCTTCCATTTGACATTTGACCCGTAACA 2133
 DB 1621 AGCTGAGATCATAGAGATGAGCTGTGCGCTTCCATTTGACATTTGACCCGTAACA 1680
 QY 2134 GCGTGTATATCTGATGCGCGACCTTCTTCCACCGGTGCAACCAAGACCCAGATCAGCTGGGT 2193
 DB 1681 GCGTGTATATCTGATGCGCGACCTTCTTCCACCGGTGCAACCAAGACCCAGATCAGCTGGGT 1740
 QY 2194 GAATATATCTGAGACAGGGCTGCAAGCATATACAGAGATGACATAGAAATATCTC 2253
 DB 1741 GAATATATCTGAGACAGGGCTGCAAGCATATACAGAGATGACATAGAAATATCTC 1800
 QY 2254 AGAGAGGTGATGACACTGCGCGGGCTTACCGTTCTGAAAGTACGTGTGAAAGCTCGA 2313
 DB 1801 AGAGAGGTGATGACACTGCGCGGGCTTACCGTTCTGAAAGTACGTGTGAAAGCTCGA 1860
 QY 2314 GAGGCTGAGAACAGAGGCGCTACCTTGAAGATGTTCAATCTGAAAGTTCGCGAGCTGGC 2373
 DB 1861 GAGGCTGAGAACAGAGGCGCTACCTTGAAGATGTTCAATCTGAAAGTTCGCGAGCTGGC 1920
 QY 2374 GAAGACCGTCCGCTTGCATATGACCAACCGAGTACCTTGCAGACCTGCACTGCTAG 2433
 DB 1921 GAAGACCGTCCGCTTGCATATGACCAACCGAGTACCTTGCAGACCTGCACTGCTAG 1980
 QY 2434 CACTGCTACAGACTGAAACCTGAGGACCTTCAATTTAGGCGCGGACAGCGTAG 2493
 DB 1981 CACTGCTACAGACTGAAACCTGAGGACCTTCAATTTAGGCGCGGACAGCGTAG 2040
 QY 2494 CCATTAATATGTCGCGAGCTGAACTGCTTTTATATATGACATTAATGAGATATACA 2553
 DB 2041 CCATTAATATGTCGCGAGCTGAACTGCTTTTATATATGACATTAATGAGATATACA 2098
 QY 2554 AAATTAATGAGAGAGTGGTGGAGTGTGAGTGTGATCTGTTTACTGATATATATGTC 2613
 DB 2099 AAATTAATGAGAGAGTGGTGGAGTGTGAGTGTGATCTGTTTACTGATATATATGTC 2158
 QY 2614 AAGCTGTGCGCTGCAATTTCTTTGCTGCGCAAGCTGCAAGCTGTAAGTCTGATATA 2673
 DB 2159 AAGCTGTGCGCTGCAATTTCTTTGCTGCGCAAGCTGCAAGCTGTAAGTCTGATATA 2218
 QY 2674 TACATCATATCTGTTGACCTGTGAAAAA 2703
 DB 2219 TACATCATATCTGTTGACCTGTGAAAAA 2248

RESULT 4

US-10-425-114-6561
 ; Sequence 6561, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 6561
LENGTH: 1874
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700571529_FU1
US-10-425-114-6561

Query Match 67.1%; Score 1837.4; DB 13; Length 1874;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1858; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 823 GGTATCCCTCATGATGATCTTGTCAAGCTAATGATATTAAGGCTGCCAGACAGAGAG 882
DB 1 GGTATCCCTCATGATGATCTTGTCAAGCTAATGATATTAAGGCTGCCAGACAGAGAG 60
QY 883 ACGATGCTATATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCGTTT 942
DB 61 ACGATGCTATATATCTGACCAAGTCCGTGCACTAGAAAATGAGATGTTCTCGTTT 120
QY 943 AAAAGAAAAGAGGCTGTGATGTTTCCCAAGATCTCTGTTACTCGGCTGATCCAGA 1002
DB 121 AAAAGAAAAGAGGCTGTGATGTTTCCCAAGATCTCTGTTACTCGGCTGATCCAGA 180
QY 1083 TGCAAAAGAAACATCATGCAATCAGCGCTTGAGAGAAATAGTGGAAACAGCATACTTA 1062
DB 181 TGCAAAAGAAACATCATGCAATCAGCGCTTGAGAGAAATAGTGGAAACAGCATACTTA 240
QY 1063 CATATTACAGATCCCTTCAGAAATGAAATGGAATCTTAAGAAATGAGATCAAGATT 1122
DB 241 CATATTACAGATCCCTTCAGAAATGAAATGGAATCTTAAGAAATGAGATCAAGATT 300
QY 1123 TGATGTCGTCATCTGAGAAACATTTGAGAGATGCTGCTGAGAAATGCTGCTGA 1182
DB 301 TGATGTCGTCATCTGAGAAACATTTGAGAGATGCTGCTGAGAAATGCTGCTGA 360
QY 1183 ATTACAGATCTCAGACTTCATTAATTGAAATCTACAGTGAATCTTGTGCGCTC 1242
DB 361 ATTACAGATCTCAGACTTCATTAATTGAAATCTACAGTGAATCTTGTGCGCTC 420
QY 1243 ATTGCTATCTTACAAAGATGGGAATTAACCAATGCAATTTGCTCATGCTCTGAAAAGAC 1302
DB 421 ATTGCTATCTTACAAAGATGGGAATTAACCAATGCAATTTGCTCATGCTCTGAAAAGAC 480
QY 1303 TAAAGATCCAGATGACATATTTTGAAGAAATTCGATGAGAGTACATTTCTCTG 1362
DB 481 TAAAGATCCAGATGACATATTTTGAAGAAATTCGATGAGAGTACATTTCTCTG 540
QY 1363 CCAAGTTCATGCTGATATTAATTGCTATGAAACATGCTGATTTTATCATCAACAGACATA 1422
DB 541 CCAAGTTCATGCTGATATTAATTGCTATGAAACATGCTGATTTTATCATCAACAGACATA 600
QY 1423 CCAAGAAATTTGCTGAAAGCAAAATTAATCTTTGAGACGATGAGAGTCAATGCTCTTAC 1482
DB 601 CCAAGAAATTTGCTGAAAGCAAAATTAATCTTTGAGACGATGAGAGTCAATGCTCTTAC 660
QY 1483 TCTGCTGGTCTGTACCGAGTGTGCATGGAATCAATGCTTCGATCCAAAGTTCAAT 1542
DB 661 TCTGCTGGTCTGTACCGAGTGTGCATGGAATCAATGCTTCGATCCAAAGTTCAAT 720
QY 1543 AGTCTCTCTGAGCTGACATCTCCATATACATTTTCCATACAGAGAGGCGCAAGGACT 1602
DB 721 AGTCTCTCTGAGCTGACATCTCCATATACATTTTCCATACAGAGAGGCGCAAGGACT 780

QY 1603 CACTCTCTTATGATGATTCGAATGCAAAATTTGATTAATGACCCGAGCAAAAGATGACA 1662
DB 781 CACTCTCTTATGATGATTCGAATGCAAAATTTGATTAATGACCCGAGCAAAAGATGACA 840
QY 1663 CATGGGATCTGATGACCGGTCAGAGCCATCTCTTCTCATGAGGACAGCTGACAG 1722
DB 841 CATGGGATCTGATGACCGGTCAGAGCCATCTCTTCTCATGAGGACAGCTGACAG 900
QY 1723 GGTGAAGAACATTAACAGGCTGATGAGCTTTTGTCTAATGTCGCTAAGCTGAGGAGCT 1782
DB 901 GGTGAAGAACATTAACAGGCTGATGAGCTTTTGTCTAATGTCGCTAAGCTGAGGAGCT 960
QY 1783 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1842
DB 961 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1843 GATGCGGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1902
DB 1021 GATGCGGAGATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1903 CCGCTGATCTCTGCGCAGACAAACAGGCGCTGTAAGCGGAGCTCTATGCTACATGCG 1962
DB 1081 CCGCTGATCTCTGCGCAGACAAACAGGCGCTGTAAGCGGAGCTCTATGCTACATGCG 1140
QY 1963 TGATPCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2022
DB 1141 TGATPCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
QY 2023 TGAGGCAATGACCTGAGGCTCTCTACTTTCGAGAGCTCATGAGAGTCCAGCTGAGAT 2082
DB 1201 TGAGGCAATGACCTGAGGCTCTCTACTTTCGAGAGCTCATGAGAGTCCAGCTGAGAT 1260
QY 2083 CATAGAGATGACCTGAGGCTCTCTACTTTCGAGAGCTCATGAGAGTCCAGCTGAGAT 2142
DB 1261 CATAGAGATGACCTGAGGCTCTCTACTTTCGAGAGCTCATGAGAGTCCAGCTGAGAT 1320
QY 2143 TCTGATGCGCATCTCTCTGACCCGCTGCAAGAGCAAGCCAGTCACTGGGCTGAATATAC 2202
DB 1321 TCTGATGCGCATCTCTCTGACCCGCTGCAAGAGCAAGCCAGTCACTGGGCTGAATATAC 1380
QY 2203 TGAGACAGGCTGACAGCGCATATACAGAGATGACATGAGATATATCTCAGAGAGAT 2262
DB 1381 TGAGACAGGCTGACAGCGCATATACAGAGATGACATGAGATATATCTCAGAGAGAT 1440
QY 2263 GATGACCTGAGCGGCTCTACGCTTTCGAAATGATGCTGAAAGCTGAGAGCTGCA 2322
DB 1441 GATGACCTGAGCGGCTCTACGCTTTCGAAATGATGCTGAAAGCTGAGAGCTGCA 1500
QY 2323 GAGGAGGCGCTACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 2382
DB 1501 GAGGAGGCGCTACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 2383 GCCGCTTGCAATTGACCAACCGAGTACCTGCGAACTGCGAGCTGCGAGCACTTGGA 2442
DB 1561 GCCGCTTGCAATTGACCAACCGAGTACCTGCGAACTGCGAGCTGCGAGCACTTGGA 1620
QY 2443 CAAAGCTGAACCTGAAAGACCTTCAATATTTAGCGCGGAGAGAGTAAAGCAATTA 2502
DB 1621 CAAAGCTGAACCTGAAAGACCTTCAATATTTAGCGCGGAGAGAGTAAAGCAATTA 1680
QY 2503 TGTGCGGAGCTGAAGTGTGTTTATTAATGATGATGATGATGATGATGATGATGATGAT 2562
DB 1681 TGTGCGGAGCTGAAGTGTGTTTATTAATGATGATGATGATGATGATGATGATGATGAT 1739
QY 2563 AAGGAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2622
DB 1740 AAGGAGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1793
QY 2623 GCTGCAATTTCTTGTGCAAGCGCAGAGCTGCTGTAAGTGTGATTAATCAATCA 2682
DB 1800 GCTGCAATTTCTTGTGCAAGCGCAGAGCTGCTGTAAGTGTGATTAATCAATCA 1853
QY 2683 TTCTGTTGACTGTG 2697

Db 1860 TTCTGTTGACCTGTG 1874

RESULT 5

US-10-425-114-15113
Sequence 15113, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5311)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15113
LENGTH: 2832
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB3051-038-E10_F11
US-10-425-114-15113

Query Match 49.0%; Score 1340.8; DB 13; Length 2832;

Best Local Similarity 72.7%; Pred. No. 0;
Matches 1748; Conservative 0; Mismatches 652; Indels 6; Gaps 1;

QY 16 CGGCGACCCGCGTGAGAGACACCTCCACGCGACCGACGAGCTCGGCGCTCGTGC 75
DB 138 CAGAGACCGAGTTGAGAGACACTCTCTGCTCAACCGTACGAACTCATTTCTCTCTC 197
QY 76 CAGTACGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 135
DB 198 CAGGATGTGGCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 257
QY 136 CGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 189
DB 258 CAGATCTCTGCGGATGATCAGACATATGATGATCTTAAATATGATCTCTCTCTCT 317
QY 190 CCTCCGCTCGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 249
DB 318 CGTCAAGTCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 377
QY 250 GCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 309
DB 378 AAGACCTGTGTGTGGAGATATGTCGTGTTAATGTCGTGAGCTCAGCTGAGCAATT 437
QY 310 CACAGTCTCGAGGAGTCTCGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
DB 438 AAGTGTCTTGATATCTCAGCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 370 CTAGGTTCTGAGCTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
DB 498 TTTGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 557
QY 430 ATATCTATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489
DB 558 AGATCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 617
QY 490 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 549
DB 618 CAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 677
QY 550 TGTATGATGCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609
DB 678 TGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 737

QY 610 AGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
DB 738 GGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 797
QY 670 ATTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 725
DB 798 ATTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 857
QY 730 GATTCATCTCTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 789
DB 858 GATTCATCTCTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 917
QY 790 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 849
DB 918 TGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 977
QY 850 AGCTAAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 909
DB 978 AGCCATCTCTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1037
QY 910 CCGTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 969
DB 1038 GCGTCCCTTGAAGATGAGATGCTCTCCGATCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1097
QY 970 AAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1029
DB 1098 AAGATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1157
QY 1030 GCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1089
DB 1158 GCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217
QY 1090 AATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1149
DB 1218 GTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1277
QY 1150 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1209
DB 1278 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1337
QY 1210 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1269
DB 1338 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1397
QY 1270 CAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1329
DB 1398 AAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1457
QY 1330 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1389
DB 1458 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517
QY 1390 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1449
DB 1518 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1577
QY 1450 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1509
DB 1578 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1637
QY 1510 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1569
DB 1638 TGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1697
QY 1570 ATATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1629
DB 1698 ATATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1757
QY 1630 TTTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1689
DB 1758 GCTATTTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1817
QY 1690 GCCATCTCTTCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1749

```

Db      1818  GCGCAATATTCTCCATGGCAAGGCTACACAGAGTAAAAACATACCTGCAATTGGTACA 1877
Qy      1750  AGCTTTGCTAAGTGGCTAAGCTGAGGAGCTGGTAAACCTTGTGCTGTCGCCGGTA 1809
Db      1878  AAGCTTTGGTAAAGAACAGAAATGAGGAACTGGTCAACTTGTATATGTCGTGTTA 1937
Qy      1810  CATATATGTCACAAAGTCCAGAGACAGGAGAGATCGCGAGATAGAGAGATGCATGA 1869
Db      1938  TATTATGATGTAAGAGAGTCAAGTACAGAGAAATGCAAAATTGAGAAATGCATGA 1997
Qy      1870  ACTATCAAGACCCCAACTGTGTGGGAGTCCGCTGATCTCTGCCCAACAACAG 1929
Db      1998  GCTCATGAAAAAGTAACTTAAGTGTGATTTTGTGGATTGCTGCCCAACAATAG 2057
Qy      1930  GACCCGTAACGGCGAGCTCTATCGCTACATCGCTGATACCCATGGTGTCTTCTGACAGCC 1989
Db      2058  GGCACGTATAGGGAGCTGTATCGCTACATACAGACACACAAAGTGCTTCTGTCAGCC 2117
Qy      1990  GACCTTGATAGAGCGTGTGGTCTCAACCGTGTGAGGCAATGACCTGTGGGCTTCTAC 2049
Db      2118  TGTCTTCTATGAGCTTTTGGACTTACAGTGTGAGAGGCAATGGAATGTGAGACTCCAC 2177
Qy      2050  TTGCGCAGCGCTCCATGAGGCTCAGCTAGATCATAGAGCATGGCGTCTCGGGCTTCCA 2109
Db      2178  TTTTCTCTCTGCGCAGTGTGCTGCGCTGAGATCTGAGCAGTGTATTCAGAGATCCA 2237
Qy      2110  CATGACCCGTAACACCCCGAAGCAGCTGTATCTGATGAGCCGACTTCTTGACCCGCTG 2169
Db      2238  CATGATCCTTATCACCCCGATCAAGCTTCAAGCTATAGTTGAAATTTTCCAAAAGAG 2297
Qy      2170  CAAAGAACCCCAATCTACTGCTGATATATCTGAGAGAGGCTGACGCTGACATATACA 2229
Db      2298  CAAAGAGAGCCCAAGCCATGTGAAAGAAATATCTATGTGTCTTCAAGAAATTTATGA 2357
Qy      2230  GAAATACATAGGAAGATATATCTCAGAGAGTGTATGACATGCGCCGCTCTACGCTTT 2289
Db      2358  AAGGTACAGCTGGAAGATTTATTCGAAAGGCTTATGACTTTGGCGGAGTTATAGTTT 2417
Qy      2290  CTGGAAGTACGTGTGAAAGCTGAGAGGCTGAGACAGGCGCTTACCTTGAATGTTCTA 2349
Db      2418  CTGGAATATACGTTTCCAAATTAGAGAGGCGTGAACACTGACGATATCTTGAATGTTCTA 2477
Qy      2350  CATCTGAAGTTCGCGAGCTGGCGAGACCGTGGCGCTTGAATGACCAACCGCAGTA 2409
Db      2478  TATCTCAAGTTCGCTGATTTGGCAAAATTCGTCCGCTAGAGATGATCAAGTTA 2537
Qy      2410  GCTTGC 2415
Db      2538  ACTAGC 2543

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RESULT 6
US-10-424-599-98889
; Sequence 98889, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 28584
; SEQ ID NO 98889
; LENGTH: 3191
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure

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; LOCATION: (1)..(3191)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1
US-10-424-599-98889

Query Match      48.0%; Score 1314; DB 13; Length 3191;
Best Local Similarity 72.5%; Pred. No. 0;
Matches 1745; Conservative 0; Mismatches 655; Indels 8; Gaps 3;

Qy      16  CGGACCGCGCTCGAGAGACACCTCCACGCGGACGCAACGAGCTGTGCGCTCTGTC 75
Db      230  CAGAGACCGAGTTGAAAGACACTCTCTGCTACCGTAAAGCACTATTTCTCTCTC 289
Qy      76  CAAATACGTGAACAAAGGGAGGAGCATCTGAGCGGACCAATCTCGAGCGCTCGA 135
Db      290  CAGGTATGTGCTCAGGGAGAGGAGATTTCACACCCCAATTTATTTGATGATGACCTTA 349
Qy      136  CGAGGTCCAGGCG-----TCCGGGGGCGCGCGCTAGCCGAGGACCTTCTCTGACGT 189
Db      350  CAAATCTCCCTGGCGATGATCAAGCAATAGTGAATCTTAAAAATGTCTTGTGTAAAT 409
Qy      190  CCTCCGCTCCGCGCAGAGGCGCATGTGCTGCCCGTTCGTGGCCATCGCGTGGCGCC 249
Db      410  CGTCAAGTTCGAAAGAGAACCAATGTTTGTCTCTTGTGTGCAATAGCACTTCTCTC 469
Qy      250  GCGCCCGGAGTTTGGAGTACGTCCGCTCAACGTTACAGACTCAGCGTGGAGTACGT 309
Db      470  AAGACTGTGTGTTGGGAATATGTCCGTATATGTCTGTGAGCTCAGCGTGGAGCAAT 529
Qy      310  CACAGTCTCGAGTACCTCCGCTTCAAGAGAGAGCTGTGCGAGCGACG-CAATATATC 368
Db      530  AAGTGTCTGATATCTCAGCTTCAAGGAAACCTGTGATGAGAAATTAATGACA 589
Qy      369  CCTACGTTCTCAGAGCTTGACTTCCAGCCGTCATATGTCTACGTCCACGCCCAATCG 428
Db      590  ATTTGTATGAGGCTGATTTTGAAGCATTTAAGCCACATTTCTCTCTCCAACTCGCT 649
Qy      429  CATCATCTATTGGAACCGGT-GTGCAATCTCTCAACCGACACTGTCTCTCAATCATGTT 487
Db      650  CAGCATTCATGGCAATATGTGTCTCCATCTTCCAAATCTCCACCTTCAATCTTATGTT 709
Qy      488  CGCAACAGGATTTGCTGGAGCCCTGTGATTTCTCTCGTGGCCACCGGCAAGGGG 547
Db      710  CGCAAGAGAGATTTCTTGAGCCCTTCTGATTTCTCTCGAGCTCAAAATTAAGGGC 789
Qy      548  CATGTTATGATCTTAAATGATGAATACAAAGCTTGGAGGCTTGAATCTGTGCTGACC 607
Db      770  CATGCTCTGATGTAAATGATGAATACAAACATTTCCAAATTTCAATCTGATGCTGAGCC 829
Qy      608  AAGCTGAGGAGACTTGTCAAAAGCTCCCTGCTGACACACATCTCAATTTGCTTAT 667
Db      830  AAGCTGAGGATTTCTCTTAAGCTTGCATATGATACCTCTATTCACAGTTGAAAT 889
Qy      668  AATTTTCAAGATGGGGCTTGGAGAAAGTTGGGGGATACAGAGGACATGTTTGGAA 727
Db      890  GATTTGCAAGAAATGGGTTTGAAGAGGTTGGGGGATACGCTGAACGGGATTTGGA 949
Qy      728  ATGATTCATCTCTCTTACAGATCAATTCAGCGCGACAGACCATCTACCTTGAAGAAATTC 787
Db      950  ATGATGATCTGCTATTTGATTTCTTTCAGGCTCTCCGATCTTCTTACATCTAGGACTTTT 1009
Qy      788  TTGGGAGAGATCCCATATGTTTAAAGTGTGTGATATCCCTCATGATGATCTTGTG 847
Db      1010  CTTGGAGAGTACCAATGATATCAATGTTGATATTTATCTCTCATGATGCTTCTTGA 1069
Qy      848  CAACTAAATGATTTAGCTTGGCAGACACAGAGAGACAGATGCTATATCTGACCA 907
Db      1070  CAAAGCAATGTCTTGGGTTTGTCTGACACTGTGTGGGAGGTTGTTATATCATAGTCA 1125
Qy      908  GTCCGTGACATGAAATAGATGTTCTCGCTTTAAAGAAACAAAGGCTTGTATGTTCC 967
Db      1130  GTGCGTCCCTTGAATAATGAGATGCTCTTCCGATCAAGAAACAGGACCTTATTTCACT 1189

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QY 968 CCAAGATCTCTATTGTTACTCGGCTGATACCAAGATGCAAAAGAACATCATGCAATCAG 1027
DB 1190 CCAAGATCTCTATTGTTACTCGGCTGATACCAAGATGCAAAAGAACATCATGCAATCAG 1249
QY 1028 CGGCTTGAGAGAAATTAGTGAACACAGCATCTTACATTAATTAACAGTTCCCTTCAGAAAT 1087
DB 1250 CGGCTTGAGAGAAATTAGTGAACACAGCATCTTACATTAATTAACAGTTCCCTTCAGAAAT 1309
QY 1088 GAAAATGGGATCTTAAAGAAATGATATCAAGATTTGATGTGGCCCATATCTGSAACA 1147
DB 1310 GAGTCAGGAATCTCCGTAATGATTTCAAGGTTTATGTGTGGCCCTTATCTAGAGACT 1369
QY 1148 TTGCTGAGAGATGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1207
DB 1370 TATGCAAGAGATGTTGCAAGTGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1429
QY 1208 ATTGGAATCTACAGTGTGGAATCTTGTGGCGCTCATTTGCTATCTTAACAAGATGGAAAT 1267
DB 1430 ATTGGAATCTACAGTGTGGAATCTTGTGGCGCTCATTTGCTATCTTAACAAGATGGAAAT 1489
QY 1268 ACCGAGTGAACATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1327
DB 1490 ACCGAGTGAACATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1549
QY 1328 TGAAGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1387
DB 1550 TGAAGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1609
QY 1388 ATGGAAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1447
DB 1610 ATGGAAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1669
QY 1448 ACTGCTGAGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1507
DB 1670 ACTGCTGAGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1729
QY 1508 CATGGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1567
DB 1730 CATGGAGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1789
QY 1568 ATATACATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1627
DB 1790 ATATACATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1849
QY 1628 AATTGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1687
DB 1850 AATTGATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1909
QY 1688 AAGCCATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1747
DB 1910 AAGCCATTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1969
QY 1748 GAAAGCTTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1807
DB 1970 GAAAGCTTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 2029
QY 1808 TACATATGTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 1867
DB 2030 TACATATGTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 2089
QY 1868 GAAATCATCAAGAACCAACACTGTTGCGGCGATTTCCGCTGATTTCTGCGCAGCAAAAC 1927
DB 2090 GAAATCATCAAGAACCAACACTGTTGCGGCGATTTCCGCTGATTTCTGCGCAGCAAAAC 2149
QY 1928 AGGGCCCGTAAACGCGAGCTCTATGCTAATCGCTGATTAACAGGTAATCCAGACTTATCATA 1987
DB 2150 AGGGCCCGTAAACGCGAGCTCTATGCTAATCGCTGATTAACAGGTAATCCAGACTTATCATA 2209
QY 1988 CCGGCTTTGATGAAGCGTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 2047
DB 2210 CCGGCTTTGATGAAGCGTTGCTGCTGCTGGAATTTGCTGCTGATTAACAGGTAATCCAGACTTATCATA 2269

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QY 2048 ACTTGGCGAGCGCTCCATGAGAGGTCGAGTCAATGATTCATAGCATGCGCTCTCGGCTTC 2107
DB 2270 ACTTGGCGAGCGCTCCATGAGAGGTCGAGTCAATGATTCATAGCATGCGCTCTCGGCTTC 2329
QY 2108 CACTTACCCGCTACGAGCCCGGAGAGAGGCTGTTATATGATGAGCCGACTCTTCGACCGG 2167
DB 2330 CACTTACCCGCTACGAGCCCGGAGAGAGGCTGTTATATGATGAGCCGACTCTTCGACCGG 2389
QY 2168 TGCAGAGAGAGCCGAGATCACTGAGGATATATCTGAGAGAGGCTGAGCGATATATAC 2227
DB 2390 AGCAGAGAGAGCCGAGATCACTGAGGATATATCTGAGAGAGGCTGAGCGATATATAC 2449
QY 2228 GAGAGATCACTGAGGATATATCTGAGAGAGGCTGAGCGATATATAC 2287
DB 2450 GAGAGATCACTGAGGATATATCTGAGAGAGGCTGAGCGATATATAC 2509
QY 2288 TTCTGAGAGATGCTGCTGAGAGCTGAGAGGCTGAGAGAGGCTGAGAGGCTTACGAGTTC 2347
DB 2510 TTCTGAGAGATGCTGCTGAGAGCTGAGAGGCTGAGAGAGGCTGAGAGGCTTACGAGTTC 2569
QY 2348 TACATACGAGATTCGCGAGCTGCGAGAGAGCGTGCCTGTCATTTGACCAACCGCAG 2407
DB 2570 TACATACGAGATTCGCGAGCTGCGAGAGAGCGTGCCTGTCATTTGACCAACCGCAG 2629
QY 2408 TAGCTTC 2415
DB 2630 TAGCTTC 2637

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RESULT 7
US-10-425-114-5285
; Sequence 5285, Application US/10425114
; Publication No. US2004003488B1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalec, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5285
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454567_F11
US-10-425-114-5285

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Query Match 47.9%; Score 1309.8; DB 13; Length 1340;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 128; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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QY 1357 CTCCTGCGAGTCACTGCTGATTAATTTGCTGAGCAATGCTGATTTATCATACCGG 1416
DB 1 CTCCTGCGAGTCACTGCTGATTAATTTGCTGAGCAATGCTGATTTATCATACCGG 60
QY 1417 CACATACGAGAAATTTGCTGAGCAAAATTTCTGTTGAGCAGTATGAGAGTATATCTGC 1476
DB 61 CACATACGAGAAATTTGCTGAGCAAAATTTCTGTTGAGCAGTATGAGAGTATATCTGC 120
QY 1477 CTTTACTGCTGCTGCTGCTGATTAATTTGCTGAGCAATGCTGATTTATCATACCGG 1536
DB 121 CTTTACTGCTGCTGCTGCTGATTAATTTGCTGAGCAATGCTGATTTATCATACCGG 180
QY 1537 CAAATATGCTGCTGCTGAGCAGTATGCTGATTTATCATACCGGAGAGGCGCA 1596
DB 181 CAAATATGCTGCTGCTGAGCAGTATGCTGATTTATCATACCGGAGAGGCGCA 240

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QY 1597 GCGACTCACCTCTCTCATGTCATCGAAATTTGATTATGACCCGAGCAAAACGA 1656
DB 241 GCGACTCACCTCTCTCATGTCATCGAAATTTGATTATGACCCGAGCAAAACGA 300
QY 1657 TGAACACATTGGGCACTGAGTACCGGTCAAAAGCCATCTTCTCCATGGCAAGACT 1716
DB 301 TGAACACATTGGGCACTGAGTACCGGTCAAAAGCCATCTTCTCCATGGCAAGACT 360
QY 1717 CGACAGGAGTAAACATTAACAGGCTGTGTCAGAGCTTTGCTAAGTGGCTTAAGTGG 1776
DB 361 CGACAGGAGTAAACATTAACAGGCTGTGTCAGAGCTTTGCTAAGTGGCTTAAGTGG 420
QY 1777 GAGAGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1836
DB 421 GAGAGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 1837 GGAAGAGATGCGGAGATAGAGAAGATGATGATGATGATGATGATGATGATGATGATGAT 1896
DB 481 GGAAGAGATGCGGAGATAGAGAAGATGATGATGATGATGATGATGATGATGATGATGAT 540
QY 1897 GCGAGTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1956
DB 541 GCGAGTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 1957 CATGCTGATACCATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2016
DB 601 CATGCTGATACCATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 2017 CGTGTGTAAGGCGCATGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2076
DB 661 CGTGTGTAAGGCGCATGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 2077 TGAAGATCATGAGCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2136
DB 721 TGAAGATCATGAGCAATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 2137 TGTATATCTGATGAGCGCACTTCTTCCAGCGGTGCAAGCAAGCAAGCAAGCAAGCAAG 2196
DB 781 TGTATATCTGATGAGCGCACTTCTTCCAGCGGTGCAAGCAAGCAAGCAAGCAAGCAAG 840
QY 2197 TATATCTGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2256
DB 841 TATATCTGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 2257 GAT 2316
DB 901 GAT 960
QY 2317 GCTGAGAGCAAGGCGCTACCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 2376
DB 961 GCTGAGAGCAAGGCGCTACCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 2377 GACCGTCCGCTTGGCAATTAACCAACGCGATGAGCTTGGCAACTGGGACTGGGTAGAC 2436
DB 1021 GACCGTCCGCTTGGCAATTAACCAACGCGATGAGCTTGGCAACTGGGACTGGGTAGAC 1080
QY 2437 TTGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2496
DB 1081 TTGATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1140
QY 2497 ATAAATATGTCGCGAGCTGAAGCTGTTTATATATATATATATATATATATATATATAT 2556
DB 1141 ATAAATATGTCGCGAGCTGAAGCTGTTTATATATATATATATATATATATATATATAT 1199
QY 2557 TTAATGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 2616
DB 1200 TTAATGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 1259
QY 2617 CTGTCGCTGCAATTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2676
DB 1260 CTGTCGCTGCAATTTCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1319

QY 2677 ATCAATTCCTGTTGACCTGTG 2697
DB 1320 ATCAATTCCTGTTGACCTGTG 1340

RESULT 8
US-09-938-842A-2415
; Sequence 2415, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krebs, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OR INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OR INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDP1300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2415
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2415

Query Match 45.2%; Score 1238.4; DB 9; Length 2430;
Best Local Similarity 70.4%; Pred. No. 0;
Matches 1672; Conservative 0; Mismatches 656; Indels 6; Gaps 1;

QY 18 GCGACGCGCTGAGAGACCTTCCAGCGGCAACGAGCTGTGCTGCTGCTGCTGCTGCTGCT 77
DB 38 GCGATGCGCTGCAAGACACGCTTCCGCTCAGCGCAAGCAAGCTGTGCTGCTGCTGCTGCT 97
QY 78 AGTACGTAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 137
DB 98 GGTATGTGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 157
QY 138 AGGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 191
DB 158 CTGTATCGGAGAGAGATGAGAAACAAAGAGAGTCTGTATGATGATGATGATGATGATGAT 217
QY 192 TCCGCTCCGCGAGAGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
DB 218 TTAATATGCAATGAGAGCTATGATGATGATGATGATGATGATGATGATGATGATGAT 277
QY 252 GCCCGGAGGAGTGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
DB 278 GACCTGTGTTGGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 337
QY 312 CAGCTTCGAGTACCTTCCGCTTCAAGAGAGCTTGTGACGCGCAGCAACATGATCCT 371
DB 338 CAGCTTCGAGTACCTTCCGCTTCAAGAGAGCTTGTGATGAGCTTGAATGATGATGAT 397
QY 372 ACGTTCGAGCTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431
DB 398 TTGTCTTGAAGCTTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 457
QY 432 CATCTATTTGAAAGCGGTGCAAGTCTTCAACGAGCACTTGTCTCAATGATGATGATGAT 491
DB 458 CTTCGATTTGATGAGAGTCAAGTCTTCAATGATGATGATGATGATGATGATGATGATGAT 517
QY 492 AAGAGATGCTTGAAGCGGCTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 551
DB 518 ACAAAGATGCTTGAAGCGGCTGTTGATGATGATGATGATGATGATGATGATGATGATGAT 577
QY 552 TTAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611

Db 578 CGTGTATGTTGATGATTCGGATTCAGAGATATCTAGGCTTCAATCCAGCTTAGTAAAG 637
 Qy 612 CTAGAGAGACCTTGTCAAAAGCTCCCTGCTGACACACCATATCTCAATTTGCTTAAT 671
 Db 638 CAGAAATCATATCTCTAAGCTTTCACAGAAATCCCGTCTCGGAATTCGATAGCCGT 697
 Qy 672 TTCAAGAGGCGGCGCTGAGAAAGGTGGGGTATACAGACAGACATGTTTGGAAATGA 731
 Db 698 TGCAGGAATGAGTTTGAAGAAAGATGGGAGATACCGAGAGAAAGTTCTTGAAATGA 757
 Qy 732 TCCATCTCTCTAGACATCATTCAGGCGCAGACCATCTACCTAGAGAAATTTCTTG 791
 Db 758 TGTATCTCTCTGTATATCTTCAAGCTCCTGATCCTTGCTTGCTTGAAGATTTCTTG 817
 Qy 792 GAGAGATCCCATGATTTTAACTGTTGTGTTGTTTCCCTCATGATCTTTGTTGAG 851
 Db 818 GATGTGACCAATGATTTTCAAGTGTGTGATCTTATCTCAATGATGATTTTGGGGAAG 877
 Qy 852 CTAATGATTTAGGCTTGCAGACACAGAGAGACAGATCGTCTATATATCTGAGACCAAGTCC 911
 Db 878 CCATGTTTATGAGCTTACCTGACATGAGAGAGAGATGTTCTATATCTTGAACCAAGTCC 937
 Qy 912 GTGCACTAGAAATGAGATGTTCTCCGTTTAAAGAAACAGAGGCTGATGTTTCCCA 971
 Db 938 GTGCCCTTGAAGATGAAATGCTGTGAGATTAAGAGACAGGGTTGATATATCACTTA 997
 Qy 972 AGATTTCTATGTTTACTCGGCTGATACAGATGCAAAAGAAATCTATGCAATCAGGCGC 1031
 Db 998 GATTTCTTATGTTGATCTAGGTTGATACCGGATCTAAAGGAACTAGCTGTACAGGCGGT 1057
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 Qy 1092 ATGGGATCTTAAAGAAATGAGATGATCAAGATTTGATGTGTGGCCATATCTGAAATCTTG 1151
 Db 1118 AAGGATCTCTCCGTAAGTGAATTTCAAGATTCGACGATAGGCTTATCTAGAGAACTATG 1177
 Qy 1152 CTGAGATGCTGCTGTAAGATGCTGCTGAATTTCAAGGATCTCCAGATCTTATATG 1211
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 Db 1238 GTACTATATGAGAGAACTTGTGATGCTTATGATGCAATGATGAGATGGGTTGATAC 1297
 Qy 1272 AGTGAACATTTGCTCATGCTCTGAAAGAACTAAGTATCCAGATTCAGACATTTTGA 1331
 Db 1298 AATGTACTATGCAATGCTTGAAGAAACCAAGTATCCAGATTCAGACATTTACTGGA 1357
 Qy 1332 AGAATTCGATGGAAGTACCATTTCTCTGCCAGTTCACTGCTGATATATTTGCTATGA 1391
 Db 1358 AAGACTTCGACAAAGATATCATTTCTCTGATCATCAAGCTGATCTTATGCAATGA 1417
 Qy 1392 AGAATGCTATTTATCATACAGACATNCCAGAAATTTGCTGAGAGAAATATCTG 1451
 Db 1418 ACAAGCGAATTTCAATCATACAGACATNCCAGAAATTCGAGAGAAACGAGACACG 1477
 Qy 1452 TTGAGACATGAGAGATCATACCTTTACTCTGCTGCTGCTGATCCAGATTTGCTATG 1511
 Db 1478 TGGGTAAATGAGAGACACGGGCTTTTACGCTCCGGGACTATATAGATGATACAG 1537
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 Db 1538 GCAATGATGCTTCTGATCCAAAGTTCAATATAGTCTCTCTGAGCTGATATGCTCAT 1597
 Qy 1572 ACTTTCACATACCGAGAGAGCCAGGACTCACTCTCTCAATGATTCGAAAT 1631
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 Qy 1632 TGAATATGACCCGAGAGAAACGATGACATTTGGGCAATCTGATGACCGGCTCAAGC 1691

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 Qy 1812 ATATGATCAACAAATCCAGAGACAGAGAAATGCGAGATAGAGAAATGATGATGAC 1871
 Db 1838 TTGATGTAACAAGTCCAAAGATGAGAAATTCGATGATGAGAAATGATGATACC 1897
 Qy 1872 TCAATGAGCCCAATTTGCTGCGAGTTCGCTGATCTCTGCCAGCAACAGAG 1931
 Db 1898 TTAAGAAATTCAGACTGATGAGAGATTTCTGTGATATCTGTGATGATGAG 1957
 Qy 1932 CCGTAAAGGCGAGCTTATGCTGATACATGCTGATACCATGATGCTTCTGATAGCCGG 1991
 Db 1958 CTGAAATGATGAGCTTTTACCGTATACATGCGAGTACAGAGATGCTTTGCTAGCCTG 2017
 Qy 1992 CTTGTATGAGGCTTCTGCTCACTGCTGTTGAGGCTATGACCTGTGAGCTTCTACTT 2051
 Db 2018 CGTCTACAGGCTTTTGAATTAAGGATGAGAGAGATGATGAGGCTTCCGACTT 2077
 Qy 2052 TCGGAGCGCTCACTGAGGCTCAAGCTGATCATAGAGATGAGGCTTCCGAGCTTCCACA 2111
 Db 2078 TTTGCACTTCTACGAGTGTGCTGACAGAGATCATGAGACAGGCTCTCGGATTTCCACA 2137
 Qy 2112 TTGACCGTATCAACCCGAAACAGGCTTATCTGATGAGGCTTCTTTCAGAGCTGCA 2171
 Db 2138 TGTATCATATCAATCTGAGACAGGCTAATATATGCTGATTTCTTTGAAAGTGTGA 2197
 Qy 2172 AGCAAGCCCAATCACTGCTGATATATCTGAGAGAGGCTGACGCTATATGAGA 2231
 Db 2198 AGCAAGATCCAAACATTTGAGAGAAATGATCAAGGCTGCTCTCAAGGATATACGAA 2257
 Qy 2232 AGTACATGAGAAATATATCTCAGAGAGTGTGATGACATGCGCGGCTTACGCTTCT 2291
 Db 2258 GGTACATGAGAAATATATCTCAGAGAGTGTGATGACATGCTGCTGATATGATGCT 2317
 Qy 2292 GGAATGATGCTGCAAGCTGAGAGGCTGAGAGAGAGGCTGATCTTGAATGTTTACA 2351
 Db 2318 GGAATGATGATGAAATTTGAGAGGCTGATGAGCTCGGCGATATCTTGAATGTTTACA 2377
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 Db 2378 TTCTCAAAATTCGCGACTGTGTGAAAATGTTCC 2411

RESULT 9
 US-09-938-842A-2415
 ; Sequence 2415, Application US/09938842A
 ; Publication No. US20040009476A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227, 866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264, 647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300, 111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2415

LENGTH: 2430
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2415

Query Match 45.2%; Score 1238.4; DB 11; Length 2430;

Best Local Similarity 70.4%; Pred. No. 0;
Matches 1672; Conservative 0; Mismatches 696; Indels 6; Gaps 1;

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QY 18 GCGACCGGCTGAGAGACACCTCCACGGCGCAACCGAAGAGCTGCTGCGCCCTCCGTCGA 77
DB 18 GCGACCGGCTGAGAGACACCTCCACGGCGCAACCGAAGAGCTGCTGCGCCCTCCGTCGA 97
QY 38 GGGAGTCGGGTCACAAACACGCTTCCGCTCACCGCAAGAACTGCTGCTCTTCTCCCA 97
DB 38 GGGAGTCGGGTCACAAACACGCTTCCGCTCACCGCAAGAACTGCTGCTCTTCTCCCA 97
QY 78 AGTACGTACAAAGGGAGAGGACATCTGACGCGCACCAACATCTGACGCGCTGACG 137
DB 78 AGTACGTACAAAGGGAGAGGACATCTGACGCGCACCAACATCTGACGCGCTGACG 157
QY 58 GGTATGTGATCAGGGGAAAGGATTTTCAACACATTAATTAAGACATCGAAT 157
DB 58 GGTATGTGATCAGGGGAAAGGATTTTCAACACATTAATTAAGACATCGAAT 157
QY 138 AGGTCCAGAGGCTCCGGGGCCCGCGC-----CTAGCCAGAGGACCTTCTCGAGTCC 191
DB 138 AGGTCCAGAGGCTCCGGGGCCCGCGC-----CTAGCCAGAGGACCTTCTCGAGTCC 217
QY 158 CTGTATCGGACAGCATGAAACAAAGAAAGTCTCTGATGCTCTTTTGGAGAGATCC 217
DB 158 CTGTATCGGACAGCATGAAACAAAGAAAGTCTCTGATGCTCTTTTGGAGAGATCC 251
QY 132 TCCGCTCCGCGCAGAGGCGATCGTCGTCGCCGCTTGGCCATCGCGTGGCGCCGC 251
DB 132 TCCGCTCCGCGCAGAGGCGATCGTCGTCGCCGCTTGGCCATCGCGTGGCGCCGC 277
QY 218 TTAAATCAGCAATGGAAGCTATAGTTGACCACTTTGTTGCGTTAGCCGTTACACAA 277
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QY 252 GCCCGGAGTTTGGAGATACGTCGCGCTCAACGTTACAGAGCTCAGCGCTGACGACTCA 311
DB 252 GCCCGGAGTTTGGAGATACGTCGCGCTCAACGTTACAGAGCTCAGCGCTGACGACTCA 337
QY 278 GACCTCGTGTGGGAAATATGTTGCTGTTAATGCTTGAAGCTAAGTGTGAACATTTA 337
DB 278 GACCTCGTGTGGGAAATATGTTGCTGTTAATGCTTGAAGCTAAGTGTGAACATTTA 371
QY 312 CAGTCTCGAGTACTCTCCGCTTCAAGAGAGCTTGTGACGCGCAACAAATGATCCCT 371
DB 312 CAGTCTCGAGTACTCTCCGCTTCAAGAGAGCTTGTGACGCGCAACAAATGATCCCT 397
QY 338 CAGTCTCGAGTACTCTCGTTCAAGAAAGAACTCGTGTGATGAGAACTATATGACCCCT 397
DB 338 CAGTCTCGAGTACTCTCGTTCAAGAAAGAACTCGTGTGATGAGAACTATATGACCCCT 431
QY 372 AGCTTCTGAGCTTACTTCCAGCGCTTCAATGCTCAGTCCCAAGCCCAATGCTCAT 431
DB 372 AGCTTCTGAGCTTACTTCCAGCGCTTCAATGCTCAGTCCCAAGCCCAATGCTCAT 457
QY 398 TTTGCTTGAAGCTTATTTGAGCCCTTTAAGCAACAGTGCAGGCTCTTCTGCTTGT 457
DB 398 TTTGCTTGAAGCTTATTTGAGCCCTTTAAGCAACAGTGCAGGCTCTTCTGCTTGT 491
QY 432 CATCATTTGMAAAGGATGTCAGTCTCTCAACGACATCTGCTCAATCATGTTCCGA 491
DB 432 CATCATTTGMAAAGGATGTCAGTCTCTCAACGACATCTGCTCAATCATGTTCCGA 517
QY 458 CTTCATTTGTAATGAGAGCTCGATTTTGAATGCTGATGCTGCTTGTATGTTCCGTA 517
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QY 518 ACAAGATTGCTTGAAGCTCTGCTGATTTCTTAGAGTCAATAGTCAAAAGGTCATC 577
DB 518 ACAAGATTGCTTGAAGCTCTGCTGATTTCTTAGAGTCAATAGTCAAAAGGTCATC 611
QY 552 TTATATGCTTATATGATGAAATCAAAAGCTTGGAGAGCTTCAAGTGTGCTGACCAAG 611
DB 552 TTATATGCTTATATGATGAAATCAAAAGCTTGGAGAGCTTCAAGTGTGCTGACCAAG 637
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QY 612 CTGAGGAGACTGTCAAAGCTCCCTGCTGACACACATCTACCAATTTGCTTAAAT 671
DB 612 CTGAGGAGACTGTCAAAGCTCCCTGCTGACACACATCTACCAATTTGCTTAAAT 697
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DB 698 TCGAAGGATGAGGTTTGGAAAGGATGAGGAGATACCCAGAGGAGTCTTGAATATA 791
QY 732 TCCATCTCCTTTAGACATCTATTCAGGGGCGCAGAACCATCTAACCTTAGAATTTGCG 791
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QY 758 TCCATCTCCTTTAGACATCTATTCAGGGGCGCAGAACCATCTAACCTTAGAATTTGCG 817
DB 758 TCCATCTCCTTTAGACATCTATTCAGGGGCGCAGAACCATCTAACCTTAGAATTTGCG 851
QY 792 GAGAGATCCCATGATTTTAAAGTGTGTGGTATCCCTCATGAGATACTTGTGTAAG 851
DB 792 GAGAGATCCCATGATTTTAAAGTGTGTGGTATCCCTCATGAGATACTTGTGTAAG 877
QY 818 GATATGATCAATATGTTTCAAGGTTGTATCTTATCTCAATGATATTTGGGCAAG 877
DB 818 GATATGATCAATATGTTTCAAGGTTGTATCTTATCTCAATGATATTTGGGCAAG 911
QY 852 CTAAATGATTAAGCTTCCAGACACAGAGGACATGCTCTAATATCTGACCAAGTCC 911
DB 852 CTAAATGATTAAGCTTCCAGACACAGAGGACATGCTCTAATATCTGACCAAGTCC 937
QY 878 CCAATGTTTAAAGCTTACCTGACACAGGAGCAACATGCTTATATTTTGAACCAAGTCC 937
DB 878 CCAATGTTTAAAGCTTACCTGACACAGGAGCAACATGCTTATATTTTGAACCAAGTCC 971
QY 912 GTGACATGAATATGATGATGCTCTCGTTTAAAGAAACAGGAGCTGATGTTCCCA 971
DB 912 GTGACATGAATATGATGATGCTCTCGTTTAAAGAAACAGGAGCTGATGTTCCCA 997
QY 938 GTGACCTTGAAGACTGAATGCTCTGAGAAATTAAGAGACAGGGGTTGATATATACCTA 997
DB 938 GTGACCTTGAAGACTGAATGCTCTGAGAAATTAAGAGACAGGGGTTGATATATACCTA 997
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QY 972 AGATTCTATTGTACTCGGCTGATACAGATGCAAAAAGAAATCATATGCAATCAGCGCC 1031
DB 972 AGATTCTATTGTACTCGGCTGATACAGATGCAAAAAGAAATCATATGCAATCAGCGCC 1057
QY 998 GTATTCTATTGTACTCGGCTGATACAGATGCAAAAAGAAATCATATGCAATCAGCGCC 1057
DB 998 GTATTCTATTGTACTCGGCTGATACAGATGCAAAAAGAAATCATATGCAATCAGCGCC 1091
QY 1032 TTGAGAGATTAATGAGAAACACAGCATCTACTTACATATTCAGAGTCCCTCAGAAATGAA 1091
DB 1032 TTGAGAGATTAATGAGAAACACAGCATCTACTTACATATTCAGAGTCCCTCAGAAATGAA 1117
QY 1058 TAGAGAGGTCAGCGGAAACAGAGCATCTACTTACATATTCAGAGTCCCTCAGAAATGAA 1117
DB 1058 TAGAGAGGTCAGCGGAAACAGAGCATCTACTTACATATTCAGAGTCCCTCAGAAATGAA 1151
QY 1092 ATGAGATCTTAAGAAATGATATCAAGATTTGATGATGAGGCAATATCTGAAACATTTG 1151
DB 1092 ATGAGATCTTAAGAAATGATATCAAGATTTGATGATGAGGCAATATCTGAAACATTTG 1177
QY 1118 AAGGATCTCTCGGTAAGTGAATTTCAAGATTTGAGATGAGATGAGCTTATCAAGAACTAG 1177
DB 1118 AAGGATCTCTCGGTAAGTGAATTTCAAGATTTGAGATGAGATGAGCTTATCAAGAACTAG 1211
QY 1152 CTGAGATCTCTGCTGTAATTTGCTGTAATTTCAAGATTTCTCAAGCTTCAATTTG 1211
DB 1152 CTGAGATCTCTGCTGTAATTTGCTGTAATTTCAAGATTTCTCAAGCTTCAATTTG 1237
QY 1178 CTGAGATCTCTGCTGTAATTTGCTGTAATTTCAAGATTTCTCAAGCTTCAATTTG 1237
DB 1178 CTGAGATCTCTGCTGTAATTTGCTGTAATTTCAAGATTTCTCAAGCTTCAATTTG 1271
QY 1212 GAAATCAAGATGAGAAATCTGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1271
DB 1212 GAAATCAAGATGAGAAATCTGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1297
QY 1238 GTATCTAATGATGAGAAATCTGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1297
DB 1238 GTATCTAATGATGAGAAATCTGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1331
QY 1272 AGTCAACATGCTCATGCTCTGAGAAAGACTAGATTCAGATTCAGATTCAGATTCAGAT 1331
DB 1272 AGTCAACATGCTCATGCTCTGAGAAAGACTAGATTCAGATTCAGATTCAGATTCAGAT 1357
QY 1298 AATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1357
DB 1298 AATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391
QY 1332 AGAATTTGATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391
DB 1332 AGAATTTGATGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
QY 1358 AAGCTCTGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1417
DB 1358 AAGCTCTGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1451
QY 1392 ACAATGCTGATTTTATCAATCAACAGACATCAACAGAAATTTCTGAGAAACAAATATCTG 1451
DB 1392 ACAATGCTGATTTTATCAATCAACAGACATCAACAGAAATTTCTGAGAAACAAATATCTG 1477
QY 1418 ACAAGGCAATTTTATCAATCAACAGACATCAACAGAAATTTCTGAGAAACAAATATCTG 1477
DB 1418 ACAAGGCAATTTTATCAATCAACAGACATCAACAGAAATTTCTGAGAAACAAATATCTG 1511
QY 1452 TTGAGAGATGAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1511
DB 1452 TTGAGAGATGAGAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1537
QY 1478 TGGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1537
DB 1478 TGGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1571
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DB 1538 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1631
QY 1572 ACTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1631
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QY 1692 CCATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1751
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QY 1718 CAATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1777
DB 1718 CAATCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1811
QY 1752 CTTTGTCTAAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1811
DB 1752 CTTTGTCTAAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1837
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DB 1778 TGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1871
QY 1812 ATGATGTCACAGTCCAGAGACAGAGGAGATGCGGAGATGAGAAATCATGATGATGATGAT 1871
DB 1812 ATGATGTCACAGTCCAGAGACAGAGGAGATGCGGAGATGAGAAATCATGATGATGATGAT 1897
QY 1838 TTAGTGTGACAGTCCAGAGACAGAGGAGATGCGGAGATGAGAAATCATGATGATGATGAT 1897
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QY 1872 TCAATCAAGACCAACATGTTGCGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAGAT 1931
DB 1872 TCAATCAAGACCAACATGTTGCGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAGAT 1957
QY 1898 TTAGTGTGACAGTCCAGAGACAGAGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAGAT 1957
DB 1898 TTAGTGTGACAGTCCAGAGACAGAGGAGATGCGGAGATGCGGAGATGCGGAGATGCGGAGAT 1991
QY 1932 CCGGTACAGGAGCTCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1991
DB 1932 CCGGTACAGGAGCTCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2017
QY 1958 CTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2017
DB 1958 CTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
QY 1992 CCTTGTATGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2051
DB 1992 CCTTGTATGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2077
QY 2018 CGTCTTACAGAGGCTTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2077
DB 2018 CGTCTTACAGAGGCTTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 2111
QY 2052 TGGCAGAGCTCATGAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
DB 2052 TGGCAGAGCTCATGAGAGTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2111
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Db 2078 TTGCACTTGTGACGGTGTGTCAGCAGAGATCATGAGCAAGGGCTCTCGGGTTTCCACA 2137
Qy 2122 TTGACCCGTAACACCCCGAAGAGGCTGTATCTGATGCGCACTTCTTGACCGGTGCA 2171
Db 2138 TCGATTCATACCATCTGAGAGACGGGTAACTAATAGCTGATTTCTTTGAAGGTGTA 2197
Qy 2172 AGCAGACCCAGATCAGCTGGGTGAATATCTGAGAGAGGGCTGACAGGCATATAGAGA 2231
Db 2198 AGGAGATCCAAACCATTTGGAGAGAGTTCAGCGCTGCTTCAAGGATATACAAA 2257
Qy 2232 AGTACATGAGAGATATCTACAGAGAGTGTATGACATGCGCGGGTCTACGGTTCT 2291
Db 2258 GTATACATGAGAGATATCTACGAGAGATTGATGACACTAGCTGCTGATAGTTCT 2317
Qy 2292 GGAAGTACGTGTGAGAGCTTGAGAGGCTGAGAGAGAGCGCTACTTGAATGTTTACA 2351
Db 2318 GGAATACGATGAGAAATTTGAGGCTGTAGAGACTCGCGATATCTGAAATGTTTACA 2377
Qy 2352 TACTGAGTCCGCGAGCTGAGAGACCGTGC 2385
Db 2378 TTCTCAATTCGCGACTTGTTGAAAATCTGTTCC 2411

RESULT 10
US-10-217-939-29
; Sequence 29, Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENDORF, VOLKER
; APPLICANT: HAERTEL, HEIKO A.
; APPLICANT: CIRPUS, PETRA
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ. ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ. ID NO 29
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-217-939-29

Query Match 43.2%; Score 1181.2; DB 15; Length 2394;
Best Local Similarity 70.5%; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 164 CTGACCGAGGAGCCCTTCTGAGCTCTCGCTCCGCGAGAGAGGAGATCGTGCCTCG 223
Db 151 CTTAACAAAGTCATTCATGAAAGTCTGAGCTCTGAGAGAGAGCATATGTTGCTT 210
Qy 224 CCGTCTGCGCAATCGGCTGCGCCGCGCGCGAGTTTGGAGTACGTCCGCTCAAC 283
Db 211 CCATTTGTTGCTTGGCTATACGTCCAGACCTGCTGTAGGGAATATGTCGCTGAT 270
Qy 284 GTTACAGAGCTCAGCTGAGAGAGCTCAAGTCTCGAGTACTCTCCGTTCAAGAGAG 343
Db 271 GTGATAGCTGAGCGTGAATCATTTAATCTGTCTCAATATCTTCGTTTAAAGAGAG 330
Qy 344 CTGTGAGAGGAGAGCAGCATGATCCCTAGCTTCTGAGAGCTGACTCGAGCGTTCAAT 403
Db 331 CTGTATATGCGCATGCGCAATGAGATATCTCTTGAATTTGAATTTGAATTTCAAT 390
Qy 404 GTCTAGTCCAGGCGCAATCGGTCAATCATATTGAAAAGGTGTGCAAGTTCTCAAC 463
Db 391 GCAACATTTGCTGCGCCCAATCGTTTATCATTCATTTGGGAATGGGGTTCAGTTCTCAAT 450
Qy 464 CGACACTTGTCTTATCATATGTTCCGCAAGAGGATGCTTGAAGCCCTGTGGATTTTC 523
Db 451 CGTCACTCTCTTCAATATATGTTCTGTAAAGAAAGCAATGAGAGCTTTGCTTGAATTT 510

Qy 524 CTCGTTGGCAACCGGCAAAAGGGCATTTATGATGCTTATGATAGATACAAAGCTTGG 583
Db 511 CTCGCACTCAAAACATGATGCGCTCTATGATGCTGAATGATGATGATGATGATGATG 570
Qy 584 GAGAGCTTCAAGTGTGTGTGACCAAAAGCTGAGAGAGCACTTGTCAAAAGCTCTCTGAC 643
Db 571 CCCATCTTCAAGGAGCTTTTGCAAGAGCAGAGAGATTCCTTTCTAAATCTCTCTGCA 630
Qy 644 ACACATCTCAAAATTTGCTTATTAATTTCAAGTGGGCTTGAGAAAGTGGGT 703
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Qy 704 GATACAGAGACATGTTTGGAAATGATCATCTCTTACAGATCATTTCAAGGCGCA 763
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Qy 764 GACCATCTCACTTGAAGAAATCTTGGAGAGATCCCATGATTTTAAAGTTGTGG 823
Db 751 GATCTCTGTCTTGAAGAGTTTCTGAGAGATTCCTATGATGTTCAATGTTGTGAT 810
Qy 824 GTATCCCTCATGATCTTGTGACAGTATGATTTAGGCTTCCAGACAGAGAGA 883
Db 811 TTGTCTCGCATGTTACTTGTGACAGCATGCTTGGCTGCTGATATCTGTGGA 870
Qy 884 CAGATCGTATATATGAGACCAAGTCCGTGCACTAGAAATGAGATGTTCTCGTTTA 943
Db 871 CAGTTGTCTTACATTTGTATCAAGTATGATGATTTGAAATGATGATGATGATGATG 930
Qy 944 AAGAAACAGAGCTGATGTTTCCCAAGATTTCTCATTTACTCGCTGATACAGAT 1003
Db 931 CAGAGCAAGAGCTGAAAGTATTTCAAAAGTTCTCATTTTAAACAGCTGTAACCCAA 990
Qy 1004 GCAAAAGAAATATGATGATGACGCTTGAAGAAATATGAGAAACAGATCTTAC 1063
Db 991 GCAAAAGAAACAGTCAACCAAGGTTAAAGATGATGATGATGATGATGATGATGATG 1050
Qy 1064 ATATTAGAGTTCCTTCAAGAAATGAAATGAGATCTTAAAGAAATGATATCAAGATTT 1123
Db 1051 ATTCTGAGATATCATTTAGAGCTGAAAGGAAATCTTCCAGAGTGAATCTCAAGTTT 1110
Qy 1124 GATGTGCGCATATCTGAAACATTTGCTGAGAGATGCTGTGTAATTTGCTGTA 1183
Db 1111 GATGTGCGCATATCTGAGAGCTTTGCAAGAGATGATCAATGAAATTTCTCGAG 1170
Qy 1184 TTCAAGTACTCGAGCTTCAATATTTGAAATGAGATGAGAAATCTTGTGCGTCA 1243
Db 1171 TTGAGAGTGTACCAATCTTATATTTGCACTGAGATGAGAAATCTGTGCTTCT 1230
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Db 1351 CAGTCACTGATATATTTGCTATGAGAAAGTGTATTTATCATCATCATCATCATCATCAT 1410
Qy 1424 CAAAGAAATGCTGAGAGCAAAATATCTGTGAGAGATGAGATGATGATGATGATGATGATG 1483
Db 1411 CAAAGAAATGCTGAGAGCAAAATATCTGTGAGAGATGAGATGATGATGATGATGATGATG 1470
Qy 1484 CTGCTGTGTCTGACCGAGTTGTCTGATGGGATGATGATGATGATGATGATGATGATGAT 1543
Db 1471 ATGCTGTGTCTTTCAGAGTTGTGATGAGATGATGATGATGATGATGATGATGATGATGAT 1530
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1591 ACTGCCCTTCAAGTCAATTAAGAACTCCCTTTAGTCCGACAGAAATGATGACAT 1650
1664 ATTGGGCACTGATGATGACCGGTCMAAGCCCATCTCTTCTCATGAGCAAGCTGACAG 1723
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1711 GTGAAGAAATTAACAGGGCTGCTGCAAGCTTTTGTCTAAGTGGCTTAAGTGAAGGCTG 1770
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1964 GATACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2023
1951 GACCAAAAGTGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2010
2024 GAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2083
2011 GAATCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2070
2084 ATGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2143
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2144 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2203
2131 ACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2190
2204 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2263
2191 GAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2250
2264 ATGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2223
2251 CTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2310
2324 AGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2383
2311 ACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2370
2384 CGGCTGCAATTA 2397
2371 CGGCTGCAACAG 2384

RESULT 11
US-10-27-939-27
; Sequence 27, Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENORF, VOLKER
; APPLICANT: HARTDEL, HEIMO A.
; APPLICANT: CIPRUS, PETRA
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-217-939-27
Query Match 42.8%; Score 1172; DB 15; Length 2418;
Best Local Similarity 70.9%; Pred. No. 0;
Matches 1556; Conservative 0; Mismatches 640; Indels 0; Gaps 0;
202 GCAGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 261
213 GCAGAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 272
262 TTGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 321
273 TGGGAGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 332
322 GTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 381
333 ATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 392
382 GCTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 441
393 ACTTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 452
442 AAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501
453 GATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 512
502 CTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 561
513 CATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
562 TAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 621
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622 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 681
633 CTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
682 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 741
693 GAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 752
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753 TCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 812
802 CATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 861
813 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872
862 AGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 921
873 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 932
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933 AAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 992
1042 TATGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1101
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1102 TATGAGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1161
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QY 484 GTTCGGCAACAGGATGCTTGGAGCCCTGATGATTTCTCCGTGGCCACCGGACAA 543
 DB 546 CTTCATGACAGAGAGAGATGATACCTTGTCTCAACTTCTTCCGGCCCAACAATACAA 605
 QY 544 GGGGCAATGTTATGATGCTTAAATGATGAAATACAAAGCTTGGAGGCTTCACTGTGCT 603
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 DB 1026 CAGCGGAGAGATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
 QY 1024 TCAGCGGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
 DB 1086 CAGCGGCTTGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
 QY 1084 AATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
 DB 1146 AACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1205
 QY 1144 AACATTTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
 DB 1206 GACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1265
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 DB 1326 TGTATCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1385
 QY 1324 AATTAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
 DB 1386 CTACTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1445
 QY 1444 AATTAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1503
 DB 1506 GAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1565
 QY 1504 TGTCAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
 DB 1566 TGTCAATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1625
 QY 1564 GTTCATATATCTTCCATACAG 1623

DB 1626 GTTCATATATCTTCCATACAG 1685
 QY 1624 CCAAAATTTGATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 DB 1686 TGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1745
 QY 1684 GTCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
 DB 1746 GAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1805
 QY 1744 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
 DB 1806 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1865
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 DB 1866 CGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
 QY 1864 GCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
 DB 1923 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
 QY 1924 AAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
 DB 1983 GAAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
 QY 1984 AGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
 DB 2043 GAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
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 DB 2103 GTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
 QY 2104 CTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
 DB 2163 CTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
 QY 2164 CGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
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 QY 2344 GTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
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 QY 2404 GC 2405
 DB 2463 GC 2464

RESULT 13
 US-10-425-114-2283
 ; Sequence 2283, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yilun
 ; APPLICANT: Kovalev, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack B.
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

Db	2105	GAAACCGGCTCCGGACAAGCGCAGCTGTACCGCTACATCTGGACACCAAGGGCCGCTTCGT	2164
QY	1984	ACAAGCCGGCCCTTGTATGAAAGCTTCGGCTCTACCCGTGTTGAGGCCATGACTCTGTGGACT	2043
Db	2165	GCAAGCCCTGCTTCTACAGAGGCTTTTCGGACTGACAGTGTGTGAGGCCATGACTTGGCGCT	2224
QY	2044	TCTCACTTCGCGAAGCTCCATGAGAGGTCCAGCTGAGATCATATAGCATGGCGCTTCGGG	2103
Db	2225	GCCCAAGTTTGCACAGCTTACAGCGGCTTCGGCGCGAGATCATGTGACAGCGCGTGTCTGG	2284
QY	2104	CTTCCACATTGACCCCGTACACCCCGAACAAGGCTGTTAATGTGATGGCCGACTTCTTCGA	2163
Db	2285	CTACCAATCATGACCCCTTACCGAGGGCGACAAAGCCCTCGCTGCTCTGTGACATTCCTTGA	2344
QY	2164	CCGGTGGAGAAGAACCCAGTCACTGCGGTGAAATATATCTGGAGCAGGGCTGCAGGCGAT	2223
Db	2345	CAAGTGCAGGCGGACCCGAGCCACTGGAGGAAATCTCCAGGGCGGGCTCCAGCGTAT	2404
QY	2224	AATACGAGAAGTACCATGGAAGATATACAGAGAGTTATGACACTGGCCGGGGTCTTA	2283
Db	2405	CGAGGAGAAGTACCTCTGGAAAGCTCTACTCGGAAGAGCTGATGTACCTTCACCCGCGGTGA	2464
QY	2284	CGGTTTCGGAAGTACGTGTGGAAGCTTCGAGAGGCTTGAGAAGCAAGAGCGTACACTGTGAGAT	2343
Db	2465	CGGGTTCGGAAGTACGTGTGGAAGCTTCGGAAGAGCGGAAGACCCGAGCGTACCTGTGAGAT	2524
QY	2344	GTTCTACACTGTAAGTTCCGCGAGCTGGCGAGAACCGTTCGCGCTTCCAAATTGACCAAC	2403
Db	2525	GCTGTAGCCGCTCAAGTACCGCACCATGTGGCAGACACGTTGCCGCTGGCCGCTGGAGGGAGA	2584
QY	2404	GC 2405	
Db	2585	GC 2586	

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Query Match	42.5%;	Score 1162;	DB 13;	Length 2986;
Best Local Similarity	68.3%;	Pred. No. 0;		
Matches 1641;	Conservative	0;	Mismatches 755;	Indels 6;
				Gaps 2

QY 7 CCACGCGTCCGGGACACCGCGTCGAGGACACCTCCACGCGACCGGACGACGACTCGTCGC 66
Db 28 CCACGCGTCAGGGAGCGCATTTGGGACACTCTCTGCGCACCCCAAGAGCTTGTGCG 247
QY 67 CCTCTGTCGACGATCGTAAACAAGGGAAAGGCACTCTGCGACGCGGACCAATCTCGA 126
Db 248 CGCTTTCAACAAGACTGAATAAACCCTTTGAAAAAGGTAAGCTGCAAGCCCACTGATCTTCG 307
QY 127 GCGCGTCGAC---GAGGTCAGAGGCTCCGAGGAGCCGCGGCTAGACCGAGGAGCACTTCCT 183

D	b	308	CGATTACA	CAAT	TCGAT	CCCTAG	GGCTGA	GGCGGAG	AAGCTCA	AGGATG	ATGCTTT	TA	367			
Q	y	184	CGAGTCT	CCGCT	CCGCGA	GAGAGG	GAATCG	TCTG	CCCGCTG	TCTG	GCACAT	TCGGGT	243			
D	b	368	GGATGTC	CTTGA	GGCACT	CAGGAG	GGGATTC	ATCC	CCCCCA	TGGT	GTAC	TTGCAAT	427			
Q	y	244	GGCGCGG	CGCCG	GGATTT	GGAGTAC	GTCCG	GGTCA	AGTTAC	AGAGCT	CACAGCT	TCGA	303			
D	b	428	CCGCCCT	TAGGCT	GTGTCT	GGAGAT	TTGTGA	GGGGT	CAATG	TCA	GTAG	GTGCTG	487			
Q	y	304	GCAGTCA	CACT	TCGAGTA	CTCCG	CTTCA	GGAAG	AGAGCT	GTTCG	ACGGC	CACACAA	363			
D	b	488	GGAGCTA	GAGAT	CTCAGTA	CTCCG	CACTTCA	AGAA	CAGCTT	GTGAA	AGAGGCC	CCCAA	547			
Q	y	364	TGATCCG	TAAGT	TCGAGCT	TGACCT	CGAG	CGGTT	CAATG	TCACAG	CCCAAG	CCCAAA	423			
D	b	548	CACAACT	TTGTCT	TGAGCT	GGAC	TTTGA	GCACAT	TAAT	TCCTTC	CCCCGCT	CTTC	607			
Q	y	424	TCGTCAT	CATCTA	TTGAAA	CGGTG	GCAGTTC	CTCA	CCGAC	CTTGTCT	CAATCAT	483				
D	b	608	TCGTCAAA	GTCCAT	TGGCAAT	GGCGG	AGATTC	CTCA	CAGGAC	CTGTAT	CAAAAGCT	667				
Q	y	484	GTTCCGA	CAACGG	ATTCCTT	GAGCCCC	CTTGG	ATTTCT	CCGTG	GGCCA	CCGGCA	CAA	543			
D	b	668	CTTCATG	ACAGG	AGACAT	TACCC	TTGCTCA	CTTCT	TCG	CCCA	CAACTAC	AA	727			
Q	y	544	GGGCGAT	GTATTGA	TGCTTAT	TGATG	ATACAA	AGCTT	GGGAG	GGCTT	CATGTGCT	603				
D	b	728	GGGATG	ATCCAT	TGATTTGA	AGAC	AGATCC	GA	GTCTC	GTG	CAAGGTG	CGCT	787			
Q	y	604	GACCAAG	CTGAG	AGACA	CTTGTCA	AAAGCT	CTCTG	CTGAC	ACACAT	TA	CTCA	ATTTC	663		
D	b	788	GAGGAGG	CTGAG	AGAC	CTGTCA	CCCTTCA	AGCTG	ATAC	CCCAT	CTGTG	ATTTCA	847			
Q	y	664	TTATTAAT	TTCAAG	GTGGG	CTCG	AGAAAG	TTGGG	GTATAC	AGAGACA	CAATG	TTT	723			
D	b	848	CCACAGT	TCAG	AGACTT	GTGTG	AGAAAG	GGTTGG	GTATTC	CCGTAA	GGCTG	AC	907			
Q	y	724	GGAAATG	ATCAT	CTCTT	CTAGAC	ATTCAT	TAC	AGGCG	CAGAC	CCCAT	TA	CTT	783		
D	b	908	GGAGACT	ATCA	CCCTCT	CTTG	AGAC	CTCTG	AGAG	CCCA	TATC	GT	CA	CCCT	786AA	967
Q	y	784	ATTCTTG	GGGAG	AGATCCC	CA	TGATTTAA	AGTTGT	GTG	ATTC	CCCTG	CA	TCG	AT	CTT	843
D	b	968	GTTCTTG	AGAC	AGATCCC	CA	TGATTTAA	AGTTGT	GTG	ATTC	CCCTG	CA	TCG	AT	CTT	1027
Q	y	844	TGATCA	ACTAT	GTAT	TAGGCT	CCAG	ACAC	AGAG	AGAC	ATCGT	CTATAT	AT	CTGA	903	
D	b	1028	CGCTACA	CTAT	GTCTT	GGGTTAC	CCGTGA	CACCG	AGGG	CAGG	TTGCT	AT	CTG	AT	CTG	1087
Q	y	904	CCAAGT	CCGTG	CACTAG	AAATG	ATG	ATG	TTCT	CCGTTTAA	AGAA	CA	AGG	CT	GTATG	963
D	b	1088	TCAAATG	CGCCT	ATGAG	AGACGA	ATTC	CTG	TAGATCA	AGCA	GTGTG	AT	CTT	AT	CTG	1147
Q	y	964	TTCCCA	AGAAAT	CTCAT	TTGTA	CTCG	CTATAC	AGAT	TC	CAAA	AGGA	CAT	CA	TATG	1203
D	b	1148	CACGCGG	AGATCT	TAT	TTGTCA	CCAG	TTGCT	CCGTAT	GA	CTGG	CA	CA	CT	GTG	1207
Q	y	1024	TCAGCGG	CTTAG	AGAAAT	TAGTGA	CA	CA	CA	CA	CA	CA	CA	CA	CA	1083
D	b	1208	CCAGGCG	CTTAG	AGAAAT	TAGTGA	CA	CA	CA	CA	CA	CA	CA	CA	CA	1257
Q	y	1084	AAATGAA	ATGGA	ACTTAA	GGAAAT	GA	TA	TA	TA	TA	TA	TA	TA	TA	1143
D	b	1268	AAAGAAA	AGGAA	CTGTTG	CGA	ATGGA	ATCT	CGG	ATTTGA	AGCT	TCG	CCG	TA	CTG	1322
Q	y	1144	AAATTTG	CTAG	AGATG	CTG	GTGA	ATTC	GTG	CTGA	ATTTA	CA	AG	TA	CT	1203
D	b	1328	GACTTAC	CTG	ATG	AGTGA	CGGCA	GAT	TTG	CTG	TA	CA	AG	CT	CA	1387
Q	y	1204</														

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Db 1388 GATCATCGAACTACAGTACGGAACCTTGTGCTGTTGCTGCCCAAGATGGG 1447
Qy 1264 AATTCCCAATGCAACATGCTGCTGCTGGAAGAAAGCTAAGATTCAGATTCAGCAT 1323
Db 1448 TGTACTCAGCTGACACATGCGCCATGCGTGAAGAAACCTAAGATTCAGATTCAGCAT 1507
Qy 1324 AATTGGAAGATTCAGATGAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1383
Db 1508 CTACTGGAAGATTCAGATGAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1567
Qy 1384 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1443
Db 1568 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1627
Qy 1444 AATTCTGTTGACAGATGAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1503
Db 1628 GAGACCGCTGACAGATGAGATGAGATTCAGATTCAGATTCAGATTCAGATTCAGAT 1687
Qy 1504 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1563
Db 1688 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1747
Qy 1564 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1623
Db 1748 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1807
Qy 1624 GGAAGATTTGATTTATGACCGGAGAGAAAGATGAGATTCAGATTCAGATTCAGATTCAGAT 1683
Db 1808 TGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1867
Qy 1684 GGAAGATTTGATTTATGACCGGAGAGAAAGATGAGATTCAGATTCAGATTCAGATTCAGAT 1743
Db 1868 GGAAGATTTGATTTATGACCGGAGAGAAAGATGAGATTCAGATTCAGATTCAGATTCAGAT 1927
Qy 1744 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1803
Db 1928 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1987
Qy 1804 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1863
Db 1988 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2044
Qy 1864 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1923
Db 2048 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2104
Qy 1924 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 1983
Db 2108 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2164
Qy 1984 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2043
Db 2168 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2224
Qy 2044 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2103
Db 2228 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2284
Qy 2104 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2163
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Qy 2164 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2223
Db 2348 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2404
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Db 2408 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2464
Qy 2284 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2343
Db 2468 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2524
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Qy 2344 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2403
Db 2528 GGTCTAAGAACATGCTGATTTTATCATACCAACCAATACCAAGAAATTCCTGGAAGCAA 2584
Qy 2404 GC 2405
Db 2585 GC 2586

RESULT 15
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; Sequence 5310, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Lnu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5310
; LENGTH: 2992
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700451030_FLI
US-10-425-114-5310

Query Match 42.5%; Score 1162; DB 13; Length 2992;
Best Local Similarity 68.3%; Pred. No. 0;
Matches 1641; Conservative 0; Mismatches 755; Indels 6; Gaps 2;

Qy 7 CCAAGCTCCGAGGACCGGCTGAGAGACCTTCACGCGGACCGGACGAGCTGCTGC 66
Db 194 CCAAGCTCCGAGGACCGGCTGAGAGACCTTCACGCGGACCGGACGAGCTGCTGC 253
Qy 67 CCTCTGTCGAAGTACGAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126
Db 254 CCTCTGTCGAAGTACGAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 313
Qy 127 CGCGCTGAC---GAGGTCAAGGAGGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 183
Db 314 CGAGTACCAACCAATGAGATTCCTGAGGCTGAGGCTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAG 373
Qy 184 CGAGTCTCCGCTCCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Db 374 GGAGTCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 433
Qy 244 CGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303
Db 434 CGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 493
Qy 304 GCAAGCTCAAGTCTGAGAGTACCTCCGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
Db 494 GGAAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 553
Qy 364 TGATCCCTAGTCTTCAAGTCTGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
Db 554 CAACCAACCTTGTCTTCAAGTCTGAGAGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 613
Qy 424 TGCTGATCAATCTTGTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 483
Db 614 TGTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673
Qy 484 GTTCGAGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 543
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Db 674 CTTCATGACAAAGAGCATGTACCCCTGCTCAACTTCCTCTGCGCCCAACACTACAA 733
QY 544 GGGGACATGTATGATGCTTAATGATATGATATACAAAGCTTGGGAGAGCTTCAGCTGCT 603
Db 734 GGGGATGACCATGATGTTGAAACAGAAATCCGACATCTCAAGTGTCTGAAAGTGGCT 793
QY 604 GACCAAGCTGAGAGACACTTGTCAAAAGCTCCCTGCTGACACACACTACTCAATTTGC 663
Db 794 GAGGAAGCTGAGAGACACTGTGCAACCTCAAAAGCTGATACCCCAATCTGAAATTTCA 853
QY 664 TATTAATTTCAAGAGTGGGCTGAGAAAGTTGGGGTGTATACAGAGACATTTT 723
Db 854 CCACAGGTTCCAGGAACCTTGGTGTGAGAAAGGTTGGGGTGTATGCTTAAAGGTGCACA 913
QY 724 GGAATGATGCAATCTCTCTGACATCAATCAAGGCGCAGACCCATCACTTACCTTGAAGA 783
Db 914 GAGATATATCACTCTCTCTGACCTCTGAGGCGCCAGATCGTTCAACCTTGAAGA 973
QY 784 ATTCTTGGAGAGATCCCATGATTTTAAAGTTGTGTGTGTATCCCTCATGATATCT 843
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QY 1084 AATATGAAATGGAATCTTAAGAAATGATATCAAGATTTGATGTCATATCTGCA 1143
Db 1274 AATGAAATGGAATCTTAAGAAATGATATCAAGATTTGATGTCATATCTGCA 1333
QY 1144 AATATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1203
Db 1334 GATTAATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1393
QY 1204 CATTAATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1263
Db 1394 GATTAATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1453
QY 1264 AATTAATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1323
Db 1454 TGTTAATGGAATGGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1513
QY 1324 ATTTTGAAGATTTGATGGAAGTACATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1383
Db 1514 CTACTGGAAGATTTGATGGAAGTACATTTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1573
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Db 1574 TGTGATGGAATGGAATGCTTATATCAATCCACACATTCAGAAATTTGCTGGAAGCA 1633
QY 1444 AATATGGAATGGAATGCTTATATCAATCCACACATTCAGAAATTTGCTGGAAGCA 1503
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QY 1564 GTTCATATGCTTCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1623
Db 1754 GTTCATATGCTTCCATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1813

QY 1624 CGAAATTTGATTTATGACCCCGAGCAAAACGATGAAACATTTGAGCATCTGATGACCG 1683
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QY 1684 GTCAAGCCCATCTCTCTTCTCAATGAGCAAGATCTGACAGGCTGAAACATTAACAGGCT 1743
Db 1874 GAAACAGCCCATCTCTCTTCTCAATGAGCAAGATCTGACAGGCTGAAACATTAACAGGCT 1933
QY 1744 GTTCAGCTTTTGTCTAAGTGGCTTACGCTGAGGAGGCTGTAAACCTTGTGCTTGC 1803
Db 1934 GTTGAAGCTTTGTCTAAGTGGCTTACGCTGAGGAGGCTGTAAACCTTGTGCTTGC 1993
QY 1804 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 1863
Db 1994 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 2050
QY 1864 GCATGATCTATCAAGACCCCAACTTGTTCGAGGCTGAGTTCGCTGATCTCTGCGACAC 1923
Db 2051 GTTGAAGCTTTGTCTAAGTGGCTTACGCTGAGGAGGCTGTAAACCTTGTGCTTGC 2110
QY 1924 AAGAGGCGCCGTAAGGAGGCTTATGCTGATGATGATGATGATGATGATGATGATGAT 1983
Db 2111 GAAAGGCGCCGTAAGGAGGCTTATGCTGATGATGATGATGATGATGATGATGATGAT 2170
QY 2044 TCTTACTTTTGGAGCGCTCCATGAGAGTCCAGTGTGATGATGATGATGATGATGATGAT 2103
Db 2231 GCCCAGTTTGGCAGCGCTTACCGCGGTCCGCGGATGATGATGATGATGATGATGATGAT 2290
QY 2104 CTTCGATTTGACCCGTTACCAACCCGACAGGCTGTTAATCTGATGAGCGCACTTCTGCA 2163
Db 2291 CTTCGATTTGACCCGTTACCAACCCGACAGGCTGTTAATCTGATGAGCGCACTTCTGCA 2350
QY 2164 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 2223
Db 2351 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 2410
QY 2224 ATTCGAGAGTACATGAGATTAATCTGAGAGGCTGATGATGATGATGATGATGATGAT 2283
Db 2411 CGAGAGAGTACATGAGATTAATCTGAGAGGCTGATGATGATGATGATGATGATGAT 2470
QY 2284 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 2343
Db 2471 CGGATCAATGATGATCAACAGTCCAAAGACAGGAGGAGATGCGGAGATTAAGAAAT 2530
QY 2344 GTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
Db 2531 GTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2590
QY 2404 GC 2405
Db 2591 GC 2592

Search completed: May 26, 2004, 02:25:54
Job time : 789.142 secs

CC modulating the level of sucrose synthase in a transgenic plant,
CC increasing cellulose production in the stalk tissue of a transgenic
CC plant, or increasing the concentration of cellulose in the tissues of a
CC seed of a transgenic plant. This is particularly useful in plant (e.g.
CC maize or soybean) breeding, especially for e.g. improving stalk length in
CC maize, reducing grain breakage during combining, transport or movement
CC into storage, or improving plant or grain strength. The present sequence
CC is corn Sus3 cDNA

SQ Sequence 2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;

Query Match 100.0%; Score 2737; DB 6; Length 2737;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2737; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCCACGCGTCCGCGACCGCTCGAGACACCTTCACAGCCGACCGCAACGCT 60
DB 1 GTGACCCACGCGTCCGCGACCGCTCGAGACACCTTCACAGCCGACCGCAACGCT 60
QY 61 CGTCCGCCCTCTGCTCCAGTACGTGAACAAAGGGGAAGGGCATCTGACGCCGACCAAT 120
DB 61 CGTCCGCCCTCTGCTCCAGTACGTGAACAAAGGGGAAGGGCATCTGACGCCGACCAAT 120
QY 121 CCTCGACGCGCTCGACGAGGCTCCAGGAGCTCCGCGGCGCGCTAGCCGAGGACCTT 180
DB 121 CCTCGACGCGCTCGACGAGGCTCCAGGAGCTCCGCGGCGCGCTAGCCGAGGACCTT 180
QY 181 CCTCGACGCTCTCCGCTCCGCGGAGAGGAGATCGTCTGCGCCCTTGTGTCGCAATCG 240
DB 181 CCTCGACGCTCTCCGCTCCGCGGAGAGGAGATCGTCTGCGCCCTTGTGTCGCAATCG 240
QY 241 GGTGCGCCCGCGCGCGGAGATTGGAGATACGTCCGCGTCAAGAGCTTCAAGAGCTCA 300
DB 241 GGTGCGCCCGCGCGCGGAGATTGGAGATACGTCCGCGTCAAGAGCTTCAAGAGCTCA 300
QY 301 CGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGAGAGAGCTTGTGACGCGCA 360
DB 301 CGAGCAGCTCACAGTCTCGAGTACCTCGCTTCAAGAGAGAGCTTGTGACGCGCA 360
QY 361 CAATGATCCCTAGCTTCTGAGAGTGAATTCGAGCGGTCGAATGTCGATCCGACGCGCC 420
DB 361 CAATGATCCCTAGCTTCTGAGAGTGAATTCGAGCGGTCGAATGTCGATCCGACGCGCC 420
QY 421 AATTCGCTCATCATCTATTGGAACCGGTGTCAGTTCCTCAACCCACACTTGTCTCAAT 480
DB 421 AATTCGCTCATCATCTATTGGAACCGGTGTCAGTTCCTCAACCCACACTTGTCTCAAT 480
QY 481 CATGTTCCGCAACAGGAGATTGCTTGAAGCCCTGTGGAATTTCTCCGTGCGCACCGGCA 540
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QY 541 CAAGGGGCGATGTTATGATGCTTAATGATTAATCAAGCTTGGGGAGGCTTCAGTCTGT 600
DB 541 CAAGGGGCGATGTTATGATGCTTAATGATTAATCAAGCTTGGGGAGGCTTCAGTCTGT 600
QY 601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGACACACCAATCACTCAATT 660
DB 601 GCTGACCAAGCTGAGAGCACTTGTCAAGCTCCGCTGACACACCAATCACTCAATT 660
QY 661 TGCTTATTAATTTCAAGAGTGGGCGCTGGAAGAGTTGGGTGATACAGAGCAATGT 720
DB 661 TGCTTATTAATTTCAAGAGTGGGCGCTGGAAGAGTTGGGTGATACAGAGCAATGT 720
QY 721 TTGGAATATGATCATCTCTCTTCAAGATATTCAGGCGCCAGACCATCTACCTTGA 780
DB 721 TTGGAATATGATCATCTCTCTTCAAGATATTCAGGCGCCAGACCATCTACCTTGA 780
QY 781 GAAATCTTGGGAGAGATCCCATGATTTTAAAGTGTGTGTGATCCCTCAATGATA 840
DB 781 GAAATCTTGGGAGAGATCCCATGATTTTAAAGTGTGTGTGATCCCTCAATGATA 840
QY 841 CTTTGTCAGCTAATGATTAAGCTTGGCGACACAGAGAGACAGATCGTCTATATCT 900

DB 841 CTTTGTCAGCTAATGATTAAGCTTGGCGACACAGAGAGACAGATCGTCTATATCT 900
QY 901 GGACCAAGCTCCGACATGAAATGAGATGCTTCCGTTTAAAGAACAAAGGCTTGA 960
DB 901 GGACCAAGCTCCGACATGAAATGAGATGCTTCCGTTTAAAGAACAAAGGCTTGA 960
QY 961 TGTTCCTCCAAAGATTCTCATTTGTACTCGCTGATACAGATGCAAAAGGAACTCATG 1020
DB 961 TGTTCCTCCAAAGATTCTCATTTGTACTCGCTGATACAGATGCAAAAGGAACTCATG 1020
QY 1021 CATACGCGGCTTGAGAAATTAAGGAAACACAGCATCTTACATTAATTAAGTCCCT 1080
DB 1021 CATACGCGGCTTGAGAAATTAAGGAAACACAGCATCTTACATTAATTAAGTCCCT 1080
QY 1081 CAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATTTGATGTGCGCATATCT 1140
DB 1081 CAGAAATGAAATGGGATCTTAAGAAATGATATCAAGATTTGATGTGCGCATATCT 1140
QY 1141 GGAAACATTTGCTGAGAGATCTGCTGTGAAATTTGCTGTAATTCAGAGTCTCGAGA 1200
DB 1141 GGAAACATTTGCTGAGAGATCTGCTGTGAAATTTGCTGTAATTCAGAGTCTCGAGA 1200
QY 1201 CTTGATTAATGAAATTAAGATGATGAAATCTTGTGGGCTCATTTGCTATCTTAACAAT 1260
DB 1201 CTTGATTAATGAAATTAAGATGATGAAATCTTGTGGGCTCATTTGCTATCTTAACAAT 1260
QY 1261 GGGAAATTAACCAAGTGCACATGCTCATGCTTGAAGAAAGATTAAGTATCCAGATTCA 1320
DB 1261 GGGAAATTAACCAAGTGCACATGCTCATGCTTGAAGAAAGATTAAGTATCCAGATTCA 1320
QY 1321 CATATTTTGGAGAAATTTGATGATGAAAGTACATTTCTCTGCGCATTTGCTGATAT 1380
DB 1321 CATATTTTGGAGAAATTTGATGATGAAAGTACATTTCTCTGCGCATTTGCTGATAT 1380
QY 1381 AATTCGATGAACATGCTGATTTTATCATACACAGACATCAAGAAATTTGCTGAG 1440
DB 1381 AATTCGATGAACATGCTGATTTTATCATACACAGACATCAAGAAATTTGCTGAG 1440
QY 1441 CAAAAATTAAGTGAACATGATGAGATGATCTGCTTTACTGCTGCTGCTGATACCG 1500
DB 1441 CAAAAATTAAGTGAACATGATGAGATGATCTGCTTTACTGCTGCTGCTGATACCG 1500
QY 1501 AGTTGTCATGAGATGATGATCTTTCGATCCAAAGTTCAATTAATCTCTCTGAGAGCTGA 1560
DB 1501 AGTTGTCATGAGATGATGATCTTTCGATCCAAAGTTCAATTAATCTCTCTGAGAGCTGA 1560
QY 1561 CATGTCATATACCTTCCATACATACCGAGAGGCGCAAGCTACCTCTCTTCAATGTTTC 1620
DB 1561 CATGTCATATACCTTCCATACATACCGAGAGGCGCAAGCTACCTCTCTTCAATGTTTC 1620
QY 1621 AATCGAAATTTTATGATCCCGAGCAAAACGATGAACATTTGGGCAATCTGATGA 1680
DB 1621 AATCGAAATTTTATGATCCCGAGCAAAACGATGAACATTTGGGCAATCTGATGA 1680
QY 1681 CCGGTCAAGCCCATCTCTTCTTCATGAGGAGCTGACAGGCGTGAAGAAATTAACAGG 1740
DB 1681 CCGGTCAAGCCCATCTCTTCTTCATGAGGAGCTGACAGGCGTGAAGAAATTAACAGG 1740
QY 1741 GCTGTGGAAGCTTTTCTAAGTGGCTAAGCTGAGGAGGCTGTGTAACCTTGTCTGT 1800
DB 1741 GCTGTGGAAGCTTTTCTAAGTGGCTAAGCTGAGGAGGCTGTGTAACCTTGTCTGT 1800
QY 1801 TGCCGGTACATGATGTCACAAAGTCCAGAGCAAGAGTTCGCGGAGTTCGATCTCTGCGCA 1860
DB 1801 TGCCGGTACATGATGTCACAAAGTCCAGAGCAAGAGTTCGCGGAGTTCGATCTCTGCGCA 1860
QY 1861 GATGATGATGATCTTCAAGAGCCCACTTGTGGGAGATTTCCGCTGATCTCTGCGCA 1920
DB 1861 GATGATGATGATCTTCAAGAGCCCACTTGTGGGAGATTTCCGCTGATCTCTGCGCA 1920
QY 1921 GACAAACAGGCGCGGTAAACGCGAGCTCTATCGCTACATCGCTGATVACCATGCTGCTT 1980
DB 1921 GACAAACAGGCGCGGTAAACGCGAGCTCTATCGCTACATCGCTGATVACCATGCTGCTT 1980

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QY 1981 CGTACAGCCGCGCTTGTATGAAGCGTTCGCTCAGCCGCTGTTAGAGCCATGACCTGGG 2040
Db 1981 CGTACAGCCGCGCTTGTATGAAGCGTTCGCTCAGCCGCTGTTAGAGCCATGACCTGGG 2040
QY 2041 GCTTCTACTCTTCCGCGAGCTCCATGAGAGTCCAGCTGAGATCATAGAGCATGAGCTGCTC 2100
Db 2041 GCTTCTACTCTTCCGCGAGCTCCATGAGAGTCCAGCTGAGATCATAGAGCATGAGCTGCTC 2100
QY 2101 GGGCTTCCACATTGACCCGTTACACCCCGAAGAGGCTTTATCTGATGCGCGACTTCTT 2160
Db 2101 GGGCTTCCACATTGACCCGTTACACCCCGAAGAGGCTTTATCTGATGCGCGACTTCTT 2160
QY 2161 CGACCGGTGCAAGAGAGACCCAGATCACTGGGTGAAATATCTGAGAGCGAGGCTTGCACG 2220
Db 2161 CGACCGGTGCAAGAGAGACCCAGATCACTGGGTGAAATATCTGAGAGCGAGGCTTGCACG 2220
QY 2221 CATATACGAGAGATACATGAGAGATATATCTCAGAGAGGTTGATGACATCGCCGGGGT 2280
Db 2221 CATATACGAGAGATACATGAGAGATATATCTCAGAGAGGTTGATGACATCGCCGGGGT 2280
QY 2281 CTACGGTTTCTGGAAGTACGTGTGAAAGCTGGAAGCTGGAAGCGGCTTACTTGA 2340
Db 2281 CTACGGTTTCTGGAAGTACGTGTGAAAGCTGGAAGCTGGAAGCGGCTTACTTGA 2340
QY 2341 GATGTTCTACATACCTGAAAGTCCGCGAGCTGCGAGAGCGTGCCTTGCATTTGACCA 2400
Db 2341 GATGTTCTACATACCTGAAAGTCCGCGAGCTGCGAGAGCGTGCCTTGCATTTGACCA 2400
QY 2401 ACCGCACTAGCTTCGCGAGCTGCGAGCTGCGAGAGCTTGTGACAACTGAACTGAAAG 2460
Db 2401 ACCGCACTAGCTTCGCGAGCTGCGAGCTGCGAGAGCTTGTGACAACTGAACTGAAAG 2460
QY 2461 GACCTTCACTATTTAGCCGCGGAGAGCGTGAAGCATTAATGTGCGGAGCTGAACTG 2520
Db 2461 GACCTTCACTATTTAGCCGCGGAGAGCGTGAAGCATTAATGTGCGGAGCTGAACTG 2520
QY 2521 GTTTTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
Db 2521 GTTTTATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2580
QY 2581 TTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
Db 2581 TTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2640
QY 2641 GCAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
Db 2641 GCAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700
QY 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737
Db 2701 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2737

RESULT 2
AAD45856
ID AAD45856 standard; DNA; 2757 BP.
AC AAD45856;
XX 29-AUG-2003 (revised)
DT 27-DEC-2002 (first entry)
DE Corn Sus3-Sorghum EST chimeric DNA.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; Sus3; chimeric; gene; ds.
XX
XX Zea mays.
OS Sorghum propinquum.
OS Chimeric.
XX

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FH Key Location/Qualifiers
FT CDS 1..2430
FT /tag= a
FT /product= "Corn Sus3-Sorghum EST chimeric protein"
FT misc_feature 1..39
FT /tag= b
FT /note= "Sorghum propinquum EST DNA"
FT misc_feature 40..2757
FT /tag= c
FT /note= "Corn Sus3 DNA"
XX
XX WC020267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhugga KS, Helentjaris TG, Niu X;
XX
XX WPI; 2002-691625/74.
XX
XX P-PSDB; AAE28502.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Claim 1; Page 116-119; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX CC maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is Corn Sus3-Sorghum EST chimeric DNA. (Updated on 29-AUG-2003 to
XX standardise OS field)
XX
XX SQ Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;
XX
XX Query Match 99.2%; Score 2714; DB 6; Length 2757;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 2717; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 16 CGGCGACCGCGCTCGAGAGACATCTTCAGCGGACCGGACCAAGCTGTCCTCTCTG 75
Db 16 CGGCGACCGCGCTCGAGAGACATCTTCAGCGGACCGGACCAAGCTGTCCTCTCTG 75
QY 36 CGGAGCCGCGCTCGAGAGACATCTTCAGCGGACCGGACCAAGCTGTCCTCTCTG 95
Db 36 CGGAGCCGCGCTCGAGAGACATCTTCAGCGGACCGGACCAAGCTGTCCTCTCTG 95
QY 76 CAAGTACGTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
Db 76 CAAGTACGTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
QY 96 CAAGTACGTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 155
Db 96 CAAGTACGTAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 155
QY 136 CGAGTCCAGAGGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
Db 136 CGAGTCCAGAGGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
QY 156 CGAGTCCAGAGGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 215
Db 156 CGAGTCCAGAGGCTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 215
QY 196 CTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
Db 196 CTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
QY 216 CTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 275
Db 216 CTCCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 275
QY 256 GGAAGTTGGAGAGTACCTCCGCTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAG 315
Db 256 GGAAGTTGGAGAGTACCTCCGCTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAG 315
QY 276 GGAAGTTGGAGAGTACCTCCGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 335
Db 276 GGAAGTTGGAGAGTACCTCCGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 335
QY 316 CTGAGATACCTCCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375

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Db 336 CTGGAGTACCTCCGCTTCAAGAGSAGCTTGTGACGGCCAGACAAATGATCCCTACGT 395
QY 376 TCTGAGCTGACTTGGAGCCGTTCAATGTCTCAGTCCCAAGCCAAATGCTCATC 435
Db 396 TCTCGAGCTGACTTGGAGCCGTTCAATGTCTCAGTCCCAAGCCAAATGCTCATC 455
QY 436 TATGGAAAGGCTGTGAGTCTCTCAACGCACTTGTCTCAATATATGTCGGAACG 495
Db 456 TATGGAAAGGCTGTGAGTCTCTCAACGCACTTGTCTCAATATATGTCGGAACG 515
QY 496 GATGCTTGAAGCCCTGTTGAGATTCTCCGCTGGCCAGCGGCAAGAGGAGATGAT 555
Db 516 GATGCTTGAAGCCCTGTTGAGATTCTCCGCTGGCCAGCGGCAAGAGGAGATGAT 575
QY 556 GATGCTTGAAGATTAGATACAAAGCTTGGGAGGCTTCACTGTGTGCTGCAAGAGCTGA 615
Db 576 GATGCTTGAAGATTAGATACAAAGCTTGGGAGGCTTCACTGTGTGCTGCAAGAGCTGA 635
QY 616 GAGACACTTGTCAAGCTCCCTGCTGACACACCATACTCAATTTGCTTATTAATTCA 675
Db 636 GAGACACTTGTCAAGCTCCCTGCTGACACACCATACTCAATTTGCTTATTAATTCA 695
QY 676 AGAGTGGGCTGTGAGAGGTTGGGGTGAATACAGACAGACATGTTTGGAAATGATCA 735
Db 696 AGAGTGGGCTGTGAGAGGTTGGGGTGAATACAGACAGACATGTTTGGAAATGATCA 755
QY 736 TCTCTTTTGAACATCTTCAAGGCGCAGACCCATCTACCTTGAAGAAATTTCTGGGAG 795
Db 756 TCTCTTTTGAACATCTTCAAGGCGCAGACCCATCTACCTTGAAGAAATTTCTGGGAG 815
QY 796 GATCCCATGATTTTAAAGCTGTGTGTGTATCCCTCATGAGATCTTGGTCAAGCTAA 855
Db 816 GATCCCATGATTTTAAAGCTGTGTGTGTATCCCTCATGAGATCTTGGTCAAGCTAA 875
QY 856 TGTATTAGGCTTGCAGACACAGAGGACAGATGCTATATATCTGACCAAGTCCGTGC 915
Db 876 TGTATTAGGCTTGCAGACACAGAGGACAGATGCTATATATCTGACCAAGTCCGTGC 935
QY 916 ACTTGAAGAAATGAGATGCTTCCGTTTAAAGAAACAAAGGCTTGAATTTTCCCAAGAT 975
Db 936 ACTTGAAGAAATGAGATGCTTCCGTTTAAAGAAACAAAGGCTTGAATTTTCCCAAGAT 995
QY 976 TCTCATATGTTACTGGGCTGATACAGAGATGCAAAAGGAAATCATGCAATGACGGGCTTGA 1035
Db 996 TCTCATATGTTACTGGGCTGATACAGAGATGCAAAAGGAAATCATGCAATGACGGGCTTGA 1055
QY 1036 GAGAAATAGTGAACACAGCATACTTACATATTAAGAGTTCCTTCAGAAATGAAATGG 1095
Db 1056 GAGAAATAGTGAACACAGCATACTTACATATTAAGAGTTCCTTCAGAAATGAAATGG 1115
QY 1096 GATATCTTAAAGAAATGAGATGATCAAGATTTGATGTGTGSCATATCTGGAACATTTGCTGA 1155
Db 1116 GATATCTTAAAGAAATGAGATGATCAAGATTTGATGTGTGSCATATCTGGAACATTTGCTGA 1175
QY 1156 GGAATGCTGCTGTAATTTGCTGATTAACAAGTATCTCAAGCTTCAAGATTTGCAAGATTTG 1215
Db 1176 GGAATGCTGCTGTAATTTGCTGATTAACAAGTATCTCAAGCTTCAAGATTTGCAAGATTTG 1235
QY 1216 CTAACAGTATGGAATCTTGTGAGGCTCATGTGCTATCTTAACAAGTGGGAATTAACCACTG 1275
Db 1236 CTAACAGTATGGAATCTTGTGAGGCTCATGTGCTATCTTAACAAGTGGGAATTAACCACTG 1295
QY 1276 CAACATGCTCATGCTCTGGAAGAAAGCTTAAGTATCAAGATTTCAAGCAATTTTGGAAAGA 1335
Db 1296 CAACATGCTCATGCTCTGGAAGAAAGCTTAAGTATCAAGATTTCAAGCAATTTTGGAAAGA 1355
QY 1336 TTTGATGAGAGAGTACATTTCTCTGCAAGTTCATCTGATATATATTTGCTATGAACA 1395
Db 1356 TTTGATGAGAGAGTACATTTCTCTGCAAGTTCATCTGATATATATTTGCTATGAACA 1415
QY 1396 TGTGATTTTATCATCACAGACATACCAAGAAATTTGCTGAGCAAAATATCTGTTGG 1455

Db 1416 TGTGATTTTATCATCACAGACATACCAAGAAATTTGCTGAGCAAAATATCTGTTGG 1475
QY 1456 ACAGTATGAGAGTACATCTGCTTTTACTGCTGCTGTGCTGACAGATTTTCCATGGAT 1515
Db 1476 ACAGTATGAGAGTACATCTGCTTTTACTGCTGCTGTGCTGACAGATTTTCCATGGAT 1535
QY 1516 CGATGCTTCCATCCAAAGTTCATATATAGTCTCTCTCTGAGCTGACATGTCATATATCTT 1575
Db 1536 CGATGCTTCCATCCAAAGTTCATATATAGTCTCTCTCTGAGCTGACATGTCATATATCTT 1595
QY 1576 TCCACATCCGAGAGAGGCTCAAGGCTACCTCTCTCATGTTCAATCCAAATTTGAT 1635
Db 1596 TCCACATCCGAGAGAGGCTCAAGGCTACCTCTCTCATGTTCAATCCAAATTTGAT 1655
QY 1636 TTTATGACCCGAGACAAAAGATGAACAATTTGGGCACTGAGATGACCGGTCAAGCCAT 1695
Db 1656 TTTATGACCCGAGAGAAAAGATGAACAATTTGGGCACTGAGATGACCGGTCAAGCCAT 1715
QY 1696 CCTCTTCTCCATGGCAAGACTGACAGAGGTGAAGAAATTAACAGGCTGTGAGCTTT 1755
Db 1716 CCTCTTCTCCATGGCAAGACTGACAGAGGTGAAGAAATTAACAGGCTGTGAGCTTT 1775
QY 1756 TGTAACTGCTTAACTGAGGAGCTGTGTAACCTTGTGTGCTGCTGCTGCTGCTGCTGCT 1815
Db 1776 TGTAACTGCTTAACTGAGGAGCTGTGTAACCTTGTGTGCTGCTGCTGCTGCTGCTGCT 1835
QY 1816 TGTCAACAAGTCCAAAGACAGGAGATGCGAGATGAGAAATGATGAATGATCAAT 1875
Db 1836 TGTCAACAAGTCCAAAGACAGGAGATGCGAGATGAGAAATGATGAATGATCAAT 1895
QY 1876 CAAGACCCCAACTTGTTCGGGAGTTCCTGCTGATCTCTCCCAAGACAAACAGGCCCCG 1935
Db 1896 CAAGACCCCAACTTGTTCGGGAGTTCCTGCTGATCTCTCCCAAGACAAACAGGCCCCG 1955
QY 1936 TAAAGGAGAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1995
Db 1956 TAAAGGAGAGCTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2015
QY 1996 GTATGAAGCTTTCGATCTCAACCGTGTGAGAGCCATGACCTGTGCTCTCTCTCTCTCT 2055
Db 2016 GTATGAAGCTTTCGATCTCAACCGTGTGAGAGCCATGACCTGTGCTCTCTCTCTCTCT 2075
QY 2056 GAGCTCCATGAGAGTCCAGCTGAGATCATGAGATGAGATGAGATGAGATGAGATGAGAT 2115
Db 2076 GAGCTCCATGAGAGTCCAGCTGAGATCATGAGATGAGATGAGATGAGATGAGATGAGAT 2135
QY 2116 CCGTATCAACCCCGAAGAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 2175
Db 2136 CCGTATCAACCCCGAAGAGCTTAACTGATGATGATGATGATGATGATGATGATGATGAT 2195
QY 2176 AGACCCAGATCACTGAGTGAATATATCTGAGCAGGCTGACAGGCTATATGAGAGTGA 2235
Db 2196 AGACCCAGATCACTGAGTGAATATATCTGAGCAGGCTGACAGGCTATATGAGAGTGA 2255
QY 2236 CACATGAGAAATATATCTGAGAGGTTGATGACTGCTCGGAGTCTACAGGTTTCTGGA 2295
Db 2256 CACATGAGAAATATATCTGAGAGGTTGATGACTGCTCGGAGTCTACAGGTTTCTGGA 2315
QY 2296 GTAGCTGCTGAAGCTTGAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2355
Db 2316 GTAGCTGCTGAAGCTTGAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 2375
QY 2356 GAACTTCCGAGAGCTGAGAGAGCTGCTGCTGCAATTTGACAAATGACCAACCGCATGCTG 2415
Db 2376 GAACTTCCGAGAGCTGAGAGAGCTGCTGCTGCAATTTGACAAATGACCAACCGCATGCTG 2435
QY 2416 GCAACTGCTGAGCTGCTGAGCACTTGTGTAACAAGCTTAAACCTGTAAGAACTTGAATAT 2475
Db 2436 GCAACTGCTGAGCTGCTGAGCACTTGTGTAACAAGCTTAAACCTGTAAGAACTTGAATAT 2495
QY 2476 AGGCGCGGAGAGCGGTAGCAATTAATATGCTGAGAGCTGATGATGATGATGATGATGAT 2535
Db 2496 AGGCGCGGAGAGCGGTAGCAATTAATATGCTGAGAGCTGATGATGATGATGATGATGAT 2555

QY	2536	CATATATGCGAGTATTAACAAAATACTCTAAGGACAGTGGGTGCGTGTGGTCTGAC	2593
Db	2556	CAATATGCGAGTATTAACAAAATACTCTAAGGACAGTGGGTGCGTGTGGTCTGAC	2615
QY	2596	TGTTACTGATATTAATGTCAGACTCTGCGCTGCATATTTCTTGCTGGCAGCCGAGGAC	2655
Db	2616	TGTTACTGATATTAATGTCAGACTCTGCGCTGCATATTTCTTGCTGGCAGCCGAGGAC	2675
QY	2656	TGCTGGAAGTCTGATTAATAATACATATATTCGTGTGACCTGTGAAAAA	2715
Db	2676	TGCTGGAAGTCTGATTAATAATACATATATTCGTGTGACCTGTGAAAAA	2735
QY	2716	AAAAAAAAAAAAAGGCGCGCGCGC	2737
Db	2736	AAAAAAAAAAAAAGGCGCGCGCGC	2757
RESULT 3			
ID	ADA69581	standard; DNA; 2412 BP.	
AC	ADA69581;		
XX	20-NOV-2003	(first entry)	
DT			
XX	Rice gene, SEQ ID 2904.		
DE			
XX	Plant; bacterial infection; fungal infection; viral infection; rice;		
KM	gene; ds.		
XX			
OS	Oryza sativa.		
XX			
XX	W02003000898-R1.		
PN			
XX	03-JAN-2003.		
PD			
XX	22-JUN-2001; 2001MO-IB001105.		
PF			
XX	22-JUN-2001; 2001MO-IB001105.		
PR			
XX	(SYGN) STINGENTA PARTICIPATIONS AG.		
PA			
XX	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,		
PI	Kategirdi F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;		
PI	WPI; 2003-175290/17.		
DR			
XX	Identifying at least one gene involved in plant resistance or response to		
XX	pathogenic infection for conferring resistance or tolerance to a plant to		
PT	bacterial, fungal or viral infection by determining or detecting plant		
PT	gene expression.		
XX			
PS	Claim 6; SEQ ID NO 2904; 899bp; English.		
XX			
CC	The present invention relates to a method (M1) for identifying genes		
CC	involved in plant resistance or response to pathogenic infection. M1		
CC	comprises identifying a gene whose expression is significantly altered in		
CC	the incompatible interaction of plant gene expression relative to		
CC	expression of the gene in an uninfected plant, in a mutant plant that		
CC	does not express a gene associated with response to pathogenic infection,		
CC	or in a corresponding incompatible or compatible interaction. (M1) is		
CC	useful for conferring resistance to resistance or tolerance to a plant to		
CC	bacterial, fungal or viral infection. The present sequence was used to		
CC	illustrate the invention.		
XX			
SQ	Sequence 2412 BP; 633 A; 573 C; 599 G; 600 T; 0 U; 7 Other;		
Query Match			
Best Local Similarity 84.9%; Pred. No. 0;			
Matches 2033; Conservative 6; Mismatches 334; Indels 22; Gaps 3			
16 CGCGGACGCGGTGAGAGACACCTTCACGCGGACCGGACGAGCTGTGCGCCTCTGTGC 75			

Db	36	CCGCGACCGCGGTGAGAGAACCTCTCCAGGCCAACCGCAACAGAGCTGTGCGCCCTCTCTCTC	95
QY	76	CAAGTACGTAAACAAGGGGAAGGGCACTCTGCAAGCCGCAACAATCTTGAAGCGCTGCA	135
Db	96	CAAGTACGTAGCCAGAGGGGAAGGGGATCTTGCAGCGCGCAACAATCTTCCAGAACGCTGCA	155
QY	136	CGAGCTCAGAGGCTCCCGGGGGCCCGCGCGTACCCAGAGGAGCCCTTCTCTGAGTCCCTCG	195
Db	156	CGAGGTCCAGAGCTCCGGCGGCGCGCCCTCTGTGAGGGCCCTTCTTGAAGTCTCCG	215
QY	196	CTCCGCGCAGAGAGCGCATGCTGTGCGCGCGCTTCCGCGCATTCGCGAGTCCGCGCC	255
Db	216	CTTCCGCCAGAGGCGCATGCTGTGCGCGCGCTTCCGCGCATTCGCGAGTCCGCGCGCGC	275
QY	256	GGGAGTTTGGAGTACGTCGCGCTCAAGCTTCAAGAGCTCAAGGTGAGCAGCTCAAGT	315
Db	276	AGGGGTGTGGAGATACGTCGCGGTGAACGTCAGAGCTCAAGGTGAGCAGCTCAAGT	335
QY	316	CTCGAGTACCTCCCGCTTCAAGAGAGAGCTTGTGACGCGCAGCAAAATGATCCCAAGT	375
Db	336	GTCCGAGTACCTCCCGCTTCAAGAGAGAGCTGTGACGCGCAGCAAAATGATCCCAAGT	395
QY	376	TCTGAGCTTGACCTTCGAGCGGTTCAATGTCCTAGATCCCAAGCGCCAAATCGGTCAATC	435
Db	396	ACTTGAAGCTTATTTTGAAGCATTCATGCTCGGTTCCAGCGCCAAATCGGTCAATC	455
QY	436	TATTGAAACGGGTGTCAGTTCCTCAACGCACTTGTCTCAATATGTTCCGCAACG	495
Db	456	AATTGAAATGGCGTGCAGTTTCTCAACAAGGCACTTGTCTTCATGATGTTCCGGAACA	515
QY	496	GGATTGCTTGAAGTCCCTGTTGATTTCTCCGCTGGCCACCGGCACAAGGGAGGATGTAT	555
Db	516	GGATTGCTTGAAGTCCCTGTTGATTTCTCCGCTGGCCACCGGCACAAGGGAGGATGTAT	571
QY	556	GATGCTTAATGATGAAATACAAAGCTTGGGAGGCTTC-AGTGTGTC- TGACCAAGCT	613
Db	572	-----ATACAGATCTGGGAAACCTTCAAGTCTGTGCTTGAACAAAGCT	615
QY	614	GAGGAGCACTTGTCAAAAGCTCCCTGCTGACACACATCTCAACAATTTGCTTAAATTT	673
Db	616	GAGGAGCACTTGTCAAAAGCTCCCTGCTGACACACATCTCAACAATTTGCTTAAATTT	675
QY	674	CAAGATGTTGGGCTCTGAGAAAGGTTGGGGGTATACAGCAGAGCAATGTTTGGAAATGTC	733
Db	676	CAAGATGTTGGGCTCTGAGAAAGGTTGGGGGTATACAGCAGAGCAATGTTTGGAAATGTC	735
QY	734	CATCTCCCTTACACATCATTCAGAGGCCAGACCACATCTACCTTACAGAAATTTCTTGGG	793
Db	736	CATCTCCCTTCTGAGATGTGCTTCAAGCGCTGATTCATCTACTTGAAGAGTCTTGGGA	795
QY	794	AGGATCCCATGATTTTAAACGTTGTGTGGTATCCCTCATGATATCTTTGCTGAAGCT	853
Db	796	AGGATCCCATGATTTTAAACGTTGTGTGGTATCCCTCATGATATTTTGGCAAGCC	855
QY	854	AATGATTAATAGCTTCCAGACACACAGAGGACAGATCCCTATATACAGGACCAAGTCGT	913
Db	856	AATGATTAATAGCTTCCAGACACACAGAGGACAGATCCCTATATACAGGACCAAGTCGT	915
QY	914	GCACTAGAAATAGAGATGTTCTCCGTTTAAAGAAACAAGGACTTGAATTTTCCCAAG	973
Db	916	GCACTAGAAATAGAGATGTTCTTAAAGTAAAGAAACAAGGACTTGAATTTTCCCAAG	975
QY	974	ATTTCATTTGTTACTCGGCTGATACAGATSCAAAGAGAACATCATGCAATCAGCGCTT	1033
Db	976	ATTTCATTTGTTACTCGGCTGATACAGATSCAAAGAGAACATCATGCAATCAGCGCTT	1035
QY	1034	GAGAGATTAATGAGAACACAGATCTTCAATATTAAGAGTCCCTTCAAGAAATGAAAT	10933
Db	1036	GAGAGATTAATGAGAACACAGATCTTCAATATTAAGAGTCCCTTCAAGAAATGAAAT	10935
QY	1094	GGGATTAATAAGATGATACAGATTTGATGTGGGCAATCTTGAAACAATTTGCT	1153

QY 78 AGTACGTGAACAAGGAGAGGCACTCTGAGCCGACCAATCTCTGACGCGCTCGAGC 137
DB 98 GGTATGTGGATCGAGGGAAAAGGATTTCTTAACACCACTAACTTAATGAGAACTCGAAT 157
QY 138 AGGTCCAGAGGCTCCGGGGGCGCGCG-----CTAGCCGAGGAGCCCTTCTCTGACGCTC 191
DB 158 CTGTATCGGAGAGATGAAACMAAGAGAGTCTCTGATGGTCTTTGGAGAGATTC 217
QY 192 TCCGCTCCGCGAGAGGCGATGCTGCTGCGCCGCTTGGCCATGCGCGTGGCCCGC 251
DB 218 TTAAATGAGAAATGAAAGCTAATAGTTTACACCTTTTGTGGCTTAGCGTTAGACAA 277
QY 252 GCGCGGAGTTTGGAGATGATCGCGCTCAAGCTTCAAGCTCAAGCTCGAGAGCTCA 311
DB 278 GACCTGCTTTGGAGATATGCTGTATATGCTTCAAGCTTCAAGCTTCAAGCTTCA 337
QY 312 CAGTCTCGAGATCTCCGCTTCAAGAGAGAGCTTGTGAGCGCCAGCAATATGCTCT 371
DB 338 CAGTCTCGAGATCTCCGCTTCAAGAGAGAGCTTGTGAGCGCTTCAAGCTTCAAGCTT 397
QY 372 AGCTTCCGAGCTTGAATCGAGCGCTTCAATGCTCAAGCTTCAAGCTTCAAGCTTCA 431
DB 398 TTGTCTTGAAGCTTGAATCGAGCGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 457
QY 432 CATCTATGAGAAAGGCTGAGCTTCTCAAGCGACATCTGCTCAATGATGTTCCGCA 491
DB 458 CTTCGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 517
QY 492 ACAAGGATGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 551
DB 518 ACAAGGATGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 577
QY 552 TTATGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 611
DB 578 CTTGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 637
QY 612 CTGAGAGCACTTGTCAAGCTTCTCTGAGCAACATCTCAATCTTCTTGAAT 671
DB 638 CAGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 697
QY 672 TTCAAGAGTGGGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 731
DB 698 TGCAGAGATGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 757
QY 732 TCCATCTCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 791
DB 758 TGCATCTCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 817
QY 792 GAGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 851
DB 818 GATGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 877
QY 852 CTATGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 911
DB 878 CCAATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 937
QY 912 GTGACATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 971
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QY 972 AGATTCATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1031
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QY 1032 TTGAGAGATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1091
DB 1058 TAGAGAGATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1117
QY 1092 ATGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1151
DB 1118 AGGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1177
QY 1152 CTGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1211

DB 1178 CTGAGATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1237
QY 1212 GAAATCAAGTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1271
DB 1238 GTATCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1297
QY 1272 AGTCAATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 1331
DB 1298 ATGTCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1357
QY 1332 AGATTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1391
DB 1358 AGATTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1417
QY 1392 ACAATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1451
DB 1418 ACAAGAGATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1477
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QY 1512 GATTCATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 1571
DB 1538 GATTCATGCTTGAATGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 1597
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QY 1752 CTTTTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1811
DB 1778 TGATTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1837
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QY 1872 TCATTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1931
DB 1898 TTATTCATGAGAAAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1957
QY 1932 CCGGTAAGAGAGATGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 1991
DB 1958 CTGAAATGAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 2017
QY 1992 CTTGATGAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 2051
DB 2018 CGTTTCATGAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2077
QY 2052 TCGAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2111
DB 2078 TTGCACTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2137
QY 2112 TTGACCGTACCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2171
DB 2138 TCGATTCATGAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTT 2197
QY 2172 AGCAAGCCAGATCACTGAGTGAATATATCTGAGAGAGGCTGAGAGCCATATAGAGA 2231
DB 2198 AGGAGATCCAAACATGAGAGAGATATAGAGAGCTGCTCCAAAGATATAGAGAA 2257
QY 2232 AGTACATGAGAGATATCTGAGAGAGATATAGAGAGCTGCTCCAAAGATATAGAGAA 2291

DB 2258 GGTACACATGGAGATATATCTCGAGAGATTGATGACACTAGCTGGTGTGATGCTTCT 2317
 QY 2292 GGAATGATGCTGTCAGAGCTCGAGAGGCTGAGACGAGCGCTACCTGAGATGCTCTCA 2351
 DB 2318 GGAATGATGCTGTCAGAGCTCGAGAGGCTGAGACGAGCGCTACCTGAGATGCTCTCA 2377
 QY 2352 TACTGAGCTCGGAGGCTGCGAGAGACCGTCC 2385
 DB 2378 TTTCAAAATTCGCGACTTGTGAAAACCTGTCC 2411

RESULT 5
 ABZ76372
 ID ABZ76372 standard, cDNA; 2394 BP.
 AC ABZ76372;
 XX 12-JUN-2003 (first entry)
 DE A. thaliana LMP encoding cDNA-clone ID PK118-1.
 XX Lipid metabolism protein; LMP; seed storage; plant; transgenic; gene; ss.
 XX Arabidopsis thaliana.
 XX Key Location/Qualifiers
 XX CDS 1..2394
 XX /tag= a
 XX /product= "LMP"
 XX /note= "lipid metabolism protein"
 XX MO2003014376-A2.
 XX 20-FEB-2003.
 XX 12-XUG-2002; 2002WO-US025586.
 XX 10-XUG-2001; 2001US-0311414P.
 XX (BAD1) BASF PLANT SCI GMBH.
 XX Miltendorf V, Haertel H, Clirpus P,
 DR WPI: 2003-256595/25.
 DR P-PSDB; ABR39586.
 PT New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX Claim 1; Fig 12C; 108pp; English.
 XX The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polymucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR7658-373 represent A. thaliana LMP encoding cDNA sequences
 XX
 SQ Sequence 2394 BP; 671 A; 480 C; 564 G; 679 T; 0 U; 0 Other;
 Query Match 43.2%; Score 1181.2; DB 7; Length 2394;
 Best Local Similarity 70.3%; Pred. No. 4e-257;
 Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;
 QY 164 CTACCGAGGAGACCTTCTGAGCTCTCCGCTCCGCGAGAGGAGTGTGCTGCG 223
 DB 151 CTTAAACAAATGTCATTCATGAAAGTCTGAGCTCTGAGAGAGGACCATGTTTCT 210

QY 224 CCGTTCGAGCATCGCGAGTGGCCGCCCGGAGTTTGGAGTACGTCCGCTCAAC 283
 DB 221 CCATTGTTGCTTGGCTATACGTCCAGACCTGGTGTAGGAAATGTCGTGTGAAAT 270
 QY 284 GTTACGAGCTCAGGCTGAGAGCTCAGCTCGGAGTACTCCGCTTCAAGAGAGG 343
 DB 271 GTGTATGAGCTGAGAGCTGAGATTTAACTGTTTGAATATCTTGGTTAAGAGAG 330
 QY 344 CTGTGAGCGGACAGCAATGATCCCTACGTTCTGAGCTTGACTTCGAGCGTCAAT 403
 DB 331 CTGTTAATGGCCATGCAATGAGATTTCTCTCTGAACTTGATTTGACCTTTCAAT 390
 QY 404 GTTCAGTCCAGCCCAATGATGATCATCTATTTGAAACGCTGACGTTCTCAAC 463
 DB 391 GGAACATGCTCGGCCAATCTGTTATCATCATCATGGAATGGAGTTCACTTCAAT 450
 QY 464 CGAACCTTGTCTCAATCATGTTCCGCAACAGGATGTTGAGGCCCTGTGATTC 523
 DB 451 CGTCACTCTCTTCAATTAATGTTCCGTACAAAGAAAGATGAGCTTGTGAGTTT 510
 QY 524 CTCCGTGGCCACGGGCAAGGAGGATGTTATGATGCTTAATGATGAATACAAAGCTT 583
 DB 511 CTCCGACCTCAAAACATGATGACCTGCTTATGATCTGATGATGATGATGATGATG 570
 QY 584 GGGAGGCTTCACTGCTGCTGACCAAGCTGAGAGCACTTGCAAACTCTCTGCTGAC 643
 DB 571 CCATTAATCAAGGAGCTTGGCAAGAGAGAGAGTCTCTTAACTCTCTGCGCA 630
 QY 644 AACCATCTCAAAATTTGCTTAAATTTCAAGAGTGGGCGCTGGAAGAAAGTTGGGT 703
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 QY 704 GATACAGAGAGCATGTTTGGAAATGATCATCTCTCTTACATCATTCAGGCGCCA 763
 DB 691 GACACAGACAGAGATTTCAAGAAATGATCATCTCTCTTACATCATTCAGGCGCCA 750
 QY 764 GACCACTACCTAGAGAAATTTCTGGAGAGATCCCATGATTTTAACTGTTGTG 823
 DB 751 GATCTTCTGCTTGGAGAGATTTCTGGAGAGATTTCTGGAGAGATTTCTGGAGAGAT 810
 QY 824 GTATCCCTCAGAGATTTGCTGCAAGATTTAGGCTGCGAGACAGAGAGAG 883
 DB 811 TTGCTTCTGATGTTTCTGCAAGATTTCTGCAAGATTTCTGCAAGATTTCTGCAAG 870
 QY 884 CAGATGCTTATATATCTGACCAAGTCTGCACTAGAAATGAGATGTTCTCCGTTTA 943
 DB 871 CAGATGCTTATATATCTGACCAAGTCTGCACTAGAAATGAGATGTTCTCCGTTTA 930
 QY 944 AAGAAACAGGCTGTTAGTTTCCCAAGATTTCTGATGTTTCTGATGTTTCTGATG 1003
 DB 931 CAGAAACAGGCTGTTAGTTTCCCAAGATTTCTGATGTTTCTGATGTTTCTGATG 990
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 DB 991 GCAAAAGCAATCATGATCATGAGGCTGAGAGATTTAGTGAACACAGATATCTTAC 1050
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 DB 1051 ATTTGAGATTTCAATTTAGATTTCAAGATTTCTTAAAGATGATATCAAGATTT 1110
 QY 1124 GATGTGCGCTATCTGAGAAACATTTCTGAGATGCTGCTGAGAAATGCTGTA 1183
 DB 1111 GATGTGCGCTATCTGAGAAACATTTCTGAGATGCTGCTGAGAAATGCTGTA 1170
 QY 1184 TTACAGGTACTCCAGACTTCAATATTTGAATCTACAGTATGAAATCTTGTGCGTCA 1243
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KM Lipid metabolism protein; LMP; seed storage; plant; transgenic; gene; ss.
 XX Arabidopsis thaliana.
 XX
 XX Key Location/Qualifiers
 FT CDS 1..2418
 FT /tag= a
 FT /product= "LMP"
 FT /note= "Lipid metabolism protein"
 XX
 XX W02003014376-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 12-AUG-2002; 2002MO-US025586.
 XX
 XX 10-AUG-2001; 2001US-0311414P.
 XX
 XX (BAD1) BASF PLANT SCI GMBH.
 XX
 XX Miltendorf V, Haertel H, Cirpus P;
 XX
 XX WPI; 2003-256595/25.
 DR P-PSDB; ABR39585.
 XX
 XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 PT producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.
 XX
 XX Claim 1; Fig 12A; 108pp; English.
 XX
 XX The invention relates to isolated lipid metabolism proteins (LMP) and
 CC polynucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC AB276558-373 represent A. thaliana LMP encoding cDNA sequences
 XX
 SQ Sequence 2418 BP; 676 A; 491 C; 562 G; 689 T; 0 U; 0 Other;
 Query Match 42.8%; Score 1172; DB 7; Length 2418;
 Best Local Similarity 70.9%; Pred. No. 4.9e-255;
 Matches 1556; Conservative 0; Mismatches 640; Indels 0; Gaps 0;

QY 562 TAATGATGAATAAAGCTTGGGAGGCTTCACTCTGTGCTGACCAAGAGTGAGAGCA 621
 DB 573 GAATGATGAAATACAGAAATATCCCATACTTCAGGAGAGCTTGGCAAGAGAGAGATT 632
 QY 622 CTGTCAAGAGCTCCCTGCTGACACACCAATCTGCAAAATTGCTTAATAATTTCAAGATG 681
 DB 633 CTTTCAAACTTCTCTGGCAACACCATACTCTGAATTTGAATTTGAACAAAGGAT 692
 QY 682 GGGCTTGAAGAAAGTTGGGATATACAGAGAGACATTTTGGAAATGATCTCTCT 741
 DB 693 GGGATTTGAAGAGGATATGGGATGACACAGCAAGAGGTTTCAGAAATGGTCACTTCT 752
 QY 742 TCTAGACATATTCAGGCGGACAGCCCATACCTACCTAGCAAAATCTTGGGAGGATCCC 801
 DB 753 TCTGACATCTCCAGGACCTGATCCTTCTGTCTTGGAGAGTTTCTTAGAGAGATTC 812
 QY 802 CATGATTTTAAAGCTTTGTGTGTATCCCTCATAGATCTTGTGCTCAAGCTTAATGTAT 861
 DB 813 TATGATTTGAATTTGATTTGTCTCCCATGTTACTTGGCAAGCAATGCTT 872
 QY 862 AGGCTTCCACACACAGAGAGACATGTCTATATCTGAGACCAATCCCTGCACTGA 921
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 QY 922 AATGAGATGGTTCCTCCGTTTAAAGAAACAAGGCTTGTATTTCCCAAGATCTCAT 981
 DB 933 AATGAGATGCTCTCTTAGATATACAGACCAAGAGCTGAGAAATTTCCAAATCTCAT 992
 QY 982 TGTACTGCTGATATCCAGATGCAAGAAAGAAACATATGCAATGACCGCTTGAAGAT 1041
 DB 993 TGTAAACAAGCTGCTACCCGAAGCAAGAGAAACAAGTGAACCAAGGTTGAAGAGAT 1052
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 DB 1053 TAGTGAACACAGCAACGACACATCTGCAATACATTTAGAGCTGAAAGAGATTTCT 1112
 QY 1102 TAGAAATGATATCAAGATTTGATGTGTGACATATCTGAAACATTTGTGAGAGATC 1161
 DB 1113 TCGAAGATGATCTCAAGATTTGATGTGTGACATATCTGCAATCTGCAAGAGATC 1172
 QY 1162 TGTGTGTAATTTGCTGTGATTAACAAGATCTCCAGCTTCATATTTGAAACTACAG 1221
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 DB 1233 TGATGAAATCTTGGGAGTATTTGATTTTCAAGATTTGAAATTTGCAAGAT 1292
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 QY 1642 CCCGAGCAAAACGATGAACACATTTGGGATCTGATGAACCGGTCAAAAGCCATCTCTT 1701


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DB 1653 TGGCGAAGAGATGATGAGCATGTTGTTTACTGAGCGAAGCATGAAAGCCATCATCTT 1712
QY 1702 CTCATGCGAAGACTTCGACAGGGTGAAGAACTAAACAGGGCTGGTGGAAAGCTTTGCTAA 1761
DB 1713 CTCATGCGAAGACTTCGACAGGGTGAAGAACTTGAAGCTGGTGGAAAGCTTTGCTAA 1772
QY 1762 GTGGGCTAGCTGAGAGGAGCTGGTAAAGCTTGTGGCTGGTGGGCTGAATGATGTGAA 1821
DB 1773 GATATGCAAGCTTGAAGAGCTTGCMAATTTTGTATGCTGGTGGCTGACATGATGAGAA 1832
QY 1822 CAAGTCCAGAGACAGAGGAAGAGATCGCGAGATAGAGAAATGATGAATCATCATCAAGAC 1881
DB 1833 TCAAGTCCAGAGATAGAGGAAGATGCTGAGATACAAAGATGCAAGCTTATTAAGAGA 1892
QY 1882 CCACAACTTTGTTGGGACAGTTCCGCTGATCTTGTGCGGACAGAAACAGGGCCCGTAAAG 1941
DB 1893 GTATGATTTAACAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1952
QY 1942 CGAGCTCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2001
DB 1953 TGAGCTTTACCTGTTATATGCGAGACACAAAGTGTGTTTGTTCAGCTGCTTTCTATTA 2012
QY 2002 AGCGTTCCGTTCTCACCGTCTGAGAGCGCAATGACCTGTGGGCTTCTTACTTTGCGAGCGT 2061
DB 2013 AGCATTTGGGCTTACGGGTGGAATGCAATGATGATGATGATGATGATGATGATGATGATGAT 2072
QY 2062 CCATGAGAGTCCAGCTGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2121
DB 2073 TCATGATGAGAGCGAGAGATGATGAGAAACGAGATGATGAGATGATGAGATGAGATGAG 2132
QY 2122 CCACCCCGGAGAGGCTGTTATCTGATGAGCGCACTTCTGACCGGTCAGACCAAGACCC 2181
DB 2133 TCATGATGAGAGCGAGATGATGAGAAACGAGATGATGAGATGATGAGATGAGATGAGATGAG 2132
QY 2182 AGATCACTGAGTGAATGATGATGAGAGCGAGGCTGAGAGCGCAATGAGAGAGATGAGATGAG 2241
DB 2193 AATATGATGAGTGAATGATGATGAGAGCGAGGCTGAGAGCGCAATGAGAGAGATGAGATGAG 2252
QY 2242 GAAATATGATGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2301
DB 2253 GAAAGATGATGAGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2312
QY 2302 GTGAGAGCTGAGAGAGGCTGAGAGCGAGGCTGATGAGATGATGATGATGATGATGATGATGAT 2361
DB 2313 GTCTAAGCTGAGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2372
QY 2362 CCGGAGCTGAGAGAGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2397
DB 2373 TCGTATTTGAGCAATTCATCCCGCTGGCAACAGA 2408

RESULT 8
AAD45852
ID AAD45852 standard; cDNA; 2908 BP.
AC
XX AAD45852;
XX
XX 27-DEC-2002 (first entry)
XX
XX Corn sucrose synthase (Sus1) cDNA.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breaker; grain strength; enzyme;
XX cellulose; corn; chromosome 9; gene; ss.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
XX CDS 28..2478
XX FT /tag= a
XX FT /product= "Corn Sus1 protein"
XX
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PN W0200267662-A1.
XX
XX 06-SEP-2002.
PD
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhusga KS, Helentjaris TG, Niu X;
XX
XX MPI; 2002-691625/74.
XX
XX P-PSDB; AAE28501.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Example 10; Page 110-114; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Sus1) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is corn Sus1 cDNA. Corn Sus1 gene is located at chromosome 9
XX
XX Sequence 2908 BP; 623 A; 815 C; 808 G; 662 T; 0 U; 0 Other;
XX
XX Query Match 42.5%; Score 1162; DB 6; Length 2908;
XX Best Local Similarity 68.3%; Pred. No. 9, 5e-253;
XX Matches 1641; Conservative 0; Mismatches 755; Indels 6; Gaps 2;
XX
XX 7 CCACGCGTCCGGGAGACCGGCTGAGAGACCCCTCCACGCGCAACGAGCTGCTGCG 66
XX 66 CCACGCGTCCGGGAGAGCGATGAGCACTGCTCTGCGCCACCAATGAGCTTGTGCG 125
XX 67 CCTCTGTCAGAGTACGTGAACAGAGGAGATCTGACAGCGGACCAATCTCTGA 126
XX 126 CGTCTTCAACAGGCTGAAAAAAGGTTGAGGATGCTGACAGCCCAACAGATGATGC 185
XX 127 CGGCTGAC--GAGTTCAGAGGCTCCGGGAGCGGCTGAGCGGAGGAGCCCTTCT 183
XX 186 CGAGTACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
XX 184 CGAGTCTCCGCTCCGCGCAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
XX 246 GATGATCTGAGAGGAGGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
XX 244 GCGCCCGCGCGCGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
XX 306 CCGCCCTAGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
XX 304 GCAGCTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363
XX 366 GAGGCTGAGAGGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
XX 364 TGAATCCATGCTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
XX 426 CAACAACTTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 485
XX 424 TCGTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483
XX 486 TCGTCAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
XX 484 GTTCCGCAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
```

546 CTTCCATGACAGAGAGCATGTATCCCTTGCTCACTTCCTTGAGGCGCCAGCAACTGACAA 605
544 GGGGCAATGTTATGATCTTATATGATATGATACAAAGCTTGAGGAGGCTTCACTGTGCT 603
606 GGGGATGACCATGATGTTGAAACGACAGAAATCCGAGTCTCAAGTCTGCAAGGTGAGCT 665
604 GACCAAGCTGAGAGCATTTGTCAMAGCTCCGCTGACACACATACCTCAAAATTTGC 663
666 GAGAGAGGCTAGAGAGCATCTGTCCACCTTCAAGAGTATACCTCAATCTTGATTTCA 725
664 TTATTAATTTCAAGAGTGGGCGCTTGAGAAAGTTGGGCTGATACAGACAGACATGTTT 723
726 CCAAGGTTCCAGGAATCTGTGTGGAGAAAGGTTGGGTTGATTGGCTTAAGGCTGACA 785
724 GGAATGATCAATCTCTTCTTACATCATTCAGGCGCCAGACCCATCTACCTTGAGAA 783
786 GGAACATACCACTCTCTCTTGTGACCTCCGAGGCGCCAGATCCGTCACCTCGAGAA 845
784 ATTCTTGGGAGAGATCCCAATGATTTTAAGTGTGTTGATACCTGATGATGATCT 843
846 GTTCTTGGACATCCCAAGTGTGTTCAATGTGTTATCTCTCCCTCAATGATCTT 905
844 TGGTCAAGCTAATGATTTAGGCTTGCCAGACAGAGAGACAGATCGTATATATCTGA 903
906 CGCTCAAGCTAATGTCTGGGTTACCTGACACGAGAGCCAGGTTCTACATCTTGA 965
904 CCAAGTCCGTGCTAGAAAATGAGATGCTTCCCTTTAAAGAAACAAGGCTTGATGT 963
966 TCAAGTCCGCTGATGAGAACAAATGCTGCTGAGATCAAGAGTGTGTCTGACAT 1025
964 TTCCCAAAAGATCTCTGTTGATCTGCTGATACAGATGCAAAAGAGATCATGCA 1023
1026 CAGCGGAGATCTTATTTGTACAGAGTGTCTCCGATGACACTGACACCTGTGG 1085
1024 TACGCGCTTGAAGAAATGAGGACACAGCATATTAATTAAGATTCCTTCAAG 1083
1086 CAGCGCTTGAAGAGTCTTGGCACACGACCTGCAATATCTTGGCGGTCATTCAG 1145
1084 AATGAAATGAGATCTTAAAGAAATGAGATCAAGTTGATGTGTGGCAATCTGGA 1143
1146 AATGAAATGAGATGTTGCAAGTGTGCAAGTGTGCAATTTGAATCTGAGCGCTACCTGGA 1205
1144 AATGATGCTGAGAGTGTGCTGTAATTTGCTGCAATTTCAAGATTCCTGAGCT 1203
1206 GATCTTACTGATGACGTGGCGCATGAGATTTGAGAGCTTCAAGCCAACTCTGACT 1265
1204 CATATTTGAAACTACAGTATGAGAAATCTTGGCGCTCATTTGCTATCTTACAGATGG 1263
1266 GATCATGGAACCTACAGTGAAGAACTTGTGCTGTGCTGCTGCGCAAGATGG 1325
1264 AATTAACCATGCACTTGTCTATCTTGAAGAAAGATTAAGTATCAAGATTCAGAT 1323
1326 TGTACTGACCTGACATTCGCAATGCGCTGAGAAATTAAGATTCCTTACCTGAGCT 1385
1324 AATTTGAGAAATTTGATGAGAAATGACATTTCTCTGCAAGTTCACTGATATAT 1383
1386 CTACTGAAATGATTTGAGATCACTACACTTCTGTGCAAGTTCACTGATCTGAT 1445
1384 TGTATGAAATGCTGATTTTATCATCACAGACATCAAGAAATTTGCTGAGACAA 1443
1446 TGCATGAAACCAATGCGAGCTTCACTACCAAGATCTTCAAGAGATTCGCGAGAA 1505
1444 AATTAATCTTGAACATGATGAGTCACTACTGCTTATCTGCTGTGTGACAGAT 1503
1506 GGAACACCTGCGAGTACAGATCAAGATGCGGTTCAATGCTGAGCTGACCGCT 1565
1504 TGTCCATGAGATGATGTTTCAATCAAGATCAATATATGCTCTGCTGAGCTGAT 1563
1566 TGTCCAGGATGATGATGTTTCAATCAAGATCAATATGCTGTCTGCTGAGCT 1625
1564 GTCCATTAATTTCAATCAAGATGAGGCAAGGCTGCTCTTCTGATGAT 1623

1626 GTCCATTAATTTCCCTGACACCGAGTGCACAGAGGCTGACCTTCCATCCGAGAT 1685
1624 CGAAATTTGATTTATATACCCGAGACAAAGATGAAACATTTGGCATCTGATGACG 1683
1686 TGAAGACTCTGTACAGCCAAACCGAGAACAGAGACAAAGTGTGTTGAAAGACAG 1745
1684 GTCAAGACCATCTCTTCTCAATGAGCAAGCTGACAGAGGTGAAACATTAACAGGCT 1743
1746 GAACAGCCATATCTTCTTCCATGCTCTGCTGACCGGTGTAAGAACTTGATGAGCT 1805
1744 GATGAGCTTTGCTAAGTGTGCTAAGCTGAGAGCTGATTAACCTTGTCTGTGCT 1803
1806 GGTGAGCTGTAGGCGCGGAAACAGCGCTGACAGAGTGTGAACTGTGTGCTG 1865
1804 CGGTCAATATGATTTCAAGATTCAGAGACAGGAAAGATTCGCGATATGAGAAAT 1863
1866 CCGGAGCC---ATGGCAACCTTCCAAAGACAGAGAGAGAGGCGGTTCAAGAAAT 1922
1864 GCATGACTCATCAAGACCAACACTGTTGAGGCAAGTTCGCTGATCTGCTGACAG 1923
1923 GTTGAACCTCATGAGCATGACATGAAAGGCAATCCGCTGATCTTCCGCAAT 1982
1924 AATCAAGGCGCTTACACGCGAGCTCTATCGCTACATGCTGATACCATGATGCTTTCG 1983
1983 GAACCGGTTCGCAACGCGGAGCTGTACCGCTTACATTCGCAACAGAGGCGCTTCT 2042
1984 ACAGCGGCTCTGTATGAAAGCTTCCGCTTCAACCGCTGTTAGAGCATGATCTGAGCT 2043
2043 GCAACCTGCTTCTTACAGAGCTTTCGAGCTGACGAGTGTGAGGCAATGACCTTGGGCT 2102
2044 TCTACTTTCGCGAGCTCCATGAGGTCGAGCTGAGATCATAGAGCATGAGCTTCCGG 2103
2103 GCCACCTTTCGACCGCTTACGCGGCTTCCGAGATCATCTGACACGCGCTTCTG 2162
2104 CTTCACATTTACCCGTAACACCCGAAACAGGCTGTTAATCTGATGCGCACTTCTGCA 2163
2163 CTACCATATGACCTTACACAGGCGCAAGAGCTGCGCTGCTGCTGAGACTTCTTGA 2222
2164 CCGGTGAGAGACCCAGATCATCTGGGTGAATTAATCTGAGACAGGCTGCGAGCT 2223
2223 CAGGTGCAAGCGAGGCGAGGCACTGAGCAATCTTCCAGAGGCGCTTCAAGCTAT 2282
2224 ATACGAGATGACATGAGAAATATCTCAGAGAGGTGATGACATGCGCGAGGCTTCA 2283
2283 CGAGGAAATGATCTGGAAGCTGTACTCGGAAAGCTGATGACCTCACCGGCTGTA 2342
2284 CCGTTTCGAAAGTACGTGTGAAAGCTCGAGAGGCTGAGAGCGCTTACCTTGAGAT 2343
2343 CCGGTTCTGAAAGTACGTGTGAAAGCTCGAGAGGCGGAGACCGGCGTACCTGAGAT 2402
2344 GTTCTATATCTGAAAGTTCGCGAGCTGAGGAAACAGCTGCGGCTTCAATTTGACCA 2403
2403 GCTGTAGCGCTTCAAGTACCGACCAATGCGAGACCGTTCGCTGCTGAGAGGAGA 2462
2404 GC 2405
2463 GC 2464
RESULT 9
ADA71337
ID ADA71337 standard; DNA; 2450 BP.
XX
AC ADA71337;
XX
XX 20-NOV-2003 (first entry)
XX
XX Rice gene, SEQ ID 4660.
XX
XX Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX
OS Oryza sativa.

[illegible]

D	519	CTTCATGACAAAGGAGAGCATGTATCCACGCTCAACTTCCTCTGTGACAACTACAA	578
Q	544	GGGCGCATGTTATGATGCTTATATATATATACAAAGCTTGGGAGGCTCATGCTGCTG	603
D	579	GGGATATACCATGATGTTGATATGACAAATCCGAGCTCATGCTCTCCAAAGTGCTCT	638
Q	604	GACCAAGAGTGAAGAGCATTTGTCAAAGCTCCCTGCTGACACCAATACTCACATTTGC	663
D	639	GAGGAAAGGCTBAGSAGCATCTTCTGGTCTTTACGACGACACCCCTTACTCAGATTCCA	698
Q	664	TTATTAATTTCCAGAGTGGGGCCCTGGAGAAAGGTTGGGGGTGATACAGCAGACATGTTT	723
D	699	CCACAGGTTCCAGGAACCTTGCTGAGAAAGGGTTGGGGTGACTGTCCAGCTTCCCA	758
Q	724	GGAAATGATCCATCTCCCTTCAGACATCTTCAGGGGCGCAGACCCATCTACCTAGAGAA	783
D	759	GGACACCATTCCTCTCTTTGGACCTTTGAGGCCCTGATCCGTCACCTTCAGAA	818
Q	784	ATTCTGGGGAGATGCCCATGATTTTAAAGTGTGTGGTATCCCTCATGGATATCTT	843
D	819	GTTCCTTGGAAACATCCCAATGGTGTTCATATGTTGATATGCCCCACAGGTTACTT	878
Q	844	TGCTCAAGCTATATGATTTAGGCTTGGCCAGACACAGGAGACAGATCCCTATATACGGA	903
D	879	CGCCCAAGCCCATGCTCTGGGTATCCCTGACATCGAGGGAGGGTGTCTACACTTTTGG	938
Q	904	CCAAGTCCGTGACATAGAAATGATAGTGTCTCCGTTTAAAGAACAGGCTTGATGT	963
D	939	CCAGTCCGTCTATGAGATATGATATGCTTCAAGGATCAAGCAGCAAGGCTCAATAT	998
Q	964	TTCCCAAGATCTCATTTGTTACTCGGCTATACAGATGCAAAAGAACATATACAA	1023
D	999	TACACACGCACTCTTATTTGTCAACAGATGCTCCCTGATGCAACTGGCACCACTCGG	1058
Q	1024	TCAGGGCTTGAAGAAATTAATGAGAACACAGCATCTTACATATTAAGATTCCTCTCAG	1083
D	1059	TCAGGCTTGAAGAGTCTTGGCACCGAGCAACCCACATCCTACGTGCTGCTTTGAG	1118
Q	1084	AAATGAATGGGATCTTAAAGAAATGATATCAAGATTGATGTGTGGCCATATCTGGA	1143
D	1119	AACGAAATGGAATGTTCCAGATGGATCTCAGTTTGAAGCTGTGGCCGTACCTGGA	1178
Q	1144	AACATTTGCTAGAGTGTGCTGGTGAATTTGCTGCTGAATTAACAAGTATCTCCAGCTT	1203
D	1179	AACATTCCTATATGTTGTGCGCACGAATTTGCTGAGAGCTCTCAGGCCAATCTGACTT	1238
Q	1204	CATAATTGAAGATCAAGTATGAGAAATCTGTGGCGTCAATGCTATCTTAAAGATGGG	1263
D	1239	GATCATGGAAACTACAGCTGACGGAAACTTTGTTCAGATGCTTGTGCACACAGATGGG	1298
Q	1264	AATTACCAATGCAACATTTGCTCATGCTCTGGAAGAAAGCTAAATATCCAGATTACAGAT	1323
D	1299	TGTTATCCATTTATACATTTGCCATGGCGCTTGAGAAACCAAGTACCCCACTCTGACT	1358
Q	1324	ATTTTGAAGAAATTCAGTGAAGAGTACATTTCTCCGCAAGTCTCATGCTGATATAT	1383
D	1359	CTACTGGAGAGATTTGAGATCACTACACTTCTCATGCGCAGTTGACAACTGACTTAT	1418
Q	1384	TGCTATGAACAACTGCTGATTTTATCATACACAGACATATCCAAAGAAATTCCTGGAAGCA	1443
D	1419	TGCGATGAACACAGCTGACTTATCATACACAGTACCTTCCAAAGATGTCGGAGAAACA	1478
Q	1444	AAATCTGTGGAAGATGATGAGAGCATATGCTTACTGCTGCTGCTGTGTCGACAGT	1503
D	1479	GGACACTGTTGTGCTATGATGTCTCACATGGCATTCCACATGCTGGTCTGTACCGTGT	1538
Q	1504	TGTTCATGGGATCATGCTTTCGATCCAAAGTTCAATATATAGTCTCTCTGAGCTGACAT	1563
D	1539	TGTTCACGGATATATGTTTGAACCCAAAGTTTAACTGTCTGCTGGGTGGGAGAT	1598
Q	1564	GTTCATATCTTTCACATACCGAAGGCCAAGGATCTACCTCTTCAATGTTCAAT	1623

Db 1599 GTCCATCTACTCCCTTACTCTGAGTCTGTAAGAGGCTCACTCCCTCCACCCAGAGAT 1658
 Qy 1624 CGAAATTTGATTTATGACCCGAGGAGAAACGATGAAACATTTGGCATCTGANTGACCG 1683
 Db 1655 TGAAGAGTGTCTCTAGAGAGTGAACAACAAGCAAGTATTAATGTAAGAGCAG 1718
 Qy 1684 GTCAAGCCCATCTCTTCTCCATGCGAAGACTCGACAGGGTGAAGAACATAACAGGGCT 1743
 Db 1719 GAACAAGCCATCATCTCTCCATGCTGCTGTGACCGGTGACAAACCTTGACTGCTGCT 1778
 Qy 1744 GGTCCGAGCTTTTGTCTGTAAGTGGCTGAGGAGGAGTGTGTAACCTGTGCTGCTG 1803
 Db 1779 GGTGTGCTGTATGAGCGAATGCAACTGTAATGAGCCACATCCGCTGATCTCCGCGAGAT 1838
 Qy 1804 CGGATCATGATGTCAGCAAGTCCAGAGACAGGAGAGAGATGCGAGATAGAGAGAT 1863
 Db 1839 TGGTGAACATG---CAACCCATCTAAGAGCAAGAGAGAGAGAGAGAGTGAAGAGAT 1895
 Qy 1864 GCAATGACTCATGAGACCAACCACTTTGTCGGCAGCTTCCGCTGATCTCTGCCAGAC 1923
 Db 1896 GTTGAACCTTATGAGCAATGCAACTGTAATGAGCCACATCCGCTGATCTCCGCGAGAT 1955
 Qy 1924 AAAAGAGCCCGGTAAGAGAGTCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1983
 Db 1956 GAACCGTGTGCGAAGAGTGAAGTCTACCGCTTAATGCTGAGACCAAGAGTCTTTGT 2015
 Qy 1984 ACAGCCGCTTGTATGAGAGCGTTCGCTACCGCTGCTGAGGCGATGCTGTGAGCT 2043
 Db 2016 GAGCCCGCTTGTATGAGAGCGTTCGCTACCGCTGCTGAGGCGATGCTGTGAGCT 2075
 Qy 2044 TCTTACTTTGCGACGCTCCATGAGAGTCCAGCTGAGATCATAGAGATGCGCTTGGG 2103
 Db 2076 CCGACATTCGCAACCGCTTATGAGTGTGCTCAGCTGAGATCATGCTGAGAGAGTGTGG 2135
 Qy 2104 CTTCGACATGACCCGCTTATGAGAGCGCTTATGAGTGTGCTGAGAGAGTGTGG 2163
 Db 2136 CTTCGACATGACCCGCTTATGAGAGCGCTTATGAGTGTGCTGAGAGAGTGTGG 2195
 Qy 2164 CCGGTCGACAGAGAGCCGCTTATGAGAGCGCTTATGAGTGTGCTGAGAGAGTGTGG 2223
 Db 2196 GAGTGTGACAGAGAGCCGCTTATGAGAGCGCTTATGAGTGTGCTGAGAGAGTGTGG 2255
 Qy 2224 ATACGAGAGTACATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGTATG 2283
 Db 2256 CGAGGAGAGTACATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGTATG 2315
 Qy 2284 CGGTTCTGAGAGAGTATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGT 2343
 Db 2316 CGGTTCTGAGAGAGTATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGT 2375
 Qy 2344 GTTCTACATGAGAGTATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGT 2403
 Db 2376 GGTGTGAGAGTATGAGAGAGTATCTGAGAGAGTATGAGAGAGTATGAGAGAGTATG 2435
 Qy 2404 GCAAGTAG 2410
 Db 2436 GCCGTGG 2442

RESULT 10
 ID AD08208
 AC AD08208;

18-DEC-2003 (first entry)

Rice DNA sequence Seq ID513 related to grain filling.

plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarcane;
 wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;

Km gene; ds; plant.
 Os Oryza sativa.
 PN MO2003000905-A2.
 XX
 XX
 PD 03-JAN-2003.
 PF 21-JUN-2002; 2002MO-IB02450.
 XX
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 26-DEC-2001; 2001US-0342327P.
 XX
 XX (SYN) SYNGENTA PARTICIPATIONS AG.
 PA Zhu T, Cheng W, Briggs S, Cooper B, Goffe SA, Moughamer T;
 PI Glazebrook J, Kargi F, Krops J, Provart N, Riecke D;
 XX
 DR NPI; 2003-229341/22.
 DR P-PSDB; AD08208.
 XX
 XX
 PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX
 XX Claim 35; SEQ ID NO 513; 130pp; English.
 PS
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarcane, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is a
 CC DNA sequence encoding a rice protein of the invention. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/publichedpct_sequences.
 CC
 SQ Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
 Query Match 42.1%; Score 1152.6; DB 9; Length 2451;
 Best Local Similarity 68.0%; Pred. No. 1.2e-254;
 Matches 1637; Conservative 0; Mismatches 764; Indels 6; Gaps 2;

364 TATCCCTACGTTCTCGAGCTTGAAGCTGAGCCGTTCAATGTCATGCCACGCCCAA 423
399 CAACAACTTGGCTGAGCTGGATTTGAGCCATTGAATGCTCTTCCCTGCTTC 458
424 TCGCTATCATCTATTGAAACGCTGTCAGTTCCTCAACCGACCTTGTCTCAATCAT 483
459 TGTGTCGAAGTCCATTGGCAATGCTGTGAGTCCCAACAGGCACTGTCTCATCAAGCT 518
484 GTTCGCAACAGGAGTTGCTGGAGCCCTGTGATTTCCCTGCTGACCGGCAACA 543
519 CTTCATGACAAAGAGAGATGATCCCACTGCTCAACTCTCTGTGACACAACTTCA 578
544 GGGCATGTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
579 GGGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 638
604 GACCAAGCTGAGAGCACTTGTCAAGCTCTGTCACACACCACTCACTCAATTTGC 663
639 GAGGAAGCTGAGAGCACTTGTGTGTCGAGAGGTTGGGCTGACTGTCCAAAGCTTCCA 698
664 TTTTAAATTTCAAGAGTGGGCTGAGAGAGTTGGGCTGATACAGCAGCAATGTTT 723
699 CCAAGGTTCCAGAACTTGTGTGAGAGGTTGGGCTGACTGTCCAAAGCTTCCA 758
724 GGAATGATCCATCTCTCTAGACATCATTCAGGCGCCAGACCCATCTACCTAGAGAA 783
759 GGAAGCATCTACCTCTTCTTGGACCTTCTTGAAGCCCTGATCCGCTCACTCGAGAA 818
784 ATTCTGGGAGAGATCCCATATTTTAAAGTGTGTGATGATGATGATGATGATGATGAT 843
819 GTTCTTGGAAATATCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 878
844 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
879 CGCGAAGCAATGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 938
904 CCAAGCTCTGACATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
939 CCAAGCTCTGACATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 998
964 TTTCCCAAGATTTCTCATTTGTTACTGCTGATCCAGATGCAAAAGAAATCATGACAA 1023
999 TACACACGATCTCTTATGTCACAGTGTGCTCTCTGATGCAATCGGACCACTGGCAG 1058
1024 TGAAGGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
1059 TGAAGGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1118
1084 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
1119 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
1144 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
1179 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1238
1204 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
1239 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1298
1264 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
1299 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1358
1324 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
1359 AATGAAATGAGATCTTAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
1384 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443
1419 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1478

1444 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1503
1479 GGAACATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1538
1504 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
1539 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1598
1564 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
1599 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1658
1624 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
1659 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1718
1684 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
1719 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1778
1744 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
1779 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1838
1804 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
1839 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1895
1864 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
1896 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1955
1924 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
1956 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2015
1984 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
2016 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2075
2044 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
2076 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2135
2104 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
2136 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2195
2164 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
2196 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2255
2224 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
2256 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2315
2284 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343
2316 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2375
2344 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
2376 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2435
2404 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2463
2436 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2495

RESULT 11
AD007855
ID AD007855 standard; DNA; 2451 BP.
XX

AC ADCC7855;
 XX 18-DEC-2003 (first entry)
 XX Rice DNA sequence Seq ID121 related to grain filling.
 XX
 XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 XX gene; ds; plant.
 OS Oryza sativa.
 XX WC2CC300905-A2.
 XX 03-JAN-2003.
 XX 21-JUN-2002; 2002WC-1B002450.
 XX 22-JUN-2001; 2001US-0300112P.
 XX 26-SEP-2001; 2001US-0325277P.
 XX 20-DEC-2001; 2001US-0342327P.
 XX (SYNEMTA PARTICIPATIONS AG.
 XX Zhu T, Cheng H, Briggs S, Cooper B, Goff SA, Moughamer T;
 XX Glazebrook J, Katagiri F, Kreps J, Frowart N, Rieke D;
 XX MPI; 2003-229341/22.
 XX P-PSDB; ADCC7856.
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 XX associated with the synthesis, metabolism or degradation of carbohydrates
 XX in the plant grain useful in generating plants having improved
 XX nutritional properties.
 XX
 XX Claim 2; SEQ ID NO 121; 130bp; English.
 XX
 XX This invention, in the area of plant biotechnology, relates to novel
 XX polynucleotides comprising a nucleotide sequence encoding a protein which
 XX is involved in or associated with the synthesis, metabolism or
 XX degradation of carbohydrates in the plant grain and the expression of
 XX which is up-regulated during grain filling. The plant is selected from
 XX corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 XX sugarbeet, wheat, and rice. The invention may be useful for the
 XX improvement of protein, oil, starch, fibre and moisture content of the
 XX cereal grains. In addition, carbohydrate levels may be modified to a more
 XX desirable level using the present invention. The present sequence is a
 XX DNA sequence encoding a rice protein of the invention. Note: The sequence
 XX data for this patent did not form part of the printed specification, but
 XX was obtained in electronic format directly from WIPD at
 XX ftp.wipd.int/pub/publicshdpc_sequences.
 SQ Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
 Query Match 42.1%; Score 1152.6; DB 9; Length 2451;
 Best Local Similarity 68.0%; Pred. No. 1.2e-250;
 Matches 1637; Conservative 0; Mismatches 764; Indels 6; Gaps 2;

Db	219	GAATGTCCTGAGAGTGCACAGAGGAGATTTGTAATCTCCCATGGAGTTCCCTTGGCAT	278
Qy	244	GCGCCCGCGCCGGAGATTGGAGTACGTCGCGCTCAAGTTCAAGAGCTCAGCGTGA	303
Db	279	CCGCCGAGGCGCGGTCTGGAGATATGAGAGGTCAATGTAAGCAGATCTGTTGA	338
Qy	304	GAGGTCACAGTCCGAGATACCTCCGCTCAAGAGAGAGCTTGTGACGCGACACAA	363
Db	339	GTTGTCGACAGTCCGAGATACCTCCGCTCAAGAGAGAGCTTGTGACGCGACACAA	398
Qy	364	TGATCCCTAAGTCTCGAGCTTGAATCTGACGCGGTCAATGTCTCACTCCAGCCCAA	423
Db	399	CACAACTTGTCTTGAAGTGAATTCAGGATTCAGGATTCAGGATTCAGGATTCAGG	458
Qy	424	TGGGTATCATCTATTGAAAGGTGTGAGTCTTCAACGACATCTTGTCTCAATCT	483
Db	459	TCTGTGAAGTTCATGGCAATGATGTGAGTCTTCAACGAGATCTGTATGAAGCT	518
Qy	484	GTTCCGGAACAGGAGATTGTTGAGGCGCTGTGATTTCTCCGCGGACCGGACAA	543
Db	519	CTTCCATGACAGAGAGATGTCACCTGCTCACTTCTTGTGACACAACTCA	578
Qy	544	GCGGCAATGTTATGATGCTTAATGATTAACAAGCTTGGAGGCTTCAATGTGCT	603
Db	579	GCGGCAATGTTATGATGCTTAATGATTAACAAGCTTGGAGGCTTCAATGTGCT	638
Qy	604	GACCAAGCTGAGAGAGCTTGTCAAGCTCCCTGTCAGACACACTATCACAATTGC	663
Db	639	GAGGAAGCTGAGAGAGCTTGTGTGCTTTGACAGACACCTTATCTAGAAATCCA	698
Qy	664	TTATTAATTTCAAGAGTGGGCTTGAGAAAGTTGGAGTGAACAGAGACATGTTT	723
Db	699	CCAGAGTTTCAAGAGCTTGTGTGCTTTGAGAGAGGTTGGAGTGAACAGAGCTTCCA	758
Qy	724	GAAATGATCAATCTCTTTGACATCAATTCAGGCGCAGACCATCTACTTACAGAA	783
Db	759	GAGAACATCACTCTTTGACATCAATTCAGGCGCAGACCATCTACTTACAGAA	818
Qy	784	ATTCTTGGGAGATCCCATGATTTTAACTTGTGTGATACCCCTCATGATACCT	843
Db	819	GTTCTTGGGAGATCCCATGATTTTAACTTGTGTGATACCCCTCATGATACCT	878
Qy	844	TGGTCAAGTAAATGTTAAGGCTTGCAGACACAGAGAGCAGATGCTTATATCTGA	903
Db	879	CAGGAGAGCAGATGCTTGTGATACCTGACACAGAGAGCAGATGCTTATATCTGA	938
Qy	904	CCAGTCCGTCAGTAAAGATGATGTTCTCGTTTAAAGAAACAAGGCTTGAATGT	963
Db	939	CCAGTCCGTCAGTAAAGATGATGTTCTCGTTTAAAGAAACAAGGCTTGAATGT	998
Qy	964	TTCCCAAGATTTCTATGTTACTGCGCTGATACCAAGTCAAGAAAGATCATGCA	1023
Db	999	TACACACAGATCTTATGTCACAGATGCTTCTGATCAACTGCAACACCTGCGG	1058
Qy	1024	TGACGCTTGAAGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1083
Db	1059	TGACGCTTGAAGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1118
Qy	1084	AAATGAAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1143
Db	1119	AAATGAAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1178
Qy	1144	AAATGAAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1203
Db	1179	AAATGAAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1238
Qy	1204	CATATTTGAAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1263
Db	1239	GATGATGAGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1298
Qy	1264	AATTAACAGATGATTAAGTGAACACAGATCACTTACATTAATTCAGATTCCTTGA	1323

Dp	1299	TGTTAACCATTGTATACCAATTCGGCCATTCGGCTTGAGAAACCAAGTAAACCCAACTGTACACT	1359
Qy	1324	ATTTTGGAGAATTTCCATGAGAAATACATTTTCTCTCCGACATTCAGTCTGATATAT	1383
Dp	1359	CTACTGGAGAAGTTTGAGATCACTACCACTTCTCATGACCAAGTTCAACAATCTGACTGAT	1418
Qy	1384	TGCTATGAACATGCTGATTTTATCATCACAGACATACCAAGAAATGCTGGAAGCA	1443
Dp	1419	TGCATGAAACACGCTGACTTCATCATACCAAGTAACTTCCAAGATATGCGGAAACA	1478
Qy	1444	AAATATCTTTGGAAGATATGAGAGTCATCTGCCCTTAATCTCGCTGCTGTACCGAGT	1503
Dp	1479	GGACACATGTGTAGATAGATGTGATCTCAATGCAATTCACCAATGCTCGTGTGTACCGGT	1538
Qy	1504	TGTCATAGGATCGATGTCTTGATCCAAATGATCAATATGATCTCTCTGGAGGTGCAT	1553
Dp	1539	TGTCACGAGTATATATGTTTGTGACCGGAGTTTAACTGTCTCGCTGAGTGGAGAT	1598
Qy	1564	GTCCATATCTTTCACATACCGAGAAAGCCAGACGCTACCTCTCTTCATGAGTTCAAT	1623
Dp	1599	GTCCATCTACTCCCTTACTCTGAGTCTCTGAAAGGCTCACTTCCTCCACCCAGAGAT	1658
Qy	1624	CGAAATTTGATTTATGACCCCGAGCAAAAGATGAACATTTGGGATCTTGATGACG	1683
Dp	1659	TGAGAGATGTCTTACACGCGAAGTTGACAAACAGACGCAAGTTTATGTGGAAGGACG	1718
Qy	1684	GTCAAGCCCATCTCTCTTCCATGCGCAAGCTGCACAGGCTGGAAGAACATPACAGGCT	1743
Dp	1719	GAAACAGCAATCATCTTCTCCATGGCTCGTCTTGACCGGTGTCAAGAACTGACTGGTCT	1778
Qy	1744	GGTGAAGCTTTTGCTAATGCTGCTTAAGCTGAGGAGCTGGTAAACCTTGTGTCTTGC	1803
Dp	1779	GGTTGAGCTGTATGATGTCGCAACCTTCGCTCCAAAGAGCTGTGTAACTGTGTGTGTG	1838
Qy	1804	CGGGTCAATATATGTCAAACATGTCACAGGAACAGGGAAGATATGCGAGATPAGAAAGAT	1853
Dp	1839	TGTGTACCATG---CAACCATCTTAAAGACAAAGAGAGCAAGGTGTGATTCAAAGAAAT	1895
Qy	1864	GCATGAATCTATCAAGACCCACAACTTGTGGGCAAGTTCGCTGATCTCTGCCCAAC	1923
Dp	1896	GTTTGACCTTATGAGCAATACAACTTGAAATGGCAACATCCGCTGATCTCGCGCAAGAT	1955
Qy	1924	AAACAGGCGCCGTAAAGCGGAGCTTATATGCTATCATGCTGATATPCCATGGTGCCTTGT	1983
Dp	1956	GAACTGTGTCCGCAACGGTGAAGCTTACCTGTTACATCTGCGAACCCAAAGGTGCTTTGT	2015
Qy	1984	ACAGCCGGCCCTGTATGAGAGCTTCGGCTCACCGCTGTAGGCAATGACTGTGGCT	2043
Dp	2016	GCACTCCGGCTTCTTAAGAGGATCTGGCTCAAGTGTGTTAGTCATGACTGTGGCT	2075
Qy	2044	TCTTACTTTGCGACGCTCCATGGAAGGTTCAGCTGAGATCATATAGCATATGCGCTCTGGG	2103
Dp	2076	CCCGACATGTGCAACCGGCTATGTGTGCTCCAGCTGAGATCATCTGAAACGAGATGTCTGG	2135
Qy	2104	CTTCCACATTTACCCGTATCCAGCCCGCAACAGGCTTTAATATGTATGGCGCACTTTTGA	2153
Dp	2136	CTTCCACATTTATCCCAATPCCAGGCTGACAAAGGCTTCGGCGCTGCTCTGTAGATCTTTGA	2195
Qy	2164	CCGGTGCACAGCAACCCCAATCACTGGGTGAATATATCTGAGACAGGCTGACAGCGAT	2223
Dp	2196	GAAATGCGCAGGAAGACCCCAACCACTGGAACCAATCTCCAGAGGCGGTCTTCAAGCGAT	2255
Qy	2224	ATAGGAAAGTACATATGGAAGATATATCTCAGAGAGTGTATGACATGCGCGCGGGGTATA	2283
Dp	2256	CGAGGAGAAATPACCTGGAAGCTCTTACTTGAGAGGTGTATGACCTCACCGGCGTCTTA	2315
Qy	2284	CGATTTCTGGAAGTACGTGTGGAAGCTCGAAGGCTGAGAGCGAGCGCTACCTTGAGAT	2343
Dp	2316	CGGATCTTGGAAAGTACGTGTGGAACCTTGAGAGGAGGTGAAACCGCGCGCTACCTTGAGAT	2375
Qy	2344	GTTCTTCAATATGAAGTTCGCGAGAGTGGCGAAGACCTGTGCGCTTGCATATGACCAAC	2403
Dp	2376	GCTATATGCCCTTCAAGTACCGCAACATATGCTATGACACGATCCGTTGGCGGTGAGAGGCGGA	2435

QY		2404	GCAAGTGA	2410
Db		2436	GCCCTCG	2442
<hr/>				
RESULT 12				
AAD45851				
ID	AAD45851	standard; DNA;	2746 BP.	
XX				
AC	AAD45851;			
XX				
DT	27-DEC-2002	(first entry)		
XX				
DE	Corn sucrose synthase shrunkn-1 (Sh1) DNA.			
XX				
KM	Sucrose synthase; shrunkn-1; Sh1; constitutive sucrose synthase; Sus1;			
KW	transgenic plant; plant breeding; grain breakage; grain strength; enzyme;			
KX	cellulose; corn; chromosome 9; gene; ds.			
XX				
OS	Zea mays.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	72..2480		
FT		/*tag= a		
FT		/product= "Corn Sh1 protein"		
XX				
PN	WO200267662-A1.			
PD				
XX	06-SEP-2002.			
XX				
PF	21-FEB-2002; 2002WO-US005137.			
XX				
PR	22-FEB-2001; 2001US-0270777P.			
XX				
PA	(PTON-) PIONEER HI-BRED INT INC.			
XX				
P1	Dhuga KS, Helentjaris TG, Niu X;			
DR	WP1: 2002-691625/74.			
XX	P-PSDB; MAE285C0.			
PT	New polynucleotide and its encoded sucrose synthase, useful for			
PT	modulating the level of sucrose synthase in transgenic plants (e.g. maize			
PT	or soybean) to improve stalk length, reduce grain breakage, or improving			
PT	plant or grain strength.			
XX				
PS	Example 10; Page 105-108; 125pp; English.			
XX				
CC	The invention relates to two sucrose synthases, shrunkn-1 (Sh1) and			
CC	constitutive sucrose synthase (Sus1) and their corresponding nucleic			
CC	acids. The polynucleotide, or its encoded protein, is useful for			
CC	modulating the level of sucrose synthase in a transgenic plant,			
CC	increasing cellulose production in the stalk tissue of a transgenic			
CC	plant, or increasing the concentration of cellulose in the tissues of a			
CC	seed of a transgenic plant. This is particularly useful in plant (e.g.			
CC	maize or soybean) breeding, especially for e.g. improving stalk length in			
CC	maize, reducing grain breakage during combining, transport or movement			
CC	into storage, or improving plant or grain strength. The present sequence			
CC	is corn Sh1 DNA. Corn Sh1 gene is located at chromosome 9			
XX				
SQ	Sequence 2746 BP; 635 A; 727 C; 710 G; 674 T; 0 U; 0 Other;			
Overy Match	41.2%; Score 1127.6; DB 6; Length 2746;			
Best Local Similarity	67.7%; Pred. No. 5.7e-245;			
Matches 1612; Conservative	0; Mismatches 755; Indels 9; Gaps 2			
QY		18	GCGACGCCGTCGAGAGACACCCTCCAGCGCACCGGCACGACGACTGTGCCCCCTCTGTTCCA	77
Db		106	GCGAAGCGCTTGATGGCCACCTTCTCTCCGCCATGCCAAATGAATGATAGACATCTTTTCCA	165
QY		78	AGTAGGTGAACAAGGGAGAGGACATCTCTGACCCGACACCAATCTCTGACGCGCTCGAG	137

QY 2299 ACGTGTGAGAGCTGAGAGGCTGAGAGGCGCTACCTTGAATGTTCTACAACTGA 2357
DB 2377 ACGTGAAGCAACTGAGAGGCGCGAGAACCCCGCTACATGAGATGTTCTACGCCCTGA 2436
QY 2358 AGTTCGCGAGCTGCGGAGAGACCGTCCCTTGCAATTGA 2397
DB 2437 AGTACCGTAGCTGCGAAGCCAGAGTCCGCTCTCTTGA 2476

RESULT 13
AAC66090
ID AAC66090 standard, cDNA, 2494 BP.
XX AAC66090;
AC AAC66090;
XX 13-FEB-2002 (first entry)
XX
XX
XX Rice sucrose synthase cDNA sequence.
XX Cold resistance; transgenic plant; sucrose decomposition; rice;
XX sucrose synthase; ss.
XX
XX Oryza sativa.
XX JP2000245279-A.
XX 12-SEP-2000.
XX 01-MAR-1999; 99JP-00052102.
XX 01-MAR-1999; 99JP-00052102.
XX (MITA) MITSUI CHEM INC.
XX
XX MPI; 2000-675173/66.
XX P-ESDB; AAY85664.
XX
XX Novel method for the reinforcement of cold resistance in a plant
XX comprising introducing a vector encoding an enzyme that decomposes
XX sucrose into the plant.
XX
XX Claim 1; Page 8-11; 22pp; Japanese.
XX
XX This invention relates to a method for the reinforcement of cold
XX resistance in a plant, comprising introducing an expression vector having
XX a DNA encoding an enzyme for decomposing sucrose connected downstream to
XX a promoter expressible in the plant, and expressing the enzyme in the
XX plant body. Included in the invention are an expression vector used in
XX the method; a transformed plant carrying the expression vector; and a
XX transformed rice carrying the above expression vector. The method is used
XX for reinforcing cold resistance in a plant. The present sequence
XX represents cDNA encoding sucrose synthase used in the method
XX
SQ Sequence 2494 BP; 622 A; 599 C; 628 G; 645 T; 0 U; 0 Other;

Query Match 41.1%; Score 1125.8; DB 3; Length 2494;
Best Local Similarity 67.5%; Pred. No. 1,4e-244;
Matches 1615; Conservative 0; Mismatches 767; Indels 9; Gaps 2;

QY 7 CCAAGCGTCGCGAGCGCGCTGAGAGACACCTCCACGCGACCGGACAGAGCTGTGCG 66
DB 47 CCAAGCGTCGCGAGCGCGCTGAGAGACACCTCCACCTTCCTCAATCCAAATGAATTAATGCG 106
QY 67 CTTCTGTCAAGTACGTGAACAAGGAGGACCTCTGACGCGGACCAATCTCTGA 126
DB 107 ACTGTTCTGTAGTATGTACCAAGGAAAGGATGCTCCAGCTCCACAGCTGCTTGC 166
QY 127 GCGGCTGAGAGAGTCAAGGCTCCGCGGCGCGCTAGCGGAGGACCTTCTCTGA 186
DB 167 GAGAGTCAATGCTCTT-----GATGAAGCTGACAAAGAAATATGCTCCCTTTGAAGA 220
QY 187 GATGCTCGGCTCGCGAGAGGAGGATGCTGTGCGCGCTTCGTCGACATCGCGGTGCG 246

DB 221 CATTCGCGGCTGTCAAGAACCATATGCTGCGCGCTCGGCTTGCACTGCGCATCAG 280
QY 247 CCCGCGCCCGGAGTTGTGAGAGTACGTCGCGCTCAAGTTCACAGAGCTCAGGTGAGCA 306
DB 281 GCAAGAGCGCTGTGTCTGAGACTTACATTCGGGTAATGTAGTGAATTTGGCAATGAGA 340
QY 307 GCTCAAGTCTCGAGTACTTCCGCTTCAAGAGAGAGCTTGTGAGAGCGGACAGCAATGA 366
DB 341 GCTGAGTGTCTGAGTACTTGGCATTCAGGAAAGAGCTGTGTAGTGAACAGCCAAAG 400
QY 367 TCCCTAAGTTCGAGCTTGAAGCTTGAAGCGCTTCAATGTCTCACTGCCCAATCG 426
DB 401 CAATCTGTCTTGAAGCTTGAAGCGCTTCAATGTCTTCCGCGCGCTTCAT 460
QY 427 GTCAATCCTATGGAAGCGGTCGAGTCTTCCAAAGCAAGCTTCTCATATGTT 486
DB 461 GTCAAGTCAATGAGAAAGGAGTGTCTTCAAGCGCTTCAAGCTTGTGCAAGTGT 520
QY 487 CCGCAACAGGAGTGTGAGCGCTTGTGAGCTTGTGAGCTTGTGAGCGGACCGCAAG 546
DB 521 CAGGACAAAGAGAGCTTACCCCTGTGAACTTCTGAAAGCCCATTAACCAAG 580
QY 547 GCATGTTATGATGCTTAATGATTAATCAAAAGCTTGGGAGGCTTCACTGTGTGAC 606
DB 581 CACGACAAATGATGCTGAATGACAGAAATTCAGAGCTTGTGAGCTTCAATCCCTAG 640
QY 607 CAAAGCTGAGAGACTTGTCAAGGCTCCCTGTGACACACCAATCTCAATCTCAAT 666
DB 641 AAGGACAGAGAAATTCATGATGAGGATTCCTCAAGACAGCTTCAAGATTCACCA 700
QY 667 TAAATTTCAAGAGTGGGCTGAGAGAAAGTTGGGCTGATACAGCAGACATGTTTGA 726
DB 701 CAGGTTCAAGAGCTGTGTTGAGAGAGGTTGGGCTGATGCAAGAGCTGTGCTTGA 760
QY 727 AATGATCAATCTCTTCTTGAATCATTAAGGCGCCCAAGCCATTAACCTTGAAGAAAT 786
DB 761 CACCAATCAATCTCTTCTTGAATCATTAAGGCGCCCAAGCCATTAAGGAAAT 820
QY 787 CTGGGAGAGATCCCATGATTTTAAAGTGTGTGATGATCCCTCATGATTAATCTTGG 846
DB 821 CTTGGAATCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 880
QY 847 TCAAGCTAATGATTAAGCTTCCAGACACAGAGAGACAGATGCTATATTAAGTGAACA 906
DB 881 CCAATTCATGATGTTGGATTAACCTGATTAAGTGTGATGATGATGATGATGATGATG 940
QY 907 AGTGTGCACTAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 966
DB 941 AGTGTGCACTAGAAATGAGATGATGATGATGATGATGATGATGATGATGATGATG 1000
QY 967 CCAAGATTTCTATGTTACTCGGCTGATACAGATGCAAAAGAAACATGCAATGA 1026
DB 1001 AACTAAGATTCATGTTACTCGGCTGATACAGATGCAAAAGAAACATGCAATGA 1060
QY 1027 GCGGCTTGAAGAAATTAAGTGAACAAGCATTAATTAATTAATTAATTAATTAATTA 1086
DB 1061 GGTGTGAGAGAGTAAATTAAGTGAACAAGCATTAATTAATTAATTAATTAATTAATTA 1120
QY 1087 TGAAGAGGAGTAAATTAAGTGAACAAGCATTAATTAATTAATTAATTAATTAATTAATTA 1146
DB 1121 TGAAGAGGAGTAAATTAAGTGAACAAGCATTAATTAATTAATTAATTAATTAATTAATTA 1180
QY 1147 ATTGCTGAGAGTGTGCTGTGTAATGCTGTAATTAATTAATTAATTAATTAATTAATTA 1206
DB 1181 ATACATGAGAGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1240
QY 1207 AATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1266
DB 1241 CATTTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1300
QY 1267 TACCGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1326
DB 1301 TACCGATGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1360

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1327 TTGAGAAATTTGATGAGAGATGACATTCTCTCCGACAGTCTGATATTAATTGC 1386
1361 CTTGGACAAATTTGACAGGACGATACCACTTCTCATGCAATTAATCTGATCTTATCGC 1420
1387 TATGAAACAATGCTGATTTTATCATCAACAGACATACCAAGAAATTCCTGGAAGCAAAA 1446
1421 CATGAATCAACATGATTTATCATCAACAGATCACTTCAAGAAATTCCTGGAAGCAAGA 1480
1447 TACTGTGGACAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
1481 CACTGTGGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1540
1507 CCATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
1541 GCATGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1603
1567 CATATCTTTCCACATACAGAGAGGACAGACATCACTCTCTCTCTCTCTCTCTCTCTCTCT 1626
1601 TGTCTATCTCCGCTACACGAGAGGCTACAGAGAGGCTACGCTTTCACCTGAAATTTGA 1660
1627 AAATTTGATTTATGACCCGAGAGCAAAAGATGAAACATTTGGGCTTGGATGACCGGTC 1686
1661 GGAGCTTCTCTACAGTGAAGTGCAGAGATGAAACACAGCTTTGATTTGAAGACAGAA 1720
1687 AAGGCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1746
1721 CAAGCCATATATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1780
1747 CGAAGCTTTTGTCTAAGTGCCTAAGCTGAGGAGCTGTTAAACCTTGTCTGTCTGCGCG 1806
1781 TGAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1840
1807 GTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
1841 TGACCAAGG---CAATGAGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1897
1867 TGAACATCATCAAGAGCCCAACTGTTGTTGGGAGATGTTCCGCTGATCTCTGCGCAGACAA 1926
1898 CGGCTCATTTGACCAAGTACAGATTTGAGAGGACATATCCGCTGATCTCAGCTCAGATGAA 1957
1927 CAGGCGCCGTTACCGGAGGCTCTATGCTGATCATGCTGATATCCCATGCTTCTTCTGATA 1986
1958 CCGGTTGCTGACCGGAGGAGTTGATCCGATCATTTTGACACCAAGGAGAGCTTTGTCGA 2017
1987 GCGGCTTGTATGAGAGCTTGTGCTCTCAACCTGCTGAGGAGCCATGACCTTGGGCTTCC 2046
2018 GCTGCAATTTATGAGAGGCTTGTGCTGCTGATGATGAGAGCCATGACATGATGATGCTCC 2077
2047 TACTTGGAGAGGCTGATGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2106
2078 AACAATGCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2137
2107 CCACATTTGACCCGCTACACCCCGAAGAGGCTGTTAATCTGATGATGATGATGATGATGATGAT 2166
2138 GCACATTTGATCTTACCAAGTACAGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 2197
2167 GTGAGACAGAGCCCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226
2198 GTGAGACAGAGATTTCAACTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2257
2227 CGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2286
2258 CGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2317
2287 TTTTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2346
2318 ATTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2377
2347 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2397
2378 CTATGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2428

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RESULT 14
ID AD68521
AD68521 standard; cDNA; 2754 BP.
AC AD68521;
DT 18-DEC-2003 (first entry)
DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:13.
XX
XX Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
XX biosynthetic pathway; plant; gene; ss.
XX
XX Schedonorus arundinaceus.
XX
XX W02003040306-A2.
XX
XX 15-MAY-2003.
XX
XX 07-NOV-2002; 2002WC-N2000239.
XX
XX 07-NOV-2001; 2001US-0337703P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (WRIGHT-) WRIGHTSON SEEDS LTD.
XX
XX Demmer J, Forster RL, Gibson JB, Shenk MA, Norris MG, Glenn M;
XX Saulsbury KW, Hall C;
XX
XX WPI: 2003-441544/41.
XX P-FSDB; AD68521.
XX
XX New polynucleotide encoding polypeptides from Lolium perenne or Festuca
XX arundinacea, useful for modulating the biosynthesis of lignin, fructan or
XX tannin in a plant.
XX
XX Claim 1; SEQ ID NO 13; 240BP; English.
XX
XX The present invention describes isolated polynucleotides (i) encoding
XX proteins (ii) from Lolium perenne and Festuca arundinacea which are
XX active in lignin, fructan and tannin biosynthetic pathways. Also
XX described: (1) an isolated oligonucleotide probe or primer comprising at
XX least 10 contiguous residues complementary to 10 contiguous residues of
XX (i); (2) a kit comprising the oligonucleotide probe or primer; (3) a
XX genetic construct comprising (i); (4) a transgenic plant cell comprising
XX the genetic construct of (3); (5) a plant or its seed, fruit or progeny
XX comprising the transgenic plant cell of (4); (6) modulating one or more
XX of the lignin, fructan or tannin compositions of a plant; (7) producing a
XX plant having one or more of the lignin, fructan or tannin compositions;
XX and (8) modifying the activity of (ii) involved in a lignin, fructan or
XX tannin biosynthetic pathway in a plant. (i) can be used for modulating
XX the biosynthesis of lignin, fructan or tannin in a plant. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 2754 BP; 652 A; 685 C; 684 G; 733 T; 0 U; 0 Other;
XX
XX Query March 41.1%; Score 1125.2; DB 9; Length 2754;
XX Best local similarity 67.5%; Pred. No. 2e-244;
XX Matches 1615; Conservative 0; Mismatches 766; Indels 9; Gaps 2;
XX
XX 7 CCAGCGCTCCGCGACACCGCTGAGAGACCTTCACGAGACCGCAAGAGCTGTGCG 66
XX 136 CCAAGATCTCCGAGAGCGCTTGTGACACTTCTCTCCATCCCAAGAGCTCATTCG 195
XX
XX 67 CTTCTCTGCAAGTACGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
XX 196 CTTCTTTTCAAGTATGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255
XX
XX 127 GCGCTGAGAGAGTCCAGAGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 186
XX 256 TGAATTTGAGAGCATTTGATGATG-----ACAAGAGAGAGATGACCTTTTCAAGA 309

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Db	24E7 CTAGCCTGTGAAGTACCGAGCCTG3GAGCTCAGCTCAGTTCATTTG3GTGTGAC 2518
Db	24E7 CTAGCCTGTGAAGTACCGAGCCTG3GAGCTCAGCTCAGTTCATTTG3GTGTGAC 2518
XX	RESULT 15
XX	ABK98516
XX	ABK98516 standard; cDNA; 2829 BP.
XX	21-OCT-2002 (first entry)
DE	cDNA sequence encoding perennial ryegrass sucrose synthase.
XX	Perennial ryegrass; sucrose phosphate synthase; SPS; invertase; INV;
XX	sucrose synthase; SS; sucrose:sucrose 1-fructosyltransferase; SST;
XX	sucrose transporter; ST; fructan:fructan 1-fructosyltransferase; FFT;
XX	sucrose:fructan 6-fructosyltransferase; soluble carbohydrate transport;
XX	SFT; soluble carbohydrate metabolism; plant; gene; ss.
XX	Sodium perenne.
XX	MO200231130-A1.
XX	18-APR-2002.
XX	10-OCT-2001; 2001WO-AU001275.
XX	10-OCT-2000; 2000AU-00000673.
XX	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
XX	(AGRE-) AGRESEARCH LTD.
XX	Spangenberg G, Sawbridge TI, Ong EK, Emerling M;
XX	WP1: 2002-444177/47.
XX	P-PSDB; ABG69063.
PT	New enzymes and transporter proteins involved in metabolism and/or
PT	transport of soluble carbohydrates, useful as molecular genetic markers,
PT	and in modifying soluble carbohydrate metabolism and/or transport in
XX	plants.
XX	Claim 5; Fig 74; 177bp; English.
CC	The present invention relates to the isolation of polynucleotide
CC	sequences encoding perennial ryegrass enzymes or transporter proteins
CC	selected from sucrose phosphate synthase (SPS), invertase (INV), sucrose
CC	synthase (SS), sucrose transporter (ST), sucrose:sucrose 1-
CC	fructosyltransferase (SST), fructan:fructan 1-fructosyltransferase (FFT),
CC	and sucrose:fructan 6-fructosyltransferase (SFT). The nucleic acid
CC	sequences of the invention are useful as molecular genetic markers, to
CC	isolate cDNAs and genes encoding homologous proteins from the same or
CC	other plant species, and for the modification of soluble carbohydrate
CC	metabolism and/or transport in plants. The polypeptide sequences may be
CC	used to immunise animals to produce antibodies with specificity for the
CC	proteins, and these antibodies may then be used to screen cDNA expression
CC	libraries to isolate full-length cDNA clones of interest. ABK98425-
CC	ABK98516 represent nucleotide sequences encoding perennial ryegrass
CC	enzymes or transporter proteins involved in the metabolism and/or
CC	transport of soluble carbohydrates
XX	Sequence 2829 BP; 697 A; 678 C; 697 G; 757 T; 0 U; 0 Other;
XX	Query Match 41.1%; Score 1124.2; DB 6; Length 2829;
XX	Best Local Similarity 67.5%; Pred. No. 3.4e-244;
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2 (bases 1 to 2710)
Helentjans, T.
Direct Submission
Submitted (10-OCT-2001) Agronomic Traits/T&D, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA

FEATURES
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Location/Qualifiers

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ACCESSION AK099406
 VERSION AK099406.1 GI:32984615
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 Echinozoideae; Oryzae; Oryza.

REFERENCE
 AUTHORS The Rice Full-Length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team;

Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kikuchi, N., Yabuchi, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Nishikawa, T., Onoda, E., Yabuchi, M., Suzuki, K., Li, C.,
 Ohtsuka, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group; Ohtsuka, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, U., Kawamata, M., Yoshimura, A., Miura, U.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice
 Science 301 (5631), 376-379 (2003)
 22752273
 12869764
 JOURNAL MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 COMMENT
 URL : http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kikuchi, N., Yabuchi, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishikawa, T.,
 Onoda, E., Yabuchi, M., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and
 Yamamoto, M.
 FALS Genome Sequencing & Analysis Group: Ohtsuka, K., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, U., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, U.,
 Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashidume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Oosato, N.,
 Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
 Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
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Oryza sativa (japonica cultivar-group)
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The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Naitoh, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohnuki, K., Shishiki, T., Foundation of Advanced Science of International
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Iida, Y., Sugano, S., Fujimura, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Naitoh, K., Sugiyama, A., Mizuno, K., Yokomizo, S., Mikura, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., RIKEN,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, U., Carninci, P., Adachi, J., Aizawa, K., Aizawa, T., Fukuda, S.,
Hara, A., Hashizume, M., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
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Saito, R., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
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Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Doi, K.,
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Nunakura, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Otsu, N., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
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Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
Yamada, H., Yamamoto, M., Yasumishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.
Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica
rice.
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NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Naitoh, T.,
Ohnuki, K., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
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Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Aizawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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Yasumishi, A. and Hayashizaki, Y.
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Best local similarity 86.1%; Pred. No. 0;
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
 Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
 Plant genes involved in defense against pathogens
 Patent: WO 03000898-A 2904 03-JAN-2003;
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Query Match 65.2%; Score 1784.2; DB 6; Length 2412;
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ORIGIN

Query Match 48.7%; Score 1332.8; DB 8; Length 2765;
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 Matches 1743; Conservative 0; Mismatches 657; Indels 6; Gaps 1;

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 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1

AUTHORS Harper, J. F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 021655-A 2415 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

FEATURES

Location/Qualifiers
1. 2430
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ORIGIN

Query Match 45.2%; Score 1238.4; DB 6; Length 2430;
Best Local Similarity 70.4%; Pred. No. 1e-208;
Matches 1672; Conservative 0; Mismatches 696; Indels 6; Gaps 1;

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VERSION AY142511.1 GI:23296412
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ORGANISM Arabidopsis thaliana
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, Y.W.,
Lee, J.M., Quach, H.L., Tang, C., Toriumi, M., Wallender, E.K., Wong, C.,
Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J.,
Narusaka, M., Nguyen, M., Palm, C.U., Sakurai, T., Satou, M., Seki, M.,
Shim, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 2506)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, Y.W.,
Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K.,
Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J.,
Narusaka, M., Nguyen, M., Palm, C.U., Sakurai, T., Satou, M., Seki, M.,
Shim, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
Submitted (16-AUG-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RFLP cDNAs (RAFL CDNA: 'RIKEN
Arabidopsis Full-length CDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGSC (SSP) Consortium members constructed and

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sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K.,
Chan, M.M., Chang, C.H., Dale, J.M., Deng, J.M., Hsuan, Y.W., Lee, J.M.,
Quach, H.L., Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C.,
Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J.,
Nguyen, M., Palm, C.U., Shim, P., Southwick, A., Tripp, M.G., Wu, T.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGSC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGSC) contributed equally to this work as PIs.
Annotation is based on the January 2002 version of the Arabidopsis
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 Shim, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
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 Direct Submission
 Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory
 (SIGAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinohara, K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Shim, P., Chen, H.,
 Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Barth, J., Bowser, L.,
 Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G.,
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 Davis, R.W., Theologis, A. and Ecker, J.R.
 Shim, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinohara, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
 contributed equally to this work as PIs.
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sequencing and annotation of the RAF1 cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banno, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Tosi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, J., Chen, R., Check, R., Jones, T., Karlin-Neumann, G., Kim, C., Kosem, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Pal, C.J., Shim, P., Sotnick, A., Tracy, S.E., Davis, R.W., Eckert, J.R. and Theologis, A. Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to Genbank.

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gene

3'UTR

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 Db 232 GCGCGGAGTTTGGAGATACGTCGCGCTCAACGTTCAAGAGTCGCGCGACGACTCA 311
 QY 492 GACCTGGGTTGGGAATAATGTTGTTAAAGTCTTCAGGCTAATGTGGAACAAATTAA 551
 Db 312 CAGCTCGGAGTACCTCCGCTCAAGAGAGAGCTTGTACGCGCGCAACAATGATCCCT 371
 QY 552 CAGCTCTGAGATATCTTCTTCAAGAGAACTGCTGATGAGACCTAATGAGACCTT 611
 Db 372 AGCTTCGAGCTGATCTGAGCGCGTTCAATGTCTCACTCCACGCGCAATGCGTAT 431
 QY 612 TTGTCTTGAAGTTATTTGAGCCCTTAAAGCAAGCTGACACGCTTCTGCTGCT 671
 Db 432 CATCTATTGAAACGGTGTGCAAGTCTCAACCGACACTTGCTGCTCAATGATGCGCA 491
 QY 672 CTTCGATGTGATGAGTCAAGTCAAGTCTCAATGCTACTGCTGCTGATGATGCTGA 731
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 Db 612 CTGAGAGACATCTGTCAAGCTCCGCTGACACCACTACATCTGCAATTTGCTATAAT 671
 QY 852 CAGAAATCATATCTTCAAGCTTCAAGAACTCCGCTGCTGAGATTTGGAATACCGCT 911
 Db 672 TTCAAGAGTGGGCTCGAGAAAGGTTGGGATGATCAGAGACATGTTTGAATAATGA 731
 QY 912 TCGAAGATGGGTTTGAAGAAAGATGGGAAATCCGAGAGAGGTTCTTGAATAATGA 971
 Db 732 TCCATCTCTTCAAGATCATCTGAGCGCGCAAGCCATCTACCTAGAGAAATCTTTGG 791
 QY 972 TGCATCTCTCTGATATCTTCAAGCTCTGATCTTCTGCTGAGAGAGTTCTTGG 1031
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 Db 912 GTGCACTGAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 971
 QY 1152 GTGCGCTTGAAGCTGAATCTGTTGAAATGAAGACAGAGGTTGATATATTCACCTTA 1211
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 Db 1272 AGTGCAACTGCTCATGCTCTGAAAGACAAAGATCCAGATTCAGATATATTTGGA 1331

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QY	1392	ACAAATGCTGATTTATTCATCCACACGACATATCCAAAGAAATTTGCTGGAAGCAAAATACTG	1451
Db	1632	ACAAAGCAGATTTCTATCATCCACACCACTTACCAAGAAATGCAAGAAACGAAACACCG	1691
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Db	1692	TGGCTCAATATGAAAGCCACCGGGCTTTTACGCTCCCGGACCTATATAGATGATGACAG	1751
QY	1512	GGATTCAGTGTCTGTCATCCCAAGTTTCATATATGTTCTCTCGAGCTGACATGTCATAT	1571
Db	1752	GCATTCAGTGTGTTGATTCGAAAGTTTCAACATATGTCCTGCTCGGTGCACATGACCATAT	1811
QY	1572	ACTTTCACATATCCGAGAGAGCCCAAGCACTCACTCTTCCATATGTTCAATCCAAATTT	1631
Db	1812	ATTTCCCGGTATTTCCGAAGAAACTGAGAGACTTACAGCTTTACATATGTTCAATAGAGAA	1871
QY	1632	TGATTTATGACCCCGAGAGAAACATGTAACATTTGGCATCTGATGACCGTCCAAAGC	1691
Db	1872	TGCTCTATAGCCCTGCACCCAGACTATAGACTATGCTGCTGACACTAGATGATGATCCAAAGC	1931
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Db	1932	CAATACTTCTCTATGCGCGAGGCTCCGACAAAGTGGAGAACATCTCCGGTTAGTTGAGA	1991
QY	1752	CTTTTGCTAAGTGGCTAAGCTGAGAGAGCTGTGTAACCTTGTGCTGCTTCCGGGTACA	1811
Db	1992	TGATATGATTAAGAACACAAAGTTGAGGGAGCTGTGTTAATCTGTTGTAATAGCTGTAAAC	2051
QY	1812	ATGATGTCACAAAGCTCCAAAGGACAGGGAAAGATCCGGAGATATGAGAAAGTGCATGAC	1871
Db	2052	CTGATGTCACAAAGCTCCAAAGATATGAGAAAGAAATGCTAGAGATTTGAGAAATGTCATAAC	2111
QY	1872	TCATCAAGACCCACAACTGTTCCGGCAGTTCCGCTGGATCTCTGCCAGACAAACAGG	1931
Db	2112	TTATGAAAGATTAACAAGCTGATGAGACAGTTTCTGTTGATACGTCTCAAGCTAACCGAG	2171
QY	1932	CCCGTAAACGAGACCTCATGCGTACATCCGTGATATCCCAAGTGTCTTGGTACAGCCG	1991
Db	2172	CTCGAAATATGGAAGCTTTACCGCTACATCCGGGATTAACAAGAGTGTCTTGGCTCAGCCTG	2231
QY	1992	CCCTGTATGAAAGCTTCGAGTCTCAACCGCTCGTTGAGGCCATACCTGTGGGCTTCTACTT	2051
Db	2232	CGTTCTACGAGGCTTTTGGACTTACGTAATCGTAATGGAAGGATATCACTTGGCGGCTCCGACTT	2291
QY	2052	TTCGAGACGCTTCATGAGAGTTCACAGTATGATCATAGACATGACGCTCCGGCTTCCACA	2111
Db	2292	TTGCACTTTGTCACGGGGGTTCACACAGATCATTCAGACACCGGCTCTCCGATTTCCACA	2351
QY	2112	TTGACCCGTACACCCCGGAACAGGCTGTGTAATTCGATGGCCGACCTTCTGACCCGGTGA	2171
Db	2352	TTCGATCTATACCACTCTGAGAGACCGGGTAACTAATATGCTGATTTCTTGAACGTTGTA	2411
QY	2172	AGCAAGACCCAGATCACTGGGTGTAATATCTGAGGACAGGCTGCAAGGCAATATACGAGA	2231
Db	2412	AGGAAGATTCGAACCATTTGGAAGAAATATACAGCGCTGCTCCAAAGGATATACGAA	2471
QY	2232	AGTACACATGGAATAATATCTACAGAGAGTTGATGACACTGGCCGGGGTCTACGCTTCT	2291
Db	2472	GGTACACATGGAATAATATCTACAGAGAGTTGATGACACTGGGGGTGTGTATGATGCTTCT	2531
QY	2292	GGAAGTACGTTGTCAGAGCTCGAGAGGCTGAGAGATGAGAGCGCTACCTTGAAGATGTTCTACA	2351
Db	2532	GGAATATCGTATCGAAATTTGAGAGCTGTGTGAGACTCGGCGCATATCTTGAATGTTCTACA	2591
QY	2352	TACTGAAGTTCCCGAGAGCTGGCCAAAGCCGTGCC	2385
Db	2592	TTGTCAAATTCGCGACTGTGTGAAATCTGTCC	2625

	RESULT	15			
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	DEFINITION	Sequence 4 from Patent WO9428146.			
	ACCESSION	A41498			
	VERSION	A41498.1	GI:2297152		
	KEYWORDS				
	SOURCE				
	ORGANISM	Beta vulgaris subsp. vulgaris Beta vulgaris subsp. vulgaris Euarctica, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta. 1 (bases 1 to 2563) Hesse,H. and Mueller-Roeber,B. DNA SEQUENCES AND PLASMIDS FOR THE PREPARATION OF SUGAR BEET WITH CHANGED SUCCROSE CONCENTRATION Patent: WO 9428146-A 4 08-DEC-1994; HOECHST SCHERING AGREVO GMBH (DE) Other publication DE 4317596 941201. Location/Qualifiers 1..2563 /organism="Beta vulgaris subsp. vulgaris" /mol_type="unassigned DNA" /sub_species="vulgatis" /db_xref="taxon:3555" /clone_id="PHAGE LAMDA ZAP"			
	REFERENCE				
	AUTHORS				
	TITLE				
JOURNAL	COMMENT				
FEATURES	source				
ORIGIN					
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	Best Local Similarity	70.9%;	Prod.No.5.2e-198;		
	Matches 1592;	Conservative 0;	Mismatches 647;	Indels 6;	Gaps 2
Oy	164	CTAGCGGAGGGACCCTTCTGTGCATGTCCTCCGCCCTCCGCAAGGAGCGCATCGTGCGCG	223		
Db	21	CTTAGCGATGCCCCCTTTAGGAAGTTCTTAGGCTGTGCTCACGAAACAATACTTGTTCT	80		
Oy	224	CCGTTGCTGGCCATTGCGGATGCGCGGCCGCCGCGAGTTTGAGAGTAAGTCCGCTCAAC	283		
Db	81	CCCTTTGTTGCTAATAGACAGTCCGTCCAAAGACTGAGTTTGGAATATGTTGTTTAAAT	140		
Oy	284	GTTAACAGCTCAACGCTGAGCACTCAAGCTTCGAGTAACCTCCGCTTCAAGAAGAGAG	343		
Db	141	GCTCTGAATCGAATGAGAGCACTTAATGTTCTGAGTAATCTTCATTTCAAGAGAGAA	200		
Oy	344	CTTGTGCAAGCGCCAGCAATGATTCCTACGTTCTGAGCTTGAATTCGAGCCGTTCAAT	403		
Db	201	CTTGTGATGTAAGAAGGCTGATGACCACTATATGTTGACTTGAATTCGAGCCCTTTAAT	260		
Oy	404	GTTCTAGTCCCAGGCCCAATCGGTATCATCTATTTGAAAACGTTGCAAGTTCTCAAC	463		
Db	261	GAATCAGTTTCACTCCAATCTCCCTTTCATCAATTGTTAATGTTGTTGTTCAAT	320		
Oy	464	CGACACTGTTCTCAATCATGTTCCGCAAGAGGATGCTTGAAGCCCTGTGGAATTC	523		
Db	321	CAGCACTGTATATACATATATGTTCTGCAACAAGATTTGTTGAGCCCTTACTTATTTTT	380		
Oy	524	CTCCGTGAGCAACCGGCAACAGGGGATGTTATGATGCTTATATGTAATCAAGAATCTG	583		
Db	381	CTTAGAGTGCACAAATCTAAAGAGTTGTCAATGATTTGAATGATCGATACAGACTATC	440		
Oy	584	GGAGGCTTCAAGTGTGCTGACCAAGCTGAGAGACACTGTTGAAAAGTCCCTGCTGAC	643		
Db	441	CAGGCTTCAAGTGTGCTGATGCTTAAGCTGAGATTTATCTTATCAAACTTCAGCAAT	500		
Oy	644	ACACACTACTCACATTTGCTTATTAATTTCAAGATGAGGAGCTGAGAAAGTTGGAGT	703		
Db	501	ACACTTACTCTGAGTTGCAATTTGTAATCCAAAGTATGGTTTTGAAAAGAGGCTGGAGT	560		
Oy	704	GATNAGCAGACATGTTTTGAAATATATCATCTCTTCTAGACATATCTACAGCGCA	763		
Db	561	GATACGTCTAAAGGGTTCTAGAAATATGATGATCTACTCAATGATATCTTCAAGGCTCC	620		

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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:28:09 ; Search time 41.6803 Seconds

(without alignments)
5413.769 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247

Sequence: -MSAPKLNRMASIRDRVEDTL.....YILKREIAKTVPLAIQDPQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications: AA:*

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2: /cgn2_6/prodata/1/pubppaa/PCR_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubppaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4247	100.0	809	14	US-10-080-114A-12
2	4177	98.4	802	14	US-10-080-114A-2
3	3427	80.7	824	12	US-10-425-114-45934
4	3420	80.5	651	12	US-10-425-114-45911
5	3407	80.2	812	12	US-10-424-599-241731
6	3129	73.7	797	14	US-10-217-939-30
7	3108.5	73.2	805	14	US-10-217-939-28
8	3011.5	70.9	802	14	US-10-080-114A-5
9	3011.5	70.9	807	12	US-10-425-114-57840
10	3011.5	70.9	811	12	US-10-425-114-53965
11	3001	70.7	823	12	US-10-425-114-53296
12	3001	70.7	823	12	US-10-425-114-56696
13	3001	70.7	823	12	US-10-425-114-57139
14	3001	70.7	823	12	US-10-425-114-72813
15	2993.5	70.6	805	12	US-10-424-599-258404

16	2997	70.6	816	14	US-10-080-114A-7	Sequence 7, Appli
17	2987.5	70.3	805	12	US-10-425-114-54297	Sequence 54297, A
18	2986.5	70.3	805	12	US-10-424-599-154986	Sequence 154986,
19	2976.5	70.1	815	14	US-10-289-757-170	Sequence 170, App
20	2972	70.0	806	13	US-10-003-405-2	Sequence 2, Appli
21	2972	70.0	814	14	US-10-289-757-76	Sequence 76, Appli
22	2949.5	69.4	806	12	US-10-424-599-154300	Sequence 154300,
23	2949.5	69.4	806	12	US-10-424-599-154301	Sequence 154301,
24	2948.5	69.4	811	12	US-10-425-114-55184	Sequence 55184, A
25	2948.5	69.4	811	12	US-10-425-114-50176	Sequence 50176, A
26	2947	69.4	816	14	US-10-289-757-169	Sequence 169, Appl
27	2942.5	69.3	808	14	US-10-289-757-169	Sequence 77, Appl
28	2938.5	69.2	808	14	US-10-289-757-74	Sequence 74, Appli
29	2924.5	68.9	808	14	US-10-289-757-75	Sequence 75, Appli
30	2892.5	68.1	805	14	US-10-137-036-77	Sequence 77, Appli
31	2892.5	68.1	805	15	US-10-393-840-44	Sequence 44, Appli
32	2892.5	68.1	805	15	US-10-393-840-144	Sequence 144, App
33	2882.5	67.9	749	12	US-10-425-114-56196	Sequence 56196, A
34	2763	65.1	528	12	US-10-425-114-48418	Sequence 48418, A
35	2595.5	61.1	670	12	US-10-425-114-49869	Sequence 49869, A
36	2534	59.7	567	12	US-10-424-599-241719	Sequence 241719,
37	2485.5	58.5	639	12	US-10-425-114-58450	Sequence 58450, A
38	2474.5	58.3	652	12	US-10-425-114-46682	Sequence 46682, A
39	2439.5	57.4	628	12	US-10-424-599-244151	Sequence 244151,
40	2423.5	57.1	619	12	US-10-425-114-68121	Sequence 68121, A
41	2362.5	55.6	596	12	US-10-425-114-62525	Sequence 62525, A
42	2361.5	55.6	593	12	US-10-425-114-50109	Sequence 50109, A
43	2193	51.6	541	12	US-10-425-114-50160	Sequence 50160, A
44	2119.5	49.9	570	12	US-10-425-114-54291	Sequence 54291, A
45	2097.5	49.4	527	12	US-10-425-114-62397	Sequence 62397, A

ALIGNMENTS

RESULT 1
US-10-080-114A-12
Sequence 12, Application US/10080114A
Publication No. US20030005482A1
GENERAL INFORMATION:
APPLICANT: Dhugga, Kanwarpal S.
TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
FILE REFERENCE: 1301P
CURRENT APPLICATION NUMBER: US/10/080, 114A
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/270, 777
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 809
TYPE: PRT
ORGANISM: Zea mays

Query Match 100.0%; Score 4247; DB 14; Length 809;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSAPKLNRMASIRDRVEDTLHAHRELVALLSKYVNGKGILOPHHIDALDEVGSGVR	60
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DB	61	ALARGPFLDVRSGOEIVLPPFAIVRPARGWEYRVNVVHLSVQULTVSEYLRKE	120
QY	121	ELVDGQNDPYVLELDEPNVSVPRNRSSISNGVOFLNRHLSITFRRDCEPLD	180
DB	121	ELVDGQNDPYVLELDEPNVSVPRNRSSISNGVOFLNRHLSITFRRDCEPLD	180
QY	181	FLRGHRKHGVMLNDRIOSIGRIQSVLTAEHLSKLPADTPYSQFAAYKQEWGJERKQW	240

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Db      181  FARGHKKHVMNMDRIQSLGRLOSVLTKAEHLSKLPAIDTPYSQFAFKPQWGLEKGM 240
Qy      241  GPAGGVLEMLHLLDITIQAPBPSTLEKLGRIPMIFNVVVSPPHYFGQANVLGLPDS 300
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Qy      301  GOIYVILDOVRALENEMVRLKKQGLDVSFKLIVTRLIPDAKGSQNRLEKISGTH 360
Db      301  GOIYVILDOVRALENEMVRLKKQGLDVSFKLIVTRLIPDAKGSQNRLEKISGTH 360
Qy      361  YLRVPPNENGILKKMISRPDWPYLETFADDAAGEIAELQGTDFLLIGVSDGNLVA 420
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Qy      421  SLSTYKMGITQCNIAHAEKTYPPSDIFWKNFDEKHYSCQFTADIIAMNADFLITST 480
Db      421  SLSTYKMGITQCNIAHAEKTYPPSDIFWKNFDEKHYSCQFTADIIAMNADFLITST 480
Qy      481  YOEIAGSKNTVQGVESHFAFTLPGYRVVHGIDVDPKFNIVSPGADMSIYEPHTEKAR 540
Db      481  YOEIAGSKNTVQGVESHFAFTLPGYRVVHGIDVDPKFNIVSPGADMSIYEPHTEKAR 540
Qy      541  LTSLSGSIENLIDYDQNDENHGHLDORSKPLIFSMARLDRYKNITGLVEAPAKCAKRE 600
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Db      601  LVNLVAVAGYDYNVSKDREELAEIKEMHLLKTNLFGQFRWISQOTRANGELRYRI 660
Qy      661  ADTHGAFVQPALYAEAGLTVFAMTCGLPTFATLHGSPALIEHGVSGFHIDPYHEQAV 720
Db      661  ADTHGAFVQPALYAEAGLTVFAMTCGLPTFATLHGSPALIEHGVSGFHIDPYHEQAV 720
Qy      721  NIMADFPDCKODPDHVNISAGLQRIYKTYKTIYSERLMTLAGVYFWKYSXLERL 780
Db      721  NIMADFPDCKODPDHVNISAGLQRIYKTYKTIYSERLMTLAGVYFWKYSXLERL 780
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Db      781  ETRRYLEMFIILKPRELAKTVPLAIDQ 809

RESULT 2
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; Sequence 2, Application US/10080114A
; Publication No. US20030005482A1
; GENERAL INFORMATION:
; APPLICANT: Zhuoga, Karwaral S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080,114A
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Zea mays
US-10-080-114a-2

Query Match      98.4%; Score 4177; DB 14; Length 802;
Best local Similarity 99.9%; Pred. No. 0;
Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      7  DREVTTLAHRNELVALSKYVKKGIIQPHIILDALDEVQSGVRALAEAPFLDVS 66

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Qy      134  ELDPFENVSVPRNRSISGNGVDFLNHLSIMFRNDCLEPLIDPLRGRHKKHVM 193
Db      127  ELDPFENVSVPRNRSISGNGVDFLNHLSIMFRNDCLEPLIDPLRGRHKKHVM 186
Qy      194  LMDRIQSLGRLOSVLTKAEHLSKLPAIDTPYSQFAFKPQWGLEKGMGDAHVLEMIH 253
Db      187  LMDRIQSLGRLOSVLTKAEHLSKLPAIDTPYSQFAFKPQWGLEKGMGDAHVLEMIH 246
Qy      254  LLDITIQAPBPSTLEKLGRIPMIFNVVVSPPHYFGQANVLGLPDSGOIYVILDOVRAL 313
Db      247  LLDITIQAPBPSTLEKLGRIPMIFNVVVSPPHYFGQANVLGLPDSGOIYVILDOVRAL 306
Qy      314  ENEWVRLKKQGLDVSFKLIVTRLIPDAKGSQNRLEKISGTHYTLIRVPPNENG 373
Db      307  ENEWVRLKKQGLDVSFKLIVTRLIPDAKGSQNRLEKISGTHYTLIRVPPNENG 366
Qy      374  LKKWISRPDWPYLETFADDAAGEIAELQGTDFLLIGVSDGNLVAASLSTYKMGITQCN 433
Db      367  LKKWISRPDWPYLETFADDAAGEIAELQGTDFLLIGVSDGNLVAASLSTYKMGITQCN 426
Qy      434  IAHAEKTYPPSDIFWKNFDEKHYSCQFTADIIAMNADFLITSTYOEIAGSKNTVQ 493
Db      427  IAHAEKTYPPSDIFWKNFDEKHYSCQFTADIIAMNADFLITSTYOEIAGSKNTVQ 486
Qy      494  YESHTAFTLPGYRVVHGIDVDPKFNIVSPGADMSIYEPHTEKARLTSLSGSIENL 553
Db      487  YESHTAFTLPGYRVVHGIDVDPKFNIVSPGADMSIYEPHTEKARLTSLSGSIENL 546
Qy      554  DEQNDENHGHLDORSKPLIFSMARLDRYKNITGLVEAPAKCAKRELVNLVAVAGYD 613
Db      547  DEQNDENHGHLDORSKPLIFSMARLDRYKNITGLVEAPAKCAKRELVNLVAVAGYD 606
Qy      614  NKSXOREELAEIKEMHLLKTNLFGQFRWISQOTRANGELRYRIADTHGAFFVQPALY 673
Db      607  NKSXOREELAEIKEMHLLKTNLFGQFRWISQOTRANGELRYRIADTHGAFFVQPALY 666
Qy      674  EAFGLTVFAMTCGLPTFATLHGSPALIEHGVSGFHIDPYHEQAVNIMADFPDCKOD 733
Db      667  EAFGLTVFAMTCGLPTFATLHGSPALIEHGVSGFHIDPYHEQAVNIMADFPDCKOD 726
Qy      734  PDHVNISAGLQRIYKTYKTIYSERLMTLAGVYFWKYSXLERLETRRYLEMFIILK 793
Db      727  PDHVNISAGLQRIYKTYKTIYSERLMTLAGVYFWKYSXLERLETRRYLEMFIILK 786
Qy      794  PRELAKTVPLAIDQ 809
Db      787  PRELAKTVPLAIDQ 802

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RESULT 3
US-10-425-114-45934
; Sequence 45934, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Iju, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 45934
; LENGTH: 824
; TYPE: PRT

```

ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3051-038-E10_FLI.pep
 US-10-425-114-45914

Query Match 80.7%; Score 3427; DB 12; Length 824;
 Best Local Similarity 79.3%; Pred. No. 3.7e-307;
 Matches 638; Conservative 81; Mismatches 84; Indels 2; Gaps 1;

```

QY 4 PKLNRAASIDRVEDTLAARNELVALLSKYVKGKGLQPHHLLDADVQ--SGVRA 61
DB 17 PKLGRIPSIDRVEDTLAARNELVALLSKYVKGKGLQPHHLLDADVQ 76
QY 62 LAEGFELVARSQEAIVLPPEVAIAVRPRGVEYRVVNHLSVQLATVSEYLRKER 121
DB 77 LKNGPFGEIYKSAKEAIVLPPEVAIAVRPRGVEYRVVNHLSVQLATVSEYLRKER 136
QY 122 LVDGQNDPVLBLEDEPFNVSVPRNRSSISGVQVFLNRHLSIMFRNDCLEPLD 181
DB 137 LVDGKINDNFEVLEDEPFNVATEPRPRRSASISGVQVFLNRHLSIMFRNDCLEPLD 196
QY 182 LRGRHRKHGMINDRQSLRQSVLTAKAEHSLKLPATPYQPAKYQEWLEKQW 241
DB 197 LRGRHRKHGMINDRQSLRQSVLTAKAEHSLKLPATPYQPAKYQEWLEKQW 256
QY 242 DTAGHVLDEMTHLLDILCAPDPSTLEKELGRIPKIFNVVVVSPHGYEQANVGLPTGG 301
DB 257 DTERERVLEWHLLDILCAPDPSTLEKELGRIPKIFNVVVVSPHGYEQANVGLPTGG 316
QY 302 QIVYIILDOVRALENEVYLRKKGGLDVSPKILVTRLLIPDAKTSNQRLERISGTHTY 361
DB 317 QIVYIILDOVRALENEVYLRKKGGLDVSPKILVTRLLIPDAKTSNQRLERISGTHTY 376
QY 362 ILRPPRRNNGILKKMISRPDVPYLETPEADAAGETAAELQGPDPDIIENYSGNIVAS 421
DB 377 ILRPPRRNNGILKKMISRPDVPYLETPEADAAGETAAELQGPDPDIIENYSGNIVAS 436
QY 422 LLSYKMGITOCNIAHALEKTKYPSDSIFMKNFDEKHYFSCQFTADIIAMNNADFIITSTY 481
DB 437 LLSYKMGITOCNIAHALEKTKYPSDSIFMKNFDEKHYFSCQFTADIIAMNNADFIITSTY 496
QY 432 QELAGSKNTVQYQESHAFLLPGLYRVVHGIDVDFEKNIVSPGADMSIYFPTBKAKRL 541
DB 437 QELAGSKNTVQYQESHAFLLPGLYRVVHGIDVDFEKNIVSPGADMSIYFPTBKAKRL 556
QY 542 TSHGSIENLIYBPQNDHEHGHLDNRSKPILFSMAHLDVKNITGIVYAPAKCAKREL 601
DB 557 TSHGSIENLIYBPQNDHEHGHLDNRSKPILFSMAHLDVKNITGIVYAPAKCAKREL 616
QY 602 VNLVAVAGYDVYKSKDREIATIEKMGHELIKTANLFGQFRMISAQTNRRANGSLYVIA 661
DB 617 VNLVAVAGYDVYKSKDREIATIEKMGHELIKTANLFGQFRMISAQTNRRANGSLYVIA 676
QY 662 DTGAFVQPALYAFGLTVVBAANTGCLPTFALHGGPAELIEHGVSGFHIDPYHPEQAVN 721
DB 677 DTGAFVQPALYAFGLTVVBAANTGCLPTFALHGGPAELIEHGVSGFHIDPYHPEQAVN 736
QY 722 LMADEPDRCKQDDHWNISGAGLQRIYKTKYKISERLMTAGYVGFKKYISKLERLE 781
DB 737 LMADEPDRCKQDDHWNISGAGLQRIYKTKYKISERLMTAGYVGFKKYISKLERLE 796
QY 782 TRRYLEMFYILKREELAKTVPLAID 806
DB 797 TRRYLEMFYILKREELAKTVPLAID 821

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RESULT 4
 US-10-425-114-49911
 ; Sequence 49911, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.
 APPLICANT: Screen, Steven E.
 APPLICANT: Tabaska, Jack E.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 49911
 LENGTH: 651
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: 700551647_FLI.pep
 US-10-425-114-49911

Query Match 80.5%; Score 3420; DB 12; Length 651;
 Best Local Similarity 99.4%; Pred. No. 1.1e-306;
 Matches 647; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 159 FLNRHLSIMFRNDCLEPLDPLRGRHKGHVMMINDRIQSLRQSVLTAKAEHSLK 218
DB 1 FLNRHLSIMFRNDCLEPLDPLRGRHKGHVMMINDRIQSLRQSVLTAKAEHSLK 60
QY 219 PACDPYQPAKYQEWLEKQWGTAGHVLAMTHLLDITCAPDPSTLEKELGRIPKIFN 278
DB 61 PACDPYQPAKYQEWLEKQWGTAGHVLAMTHLLDITCAPDPSTLEKELGRIPKIFN 120
QY 279 VVVVSPHGYEQANVGLPTGGQIVYILDOVRALENEVYLRKKGGLDVSPKILVTRL 338
DB 121 VVVVSPHGYEQANVGLPTGGQIVYILDOVRALENEVYLRKKGGLDVSPKILVTRL 180
QY 339 IPDAKTSNQRLERISGTHTYILRVPPFENNGILKKMISRPDVPYLETPEADAAGEI 398
DB 181 IPDAKTSNQRLERISGTHTYILRVPPFENNGILKKMISRPDVPYLETPEADAAGEI 240
QY 399 AAELOGPDPDIIENYSGNIVASLSYKMGITOCNIAHALEKTKYPSDSIFMKNFDEK 458
DB 241 AAELOGPDPDIIENYSGNIVASLSYKMGITOCNIAHALEKTKYPSDSIFMKNFDEK 300
QY 459 FSCQFTADIIAMNNADFIITSTYQELAGSKNTVQYQESHAFLLPGLYRVVHGIDV 518
DB 301 FSCQFTADIIAMNNADFIITSTYQELAGSKNTVQYQESHAFLLPGLYRVVHGIDV 360
QY 519 FNIVSPGADMSIYFPTBKAKRLTSHGSIENLIYDEQNDHEHGHLDNRSKPILFSMA 578
DB 361 FNIVSPGADMSIYFPTBKAKRLTSHGSIENLIYDEQNDHEHGHLDNRSKPILFSMA 420
QY 579 LDRVKNITGLVYAPAKCAKRELNVLVVAGYDVYKSKDREIATIEKMGHELIKTANL 638
DB 421 LDRVKNITGLVYAPAKCAKRELNVLVVAGYDVYKSKDREIATIEKMGHELIKTANL 480
QY 639 GQFRMISAQTNRRANGSLYVIA DTGAFVQPALYAFGLTVVBAANTGCLPTFALHGG 698
DB 481 GQFRMISAQTNRRANGSLYVIA DTGAFVQPALYAFGLTVVBAANTGCLPTFALHGG 540
QY 699 ABIIIEHGVSGFHIDPYHPEQAVN LMADEPDRCKQDDHWNISGAGLQRIYKTKY 758
DB 541 ABIIIEHGVSGFHIDPYHPEQAVN LMADEPDRCKQDDHWNISGAGLQRIYKTKY 700
QY 759 BRMLTAGYVGFKKYISKLERLE TRRYLEMFYILKREELAKTVPLAID 803
DB 601 BRMLTAGYVGFKKYISKLERLE TRRYLEMFYILKREELAKTVPLAID 651

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RESULT 5
 US-10-424-599-241731
 ; Sequence 241731, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J

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; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 241731
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(812)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1.pep
US-10-424-599-241731

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Query Match      80.2%; Score 3407; DB 12; Length 812;
Best Local Similarity 78.9%; Pred. No. 2,6e-305;
Matches 635; Conservative 81; Mismatches 87; Indels 2; Gaps 1;

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QY 4 PKLNRASTIRDRVEDTLHAHRLNELVALLSKYVKGKGIQLPHIILALDEVQ--SGVRA 61
DB 5 PKLGRLESTEDRVEDTLHAHRLNELVALLSKRYAQGGIQLPHIILALDEVQDAIYD 64
QY 62 LAEGPELDYLSAOEALVLPFVAIAVRPRGWEYRVVNHLSYEOLTVSEYLFKEK 121
DB 65 LKNGPEGLIYKSKAEIVLPFVAIAVRPRGWEYRVVNHLSYEOLTVSEYLFKEK 124
QY 122 LVDGQNDYVLELDEPPENVSVPRNRSSIGNQVQFNRHLSIMFNRDCLPDLDF 181
DB 125 LVDGKXNDYVLELDEPPENVSVPRNRSSIGNQVQFNRHLSIMFNRDCLPDLDF 184
QY 182 LSHRHKGVMMLNDRISIGRLQSVLTAEHLSLDPDTPYSCAPYKQEWLEKKG 241
DB 135 LRAKKGALMLNDRISIGRLQSVLTAEHLSLDPDTPYSCAPYKQEWLEKKG 244
QY 242 LTAGVLEMIHLDDIIOADPSTLEKFLGRIMIFNVVSPHGYFGQANVGLPDTG 301
DB 245 DTAERLEMMHLLDIOADPSTLEKFLGRIMIFNVVSPHGYFGQANVGLPDTG 304
QY 302 QIVYILDOYVALENEMVLRKKGGLVSPKILLVTRILIPAKGTSNORLRSIGQHTY 361
DB 305 QVVYILDOYVALENEMVLRKKGGLVSPKILLVTRILIPAKGTSNORLRSIGQHTY 364
QY 362 ILRVPRNENGLIKKMSREDVWPLYETFAEDAAAGETIAELQGPDTIGNYSQDNLVAS 421
DB 365 ILRVPRNENGLIKKMSREDVWPLYETFAEDAAAGETIAELQGPDTIGNYSQDNLVAS 424
QY 422 LLSYKNGITQCNIAHALLEKTYPSDSIFWNPDEKHYFSCOPTADIIAMNADPITSTY 481
DB 425 LLAAYKGVITQCNIAHALLEKTKYPSDSILYWKKEFKHFSQPTADIIAMNADPITSTY 484
QY 482 QETIASKNATYQYESTHATFLPGIYRVVHGIDVDFPKFNIVSPGALMSIYFPYSEKQNL 541
DB 485 QETIASKNATYQYESTHATFLPGIYRVVHGIDVDFPKFNIVSPGALMSIYFPYSEKQNL 544
QY 542 TSHGSIENLIYDPECNDEHIGLDRSKDILFSMALDRVKNITGTVAFACAKIREL 601
DB 545 TSHGSIENLIYDPECNDEHIGLDRSKDILFSMALDRVKNITGTVAFACAKIREL 604
QY 602 VNLVYAGYDVVSKDREIAIEIKMHELKTHNTFGQFRMI SAQTNRAANGELYEYA 661
DB 605 VNLVYAGYDVVSKDREIAIEIKMHELKTHNTFGQFRMI SAQTNRAANGELYEYA 664
QY 662 DTGGAIVQRLYAFAGITVEAMTCGLPTATLHGGAAITIEHGVSGHTDPVHBRAN 721
DB 665 DTGGAIVQRLYAFAGITVEAMTCGLPTATLHGGAAITIEHGVSGHTDPVHBRAN 724

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QY 722 LMAFEDRCODPDHWNVNSGAGLRIYERYKTIYSERLMTLAGVYGFMYVSKLERLE 781
DB 725 LVEFFQKSKEDSHMKKISDQGLQRIYERYKTIYSERLMTLAGVYGFMYVSKLERLE 784
QY 782 TRRYLEMFYILKRELAKTVPLAID 806
DB 785 TRRYLEMFYILKRELAKTVPLAID 809

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RESULT 6
US-10-217-939-30

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; Sequence 30; Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENDORF, VOLKER
; APPLICANT: HAERTEL, HEIKO A.
; APPLICANT: CIRPUS, BETTA
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS 111
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-939-30

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Query Match      73.7%; Score 3129; DB 14; Length 797;
Best Local Similarity 74.1%; Pred. No. 1.2e-279;
Matches 580; Conservative 102; Mismatches 99; Indels 2; Gaps 2;

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QY 27 LVALLSKYVKGKGIQLPHIILDA-LDEVQSG-VBALGPELDYLSAOEALVLPFV 84
DB 14 LVVIFIRYVAAQGGIQLSHQIDLEFLKTYVNDGTELDNKSPTMKYLQSAEBAIVLPFV 73
QY 85 AIAVRPRGWEYRVVNHLSYEOLTVSEYLFKEELVLDGQNDYVLELDEPPENVSV 144
DB 74 AIAVRPRGWEYRVVNHLSYEOLTVSEYLFKEELVNGHANGDYVLELDEPPENVATL 133
QY 145 PRNRSSIGNQVQFNRHLSIMFNRDCLPDLDFRHRKKGVMMLNDRISIGRL 204
DB 134 PRNRSSIGNQVQFNRHLSIMFNRDCLPDLDFRHRKKGVMMLNDRISIGRL 193
QY 205 QSVLTAEHLSKLPADTPYSCAPYKQEWLEKGGDTAGVLEMIHLDDIIOADPDS 264
DB 194 QGALAAAEELSLPLATPSESEFELQGMGFERGGDTAKVSEMHVHLLDIOADPDS 253
QY 265 TLEKPIGRIMIFNVVSPHGYFGQANVGLPDTGGQIVYIILDOYVALENEMVLRKKG 324
DB 254 VLETFPGRIMIFNVVSPHGYFGQANVGLPDTGGQIVYIILDOYVALENEMVLRKKG 313
QY 325 GLDVPKILLVTRILIPAKGTSNORLRSIGQHTYILRVPRNENGLIKKMSREDVW 384
DB 314 GLDVPKILLVTRILIPAKGTSNORLRSIGQHTYILRVPRNENGLIKKMSREDVW 373
QY 385 PYLETFAEDAAAGETIAELQGPDTIGNYSQDNLVASLSYKNGITQCNIAHALLEKTYP 444
DB 374 PYLETFAEDAAAGETIAELQGPDTIGNYSQDNLVASLSYKNGITQCNIAHALLEKTYP 433
QY 445 DSDIFWNPDEKHYFSCOPTADIIAMNADPITSTYQETIASKNATYQYESTHATFLPG 504
DB 434 BSDIYWNHEDKHFSSQPTADIIAMNADPITSTYQETIASKNATYQYESTHATFLPG 493
QY 505 LRVVHGIDVDFPKFNIVSPGALMSIYFPYSEKQNL 564
DB 494 LRVVHGIDVDFPKFNIVSPGALMSIYFPYSEKQNL 553
QY 565 LDRSKDILFSMALDRVKNITGTVAFACAKIRELVNLVYAGYDVVSKDREIAIEIKMHEL 624

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Db 554 LSDOSKPIIFSEVADLDRVKNLTGLVECYAKNSKXLEIANLVIYGGYIDENOSRDEBMAE 613
Qy 625 IEKHEILIKTNLFGOPRWMISAQTRARANGELYRIADTHGAFYOPALYEAFAGLTVYAM 684
Db 614 IQKHSILIEQYDLGGERMIAAOMRANRANGELYRIADTKVFPQAPAYEAFGLTVESM 673
Qy 685 TCGI:PTFATLHGPAEIIIEHVSGFHIDPYAPBQAVNLMADEPDRCKODPHVNIISGAG 744
Db 574 TCAI:PTFATCGHGPABIIENGVSGFHIDPYAPBQAVNLMADEPDRCKODPHVNIISGAG 733
Qy 745 LORIEKYTWKTYEERLMTAGVYGFMYYSKLELETRRYLEMYIILKEFLAKTVPLA 804
Db 734 LKRIYETWKYKSERLTLTAGVYAFWKVSKLERRETRYLEMYISLKEFLANSIPLA 793
Qy 805 IDQ 807
Db 794 TDE 796

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RESULT 7
US-10-217-939-28
; Sequence 28, Application US/10217939
; Publication No. US20030154512A1
; GENERAL INFORMATION:
; APPLICANT: MITTENDORF, VOLKER
; APPLICANT: HAERTEL, HEIKO A.
; APPLICANT: CIRPUS, PETRA
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
; FILE REFERENCE: 16313-0157
; CURRENT APPLICATION NUMBER: US/10/217,939
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/311,414
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 28
; LENGTH: 805
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-939-28

```

```

Query Match 73.2%; Score 3108.5; DB 14; Length 805;
Best Local Similarity 74.3%; Pred. No. 1e-277;
Matches 579; Conservative 98; Mismatches 97; Indels 5; Gaps 3;

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```

Qy 31 LSKYKNGKGI:OPHILDA-LDEVQSG-VRALABGPF:DLRSQEAIVLPPVLAIV 98
Db 29 LKRYVAGKAILQSHQI:IDFLKTVKVDGTLDELNKSPPMKVL--QEAIVLPPVLAIV 95
Qy 89 RRPQYVWEYRVVNVHLSVYQLTVSEYLRFEKEILDGQNDPVYLELDFEPNVSVPRPN 148
Db 86 RRPQYVWEYRVVNVHLSVYQLTVSEYLRFEKEILDGQNDPVYLELDFEPNVSVPRPN 145
Qy 149 RSSISGNGVOLFNRHLSIFNRNDCL:EPILDLRGHRKHGVMMLNDRIQSLGRLQSVL 208
Db 146 RSSISGNGVOLFNRHLSIFNRNDCL:EPILDLRGHRKHGVMMLNDRIQSLGRLQSVL 205
Qy 209 TKAEHLSKLPATPYSCEAYKFOEWGELKMGDTAGHVLVEMTHLLDITIOADPSTLEK 268
Db 206 ARKEEELSKLPATPYSCEAYKFOEWGELKMGDTAGHVLVEMTHLLDITIOADPSTLEK 265
Qy 269 FLGRIMENNVVVSHPGYFGQANVLGLPTGGQIVILIDQVRLAENEMVLRLKKQGLDV 328
Db 266 FLGRIMENNVVVSHPGYFGQANVLGLPTGGQIVILIDQVRLAENEMVLRLKKQGLDV 325
Qy 329 SPKLLIVTRLIPAKGTSNORLERISGTOHTYILRVPPNENGILKKMISRPDVPYLE 388
Db 326 IPKLLIVTRLIPAKGTSNORLERISGTOHTYILRVPPNENGILKKMISRPDVPYLE 385
Qy 389 TPAEDAGRIAEALOGTPDFTIGNYSQNLVYSLSYKMGITQCNIAHALEKTKYPSDF 448
Db 386 TPAEDAGRIAEALOGTPDFTIGNYSQNLVYSLSYKMGITQCNIAHALEKTKYPSDF 445

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Qy 449 FMKNDEKYPHSCOPTADIIAMNNADPITSTYOBIASSKNTVGOYESHATAFTLPGLYRV 508
Db 446 YMRHEBKYHSSQPTADIIAMNNADPITSTYOBIASSKNTVGOYESHATAFTLPGLYRV 505
Qy 509 VHGIDVDPKXENIVSPGADMSIYPPHTEKAKRLTSIHGSIENLYDPEONDEHIGLDR 568
Db 506 VHGIDVDPKXENIVSPGADMSIYPPHTEKAKRLTSIHGSIENLYDPEONDEHIGLDR 565
Qy 569 SKPLIFSAARLDKRYKNTGLVEAPKAKLRELVLNVVYAGNDVYKSKDEKRIAEIEM 628
Db 566 SKPLIFSAARLDKRYKNTGLVEAPKAKLRELVLNVVYAGNDVYKSKDEKRIAEIEM 625
Qy 629 HELIKTNLFGOPRWMISAQTRARANGELYRIADTHGAFYOPALYEAAGLTVYEMTGL 688
Db 626 HSLIEQYDLGGERMIAAOMRANRANGELYRIADTKVFPQAPAYEAFGLTVESMTCAL 685
Qy 689 PTFATLHGPAEIIIEHVSGFHIDPYAPBQAVNLMADEPDRCKODPHVNIISGAGLORI 748
Db 686 PTFATCGHGPABIIENGVSGFHIDPYAPBQAVNLMADEPDRCKODPHVNIISGAGLORI 745
Qy 749 YERYTWKYSERLTLTAGVYAFWKVSKLERRETRYLEMYISLKEFLANSIPLATDE 804
Db 746 YERYTWKYSERLTLTAGVYAFWKVSKLERRETRYLEMYISLKEFLANSIPLATDE 804

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RESULT 8
US-10-080-114A-5
; Sequence 5, Application US/10080114A
; Publication No. US20030005482A1
; GENERAL INFORMATION:
; APPLICANT: Dhugaa, Kanwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080,114A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270,777
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 802
; TYPE: PRT
; ORGANISM: Zea mays
US-10-080-114A-5

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```

Query Match 70.9%; Score 3011.5; DB 14; Length 802;
Best Local Similarity 70.0%; Pred. No. 9.2e-269;
Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;

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Qy 3 APTLNRASTRDVEOTLHARRNLVALLSKYVNGKGI:OPHILDA-LDEVQSGVRAL 62
Db 2 APTLNRASTRDVEOTLHARRNLVALLSKYVNGKGI:OPHILDA-LDEVQSGVRAL 61
Qy 63 AEGPFLVLSAQAIVLPPVLAIVRPPQYVWEYRVVNVHLSVYQLTVSEYLRFEKEIL 122
Db 62 A--PFEILRAAQAIVLPPVLAIVRPPQYVWEYRVVNVHLSVYQLTVSEYLRFEKEIL 119
Qy 123 VDGQNDPVYLELDFEPNVSVPRPNSSISGNGVOLFNRHLSIFNRNDCL:EPILDL 182
Db 120 VDGQNDPVYLELDFEPNVSVPRPNSSISGNGVOLFNRHLSIFNRNDCL:EPILDL 179
Qy 183 RGRHKGHWMMNDRIQSLGRLQSVLTKAEHLSKLPADPYSQFAKFOEWGELKMGD 242
Db 180 RGRHKGHWMMNDRIQSLGRLQSVLTKAEHLSKLPADPYSQFAKFOEWGELKMGD 239
Qy 243 TAGVLEMIHLLDITIOADPSTLEKFLGRIPMIFNVVVSHPGYFGQANVLGLPTGGQ 302
Db 240 TAGVLEMIHLLDITIOADPSTLEKFLGRIPMIFNVVVSHPGYFGQANVLGLPTGGQ 299
Qy 303 IVTILDOVRLAENEMVLRLKKQGLDVSFKLLIVTRLIPAKGTSNORLERISGTOHTYI 362
Db 300 IVTILDOVRLAENEMVLRLKKQGLDVSFKLLIVTRLIPAKGTSNORLERISGTOHTYI 359

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QY 363 LRVFENNGILKKMISRPDVPYLETFADAGELAELOGTPTPIGNYSOENIVASTL 422
DB 360 IRVFPENNGILKKMISRPDVPYLETFADAGELAELOGTPTPIGNYSOENIVASTL 419
QY 423 LSKKGIITQCNIAHALEKTYPSDIFWKAFDEKHYSCQFTADIIAMNADFIITSTYQ 482
DB 420 LAHKGVTOCTIAHALEKTYPSDIFWKAFDEKHYSCQFTADIIAMNADFIITSTYQ 479
QY 483 ELAGSKNTYGVQYSHAFITLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 542
DB 480 ELAGSKNTYGVQYSHAFITLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 539
QY 543 SLHGSIENTIYDEPNDENHGHLDPSKPIIFSMARDKYNITGVEAFKAKRLRELY 602
DB 540 AFHPELBELIYSVENSEHFVKDKKKPIIFSMARDKYNITGVEAFKAKRLRELY 599
QY 603 NLVAVAGYDVKSKDREBELIAIEKHELIKTNLFQGFPMISAOQNRANBELYRIAD 662
DB 600 NLVAVAG-DHGKSKDREBELIAIEKHELIKTNLFQGFPMISAOQNRANBELYRIAD 658
QY 663 THGAFVQPALYEAFTLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 722
DB 659 THGAFVQPALYEAFTLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 718
QY 723 MADFPRCKODPDHWNISGAGLQRIYKTYMTWISERLMTLAGVGFMYVSKLEPLET 782
DB 719 LVNFPKCKADPSYWKISGGLQRIYKTYMTWISERLMTLAGVGFMYVSKLEPLET 778
QY 783 RRYLEMFYLIKREBELIAKTYPLAID 806
DB 779 RRYLEMFYLIKREBELIAKTYPLAID 802

RESULT 9
US-10-425-114-57840
; Sequence 57840, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 71128
; SEQ ID NO 57840
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73215F06_FLI.pep
US-10-425-114-57840

Query Match 70.9%; Score 3011.5; DB 12; Length 807;
Best Local Similarity 70.0%; Pred. No. 9,3e-269;
Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;
QY 3 APGLNNAISIRDEVEDTTLHNRNELVALSKYVKNKGKGIQPHILIDALDEYGGSGVRL 62
DB 7 AKULTLHSLREKLGITPSHREHVALSKRYHOGKGMQKQILAFPAALDSOKEK 66
QY 63 AEGPFLDVLRSAGEALVDPFVAIAVRPQVMEYVAVVHLSVQLTVSEYLAKREEL 122
DB 67 A--PFEDILRAAGEALVLPFWALIRPRGVMDYIRVNVSELAVELSVSEYLAKEQL 124
QY 123 VVGQNDPVYLDLDEFPNVSVPRRSSSIGNGVFLNRHLSIMFRNDCLEPLLDPL 182

DB 125 VVGQNSNPFVLBDPEFNAAPRPSMSKISGNGVFLNRHLSKLFQDKESLYPLNPL 184
QY 183 RGRHRGVMAMNDRQSGLQSVLTAKREHLSKLPADTPYQPAFKPQWGLEKGM 242
DB 185 KAHNYGTTMMLNDRLQSLRGLOSIRKAEYLLSPQDTPYSPFNRPQALGLEKGM 244
QY 243 TGHVLEMIHLDDIIOADDPSTLEKFLGRIPIFVNVVVSPPGYPQGANVAGLPTGQ 302
DB 245 TAKRVLDIHLDDILEADDPANLEKFLGRIPIFVNVVVSPPGYPQGANVAGLPTGQ 304
QY 303 IYVILDQVPALENEMVRLKKGLDVSFKLITVRLIPDAKTSQCNORLRIISGQHYI 362
DB 305 VVYILDQVPALENEMVRLKKGLDVSFKLITVRLIPDAKTSQCNORLRIISGQHYI 364
QY 363 LRVFENNGILKKMISRPDVPYLETFADAGELAELOGTPTPIGNYSOENIVASTL 422
DB 365 IRVFPENNGILKKMISRPDVPYLETFADAGELAELOGTPTPIGNYSOENIVASTL 424
QY 423 LSKKGIITQCNIAHALEKTYPSDIFWKAFDEKHYSCQFTADIIAMNADFIITSTYQ 482
DB 425 LAHKGVTOCTIAHALEKTYPSDIFWKAFDEKHYSCQFTADIIAMNADFIITSTYQ 484
QY 483 ELAGSKNTYGVQYSHAFITLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 542
DB 485 ELAGSKNTYGVQYSHAFITLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 544
QY 543 SLHGSIENTIYDEPNDENHGHLDPSKPIIFSMARDKYNITGVEAFKAKRLRELY 602
DB 545 AFHPELBELIYSVENSEHFVKDKKKPIIFSMARDKYNITGVEAFKAKRLRELY 604
QY 603 NLVAVAGYDVKSKDREBELIAIEKHELIKTNLFQGFPMISAOQNRANBELYRIAD 662
DB 605 NLVAVAG-DHGKSKDREBELIAIEKHELIKTNLFQGFPMISAOQNRANBELYRIAD 663
QY 663 THGAFVQPALYEAFTLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 722
DB 664 THGAFVQPALYEAFTLPGLYRVHGDVDPKFNIVSPGADMSVYPPYETDRLT 723
QY 723 MADFPRCKODPDHWNISGAGLQRIYKTYMTWISERLMTLAGVGFMYVSKLEPLET 782
DB 724 LVNFPKCKADPSYWKISGGLQRIYKTYMTWISERLMTLAGVGFMYVSKLEPLET 783
QY 783 RRYLEMFYLIKREBELIAKTYPLAID 806
DB 784 RRYLEMFYLIKREBELIAKTYPLAID 807

RESULT 10
US-10-425-114-53965
; Sequence 53965, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 53965
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM01713EB11_FLI.pep
US-10-425-114-53965

Query Match 70.9%; Score 3011.5; DB 12; Length 811;

Best Local Similarity 70.0%; Pred. No. 9,46-269;
Matches 563; Conservative 106; Mismatches 133; Indels 3; Gaps 2;

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QY 3 APLINNASIRDEVDLTAAHRELVALLSKYVKKGGIIQPHHLLADLDEVOSSGRAL 62
Db 11 AALTLRHSLRELGAFSPSHPELLLFSTRVHQGKMLQRIQLAEFLAEPSDEKEXY 70
QY AEGPFLDVIRSAQEAIVLPFVAIAVRPQGWEEYVAVVNHLSVEQLTVEYLRFKEEL 122
Db 71 A--PFEDILRAAOEAIVLPFVAIAVRPQGWVDIRVNVSELAVELSESELAPEQL 128
QY 123 VDCQHNDPVYLELDEPPFNVSVPKRRSSISNGVQFLNRHLSIMFRNDCLEPLDPL 182
Db 129 VDCQSNMFLLELDEPFNVSPPKRRSSISNGVQFLNRHLSIMFRNDCLEPLDPL 188
QY 183 RGRHKGVMMLNDRIQSLQSLRKAEHLSKLPADTPYSQFAKFEQWGLKMGD 242
Db 189 KANVYGTMMNDRIQSLQSLRKAEHLSKLPADTPYSQFAKFEQWGLKMGD 248
QY 243 TAGHVLMTLLDDIICAPDPSTLEKFLGRIPMIFNVVVSPPHGFQANVGLPDTGG 302
Db 249 TAKRVLDTHLLDLLEAPDPALKEFLGITKMFNVVLSPHGYFAQSNVGLPDTGG 308
QY 303 IYVILLDQVRALENEMVLRLKQGLDVSFKLITVRLIPDAKGTSCNQLRISGTQHTYI 362
Db 309 VYVILLDQVRALENEMVLRLKQGLDVSFKLITVRLIPDAKGTSCNQLRISGTQHTYI 368
QY 363 LKVPFENNGILKKMISRPDVPYLETFAEDAAAGETIAELQSTPDTITNGVSGNIVASL 422
Db 369 IAVPPFNENGILKKMISRPDVPYLETFAEDAAAGETIAELQSTPDTITNGVSGNIVASL 428
QY 423 LSYKMGITQCNIAHALKTKYPPDSIFMKNFDEKHFSCQFTADIIAMNADPILITSTYQ 482
Db 429 LAHKLGVTQCTIAHALKTKYPPDSIFMKNFDEKHFSCQFTADIIAMNADPILITSTYQ 488
QY 483 ETAGSNNTGQYESHTAFPLDGLYRVVHGIDVDFPKENIVSPGADMSIYFPHTKAKRLT 542
Db 489 ETAGSNNTGQYESHTAFPLDGLYRVVHGIDVDFPKENIVSPGADMSIYFPHTKAKRLT 548
QY 543 SLHGSIENTLYDPEONDEHIGHLDDRSKPLTSMAALDVRKNTGTGLVEAFKAKKRELV 602
Db 549 AHPPELEILLYDVENSEHKEFVLKDKKKPLISMAALDVRKNTGTGLVEAFKAKKRELV 608
QY 603 NLVYVAGYNDVYKSKOREELIAIEKHEHILKTNHFGQFRMISAQTNRAANGELYIAD 662
Db 609 NLVYVAG--DHGKSKOREEQAEFKKMYSLIDELKLGKHMISAQNNRANGELYIAD 667
QY 663 THGATVQPALYFAFGITVEAMTCGLPTFATLHGGPAILIIEHGVSGFHIDPHYEQAVNL 722
Db 669 THGATVQPALYFAFGITVEAMTCGLPTFATLHGGPAILIIEHGVSGFHIDPHYEQAVNL 727
QY 723 MADPFRCKODPDHWNISGAGLQRIYKTYTWKISERIMTLAGVYGFMYKSKLERLE 782
Db 729 LNFDFDKCAQDPSSYNDKISQSGGLQRIYKTYTWKISERIMTLAGVYGFMYKSKLERLE 787
QY 783 RRYLEMFYLLKFRILAKTVPLAID 806
Db 788 RRYLEMFYLLKFRILAKTVPLAID 811

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RESULT 11

US-10-425-114-53296

; Sequence 53296, Application US/10425114

; Publication No. US2004003488A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 53296

; LENGTH: 823

; TYPE: PR

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 700451030_FLI pep

; US-10-425-114-53296

Query Match 70.7%; Score 3001; DB 12; Length 823;

Best Local Similarity 69.9%; Pred. No. 9e-268;
Matches 563; Conservative 106; Mismatches 128; Indels 3; Gaps 3;

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QY 6 LBNASIRDEVDLTAAHRELVALLSKYVKKGGIIQPHHLLADLDEVOSSGRAL 61
Db 17 LSRHLSVREIRIGSLSHAPNELVAVFTRKLGKMLQPHQIIAEVNNALPEAR---EK 73
QY 62 LAEGPFLDVIRSAQEAIVLPFVAIAVRPQGWEEYVAVVNHLSVEQLTVEYLRFKEEL 121
Db 74 LKQAFEDVLRSAQEAIVLPFVAIAVRPQGWEEYVAVVNHLSVEQLTVEYLRFKEEL 133
QY 122 VDCQHNDPVYLELDEPPFNVSVPKRRSSISNGVQFLNRHLSIMFRNDCLEPLDPL 181
Db 134 VDCQSNMFLLELDEPFNVSPPKRRSSISNGVQFLNRHLSIMFRNDCLEPLDPL 193
QY 183 RGRHKGVMMLNDRIQSLQSLRKAEHLSKLPADTPYSQFAKFEQWGLKMGD 242
Db 189 KANVYGTMMNDRIQSLQSLRKAEHLSKLPADTPYSQFAKFEQWGLKMGD 248
QY 243 TAGHVLMTLLDDIICAPDPSTLEKFLGRIPMIFNVVVSPPHGFQANVGLPDTGG 302
Db 249 TAKRVLDTHLLDLLEAPDPALKEFLGITKMFNVVLSPHGYFAQSNVGLPDTGG 308
QY 303 IYVILLDQVRALENEMVLRLKQGLDVSFKLITVRLIPDAKGTSCNQLRISGTQHTYI 362
Db 309 VYVILLDQVRALENEMVLRLKQGLDVSFKLITVRLIPDAKGTSCNQLRISGTQHTYI 368
QY 363 LKVPFENNGILKKMISRPDVPYLETFAEDAAAGETIAELQSTPDTITNGVSGNIVASL 422
Db 369 IAVPPFNENGILKKMISRPDVPYLETFAEDAAAGETIAELQSTPDTITNGVSGNIVASL 428
QY 423 LSYKMGITQCNIAHALKTKYPPDSIFMKNFDEKHFSCQFTADIIAMNADPILITSTYQ 482
Db 429 LAHKLGVTQCTIAHALKTKYPPDSIFMKNFDEKHFSCQFTADIIAMNADPILITSTYQ 488
QY 483 ETAGSNNTGQYESHTAFPLDGLYRVVHGIDVDFPKENIVSPGADMSIYFPHTKAKRLT 542
Db 489 ETAGSNNTGQYESHTAFPLDGLYRVVHGIDVDFPKENIVSPGADMSIYFPHTKAKRLT 548
QY 543 SLHGSIENTLYDPEONDEHIGHLDDRSKPLTSMAALDVRKNTGTGLVEAFKAKKRELV 602
Db 549 AHPPELEILLYDVENSEHKEFVLKDKKKPLISMAALDVRKNTGTGLVEAFKAKKRELV 608
QY 603 NLVYVAGYNDVYKSKOREELIAIEKHEHILKTNHFGQFRMISAQTNRAANGELYIAD 662
Db 609 NLVYVAG--DHGKSKOREEQAEFKKMYSLIDELKLGKHMISAQNNRANGELYIAD 667
QY 663 THGATVQPALYFAFGITVEAMTCGLPTFATLHGGPAILIIEHGVSGFHIDPHYEQAVNL 722
Db 669 THGATVQPALYFAFGITVEAMTCGLPTFATLHGGPAILIIEHGVSGFHIDPHYEQAVNL 727
QY 723 MADPFRCKODPDHWNISGAGLQRIYKTYTWKISERIMTLAGVYGFMYKSKLERLE 782
Db 729 LNFDFDKCAQDPSSYNDKISQSGGLQRIYKTYTWKISERIMTLAGVYGFMYKSKLERLE 787
QY 783 RRYLEMFYLLKFRILAKTVPLAID 806
Db 788 RRYLEMFYLLKFRILAKTVPLAID 811

```


QY 482 QELASGKNTVQGYSHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYEPHTKAKRL 541
 DB 494 QELASGKNTVQGYSHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYEPHTKAKRL 553
 QY 542 TSLHGSLENTLYDEQNDENHIGLIDRSKPLIFSMARLDVKNITGLVEAFKCAKREL 601
 DB 554 TSLHGSLENTLYDEQNDENHIGLIDRSKPLIFSMARLDVKNITGLVEAFKCAKREL 613
 QY 602 VNLVAVGYNDVNSKXDEEIAETEMHETLKTNLGQGFPMISACTNRANAGELRYIA 661
 DB 614 VNLVAVCG-DHGNPSKXKEQBAEPKMFDLIEQVNLNGHIFMISQNRVRNGELRYIC 672
 QY 662 DTHGAFQAPALYEAFFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGFHIDPYHDAQVN 721
 DB 673 DTHGAFQAPALYEAFFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGFHIDPYHDAQVN 732
 QY 722 LMADEFRCODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERL 781
 DB 733 LMADEFRCODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERL 792
 QY 782 TRRYLEMLYALKYRTMASTVPLAVE 806
 DB 793 TRRYLEMLYALKYRTMASTVPLAVE 817

RESULT 14
 US-10-425-114-72813
 / Sequence 72813, Application US/10425114
 / Publication No. US20040034888A1
 / GENERAL INFORMATION:
 / APPLICANT: Liu, Jindong
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Kovalic, David K.
 / APPLICANT: Screen, Steven E.
 / APPLICANT: Tabaska, Jack E.
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(5313)B
 / CURRENT APPLICATION NUMBER: US/10/425,114
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 73128
 / SEQ ID NO 72813
 / LENGTH: 823
 / TYPE: PRT
 / ORGANISM: Zea mays
 / FEATURE:
 / OTHER INFORMATION: Clone ID: LIB4172-051-C3_F11.pep
 US-10-425-114-72813

Query Match 70.7%; Score 3001; DB 12; Length 823;
 Best Local Similarity 69.9%; Pred. No. 9e-268;
 Matches 563; Conservative 106; Mismatches 128; Indels 8; Gaps 3;

QY 6 INENASIRDRVEDTLHAHNEELVALSKYVNGKGLIOPHIL- - -DALDEWQSGSVRA 61
 DB 17 LSLRLHVSREHIGSLSHAPHELVAVFTRRLKULSKMLOPHQIILAEYNNALPEAER- - -EK 73
 QY 62 LAGEPFLDVLRSQAEIVLPFVALAVRPPGWEYVAVNVVHLSVQLTVSEYLRKEE 121
 DB 74 LKDGAFEDVLRARQAEIVLPFVALAVRPPGWEYVAVNVVHLSVQLTVSEYLRKEE 133
 QY 122 LVDCGNDPVLVLEDEPENVSVPRPKRSSISNGVQFLMRHSSIMFRKDCLEPLDR 181
 DB 134 LVEEGPNNVLELDEPENVSPRPSLSKISNGVQFLMRHSSIMFRKDCLEPLDR 193
 QY 182 LKGRHKGWYMLNDRISQSLQSV/TKAEHLSKXLPATPYQAPYKFOEWGLKQWG 241
 DB 194 LKGRHKGWYMLNDRISQSLQSV/TKAEHLSKXLPATPYQAPYKFOEWGLKQWG 253
 QY 242 DTAGHVLMIHLLDITQADPSTLEKFLGRIPMIVNVVSPHGVQGANVLGLPDTGG 301

DB 254 DCARAOETIHLDDLLEAPDPSTLEKFLGTIPWFNVVILSPHGFAGQANVLYGPDTCG 313
 QY 302 QIVVITLOVRLENEMTSLKXQGLDVSPKLLITVRLIPDAKGSQNRLEISTQRTY 361
 DB 314 QIVVITLOVRLENEMTSLKXQGLDVSPKLLITVRLIPDAKGSQNRLEISTQRTY 373
 QY 362 ILRVPFENGILKMWISRPDPWYLETFAADAGEIAAEIQTGDFITIGNSDNLVNS 421
 DB 374 ILRVPFENGILKMWISRPDPWYLETFAADAGEIAAEIQTGDFITIGNSDNLVNS 433
 QY 422 LLSYMGITQCNIAHALEKTYKPSDIFWKNFDEKHYSCOPTADIIAMNADFITITSY 481
 DB 434 LLAHMGVYCTIHALEKTYKPSDILYKKEFBHHSQCFITDILAMNADFITITSY 493
 QY 482 QELASGKNTVQGYSHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYEPHTKAKRL 541
 DB 494 QELASGKNTVQGYSHAFETLPGLYRVVHGIDVDPKFNIVSPGALMSIYEPHTKAKRL 553
 QY 542 TSLHGSLENTLYDEQNDENHIGLIDRSKPLIFSMARLDVKNITGLVEAFKCAKREL 601
 DB 554 TSLHGSLENTLYDEQNDENHIGLIDRSKPLIFSMARLDVKNITGLVEAFKCAKREL 613
 QY 602 VNLVAVGYNDVNSKXDEEIAETEMHETLKTNLGQGFPMISACTNRANAGELRYIA 661
 DB 614 VNLVAVCG-DHGNPSKXKEQBAEPKMFDLIEQVNLNGHIFMISQNRVRNGELRYIC 672
 QY 662 DTHGAFQAPALYEAFFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGFHIDPYHDAQVN 721
 DB 673 DTHGAFQAPALYEAFFGLTVVEAMTCGLPTPATLHGPAEITIEHGVSGFHIDPYHDAQVN 732
 QY 722 LMADEFRCODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERL 781
 DB 733 LMADEFRCODPDHWNISGAGLQRIYEXYTKIYSERLMTLAGVGFWMKYVSKLERL 792
 QY 782 TRRYLEMLYALKYRTMASTVPLAVE 806
 DB 793 TRRYLEMLYALKYRTMASTVPLAVE 817

RESULT 15
 US-10-424-599-258404
 / Sequence 258404, Application US/10424599
 / Publication No. US20040031072A1
 / GENERAL INFORMATION:
 / APPLICANT: La Rosa, Thomas J
 / APPLICANT: Kovalic, David K
 / APPLICANT: Zhou, Yihua
 / APPLICANT: Cao, Yongwei
 / TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 / TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 / FILE REFERENCE: 38-21(53223)B
 / CURRENT APPLICATION NUMBER: US/10/424,599
 / CURRENT FILING DATE: 2003-04-28
 / NUMBER OF SEQ ID NOS: 285684
 / SEQ ID NO 258404
 / LENGTH: 805
 / TYPE: PRT
 / ORGANISM: Glycine max
 / FEATURE:
 / OTHER INFORMATION: Clone ID: PAT_MR13847_75363C.1.pep
 US-10-424-599-258404

Query Match 70.6%; Score 2999.5; DB 12; Length 805;
 Best Local Similarity 69.5%; Pred. No. 1.2e-267;
 Matches 560; Conservative 115; Mismatches 130; Indels 1; Gaps 1;

QY 1 MSAPKLRNASIRDRVEDTLHAHNEELVALSKYVNGKGLIOPHILDALDEVQSGSVR 60
 DB 1 MARDRLRVHSIKRDLDTLANNEELVALSKYVNGKGLIOPHILDALDEVQSGSVR 60
 QY 61 ALAEGPFLDVLRSQAEIVLPFVALAVRPPGWEYVAVNVVHLSVQLTVSEYLRKEE 120
 DB 61 KLDGAFGEVLRSTQAEIVLPFVALAVRPPGWEYVAVNVVHLSVQLTVSEYLRKEE 120

QY 121 EIVDGGHNDPYVLELDFEPPNVSVPBPNSSTIGNGVOFLNRHLSIMFNRNDCLPILD 180
Db 121 EIVDSSNGNPFVLELDFEPPNNAFPPTANKSIGNGVOFLNRHLSAKLPHDKSIFPLD 180
QY 181 FLRGHRAKHVMMLNDRIQSLQSVLTKEBHLKLPADTPYSQFAYKQFQWGLEKGM 240
Db 181 FLRHSEVKGKTMNDRIQNPDALQHVLRKABEYLGTVPETPYSSEHKFQELIGERGM 240
QY 241 SDTAGHVEIMHLLDIIQAPDPSTIEKLGRIEMIPNVVVSPPHGYEQANYLGIPDTG 300
Db 241 GNAERVESIQLLDLLEAPDECTLETGRIPWFFNVVILSPHGYFAQDNYLGYPDTG 300
QY 301 GOIVYLLDQVRALNENYVLRKQGLDVPKILIVTRLIPDAKGSQNGRLERISGTCAT 360
Db 301 GOVVYLLDQVRALNENYVLRKQGLDVPKILIVTRLIPDAVGTTCQRLERKVPSTERS 360
QY 361 YLRVFPFNENGILKKMISRPVWPYLETFAADAGEIAELQGTPTDPIIGVSDGNLYA 420
Db 361 HILRVFPFTEKIVKMKISRPFWPYLETYTEDVAHELAKELQKPDILVGNVSDGNLYA 420
QY 421 SLSTYMGITOCNIAHLEKTYPPSDIFPKNFDEKXHCQFTADITAMNADPIITST 480
Db 421 SLAHKLGVTCTIAHLEKTYPPSDIYWKLEBRVHFSQFTADIFAMNHTDPIITST 480
QY 481 YQELAGSXNTVQYESHTAFTLPGLYRVVHGIDVDPKFNIVSPGADWSIYEPHTEKAKR 540
Db 481 FQELAGSKDVTQYESHTAFTLPGLYRVVHGIDVDPKFNIVSPGADQTIYEFHETSRR 540
QY 541 LTSHGSTEMLIYDEQONDERIGHLDNRKPIIFSMARLDRVKNITGLVBAFACAKLRE 600
Db 541 LTSFHPRIEELIYSSVENNEH:CVLXDRSKPIIFTMARLDRVKNITGLVBAFACAKLRE 600
QY 601 LYNLVVAGYNVNSKDBEEIAELEKMEELIKTNLFGQFHWISAOQTRANGELRYI 660
Db 601 LYNLVVWAG-DBRKESKDLBEKAEMKMKMGLIETKLNQFHWISSQMNVRNNGELRYI 660
QY 661 ADTHGAFVQPALYEAFGILVVEAMTCGLPTFATLHGSEALIEHGVSGFHIDPYHPOAY 720
Db 660 CDTREAFVQPALYEAFGILVVEAMTCGLPTFATCNGSPREILIVHGSGFHIDPYHGRNA 720
QY 721 NIMADFPDRCKODPDHWNISAGLQRIYEXYTKIYSERLMTLAGVYGFWRYSKLEBL 780
Db 720 DLIVDFPEKCKLDPHMDKISKAGLQRIEEXYTKIYISQRLTLTGAVYGFWRVSNLDR 780
QY 781 FTRRYLEMFXILXRELAQVPLAD 806
Db 780 ESRRYLEMFXILXRELAQVPLAE 806

Search completed: May 24, 2004, 11:38:09
Job time : 44.6803 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 22:35:47 ; Search time 7009.39 seconds

(without alignments)
16924.423 Million cell updates/sec

Title: US-10-080-114A-1
Perfect score: 2737
Sequence: 1 gtcgaccacgcgtccgagc.....aaaaaaaaagggcgccgc 2737

Scoring table: Oligo_NWC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 2167151695 residues

Word size: 50

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pac:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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24: em_ph:*
25: em_pl:*
26: em_ro:*
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39: em_hlg_hum:*
40: em_hlg_mus:*
41: em_hlg_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2710	99.0	2710	8 AY059416	Zea mays
2	2138	78.1	2837	8 AY124703	Zea mays
3	192	7.0	297	6 AX756452	Sequence
4	191	7.0	258	6 AX756409	Sequence
5	122	4.5	265	6 AR246503	Sequence
6	103	3.8	221	11 BV079817	sc1180_p3
7	103	3.8	225	11 BV079815	sc1180_p3
8	103	3.8	234	11 BV079813	sc1180_p3
9	103	3.8	239	11 BV079812	sc1180_p3
10	103	3.8	239	11 BV079814	sc1180_p3
11	103	3.8	239	11 BV079819	sc1180_p3
12	72	2.6	240	11 BV079818	sc1180_p3
13	69	2.5	234	11 BV079820	sc1180_p3
14	69	2.5	246	11 BV079821	sc1180_p3

ALIGNMENTS

RESULT 1
AY059416
LOCUS AY059416 2710 bp mRNA linear PLN 07-NOV-2001
DEFINITION Zea mays sucrose synthase mRNA, partial cds.
ACCESSION AY059416
VERSION AY059416.1 GI:16797784
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
AUTHORS Carlson, S.J., Chourey, P.S., Helentjaris, T. and Datta, R.
TITLE Gene expression studies on developing kernels of maize sucrose
synthase (Susy) mutants show evidence for a third Susy gene
JOURNAL Plant Mol. Biol. (2001) In press
REFERENCE
AUTHORS Helentjaris, T.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2001) Agronomic Traits/T&T, Pioneer Hi-Bred,
7250 NW 62nd Avenue - PO Box 552, Johnston, IA 50131-0552, USA
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Pred. No. is the number of results predicted by chance to have a


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DB 2101 CGTACCCACCCCGGACAGGCTGTATCTGATGAGCCGCACTTTTGACCGCGTCAAGCAAG 2160
QY 2178 ACCGAGTCACTGAGTATATCTGAGAGCGGCTGACGCGCATATAGAGAGATGACA 2237
DB 2161 ACCGAGTCACTGAGTATATCTGAGAGCGGCTGACGCGCATATAGAGAGATGACA 2220
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QY 2718 AAAAAAAAAA 2727
DB 2701 AAAAAAAAAA 2710

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RESULT 2
LOCUS AY124703 2837 bp mRNA linear PLN 05-AUG-2002
DEFINITION Zea mays sucrose synthase 3 mRNA, complete cds.
ACCESSION AY124703
VERSION AY124703.1 GI:22121989
KEYWORDS
SOURCE
ORGANISM Zea mays

```

REFERENCE

1 Holtrawie, D.L., Scholz, A., Altmann, B. and Winter, H. Complete coding sequence of a third sucrose synthase isoform in

AUTHORS

Holtrawie, D.L., Scholz, A., Altmann, B. and Winter, H.

JOURNAL

Submitted (20-JUN-2002) Biology, University of Osnabrueck, Barbara

FEATURES

Location/Qualifiers

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CDS

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polysite

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Query Match 78.1%; Score 2138; DB 8; Length 2837;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2386; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 218 AGTACGGAACAAAGGGGAAGGGACCTCTGACCGCGCAACCATCTGACCGCGTCTGACG 277
QY 138 AGGTCCAGGGCTCCGGGGGCGCGCGCTAGCGCGAGGACCTTCTCTGACGCTCTCGCT 197
DB 278 AGGTCCAGGGCTCCGGGGGCGCGCGCTAGCGCGAGGACCTTCTCTGACGCTCTCGCT 337
QY 198 CCGCGCAGAGGCGATGTCGTCGCGCTTGTGTCATGCGGCTGCGCGCGCG 257
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QY 618 ACCACTGTCAAGAGTCCCTGCTGACACACCACTACTACAAATTTGCTATTAATTTCAAG 677
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RESULT 3
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 SEQUENCE 1191 from Patent W003000905.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 1
 Zea mays
 Glazebrook, J., Katagiri, F., Kreis, J., Provart, N. and Riecke, D.
 Identification and characterization of plant genes
 Patent: WO 03000905-A 1191 03-PAN-2003;
 Syngenta Participations AG (CH)
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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1433 GCTGGAAGCAAAATATCTGTGACAGATATGAGTATGCTATCTCTTCTCTCT 1492
DB 183 GCTGGAAGCAAAATATCTGTGACAGATATGAGTATGCTATCTCTTCTCTCT 124

QY 1493 CTGTACAGAGTTGCTATGAGATGCTGTCTGTGATCCAAAGTCAATATAGTCTCT 1552
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QY 1553 GGAAGCTGACATGCTCATATATCTTCCACATACGAGAGGCAAGCACTACCTCTT 1612
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QY 1613 CAT 1615
DB 3 CAT 1

RESULT 4
AX756409/c 258 bp DNA linear PAT 24-JUN-2003
LOCUS AX756409
DEFINITION Sequence 1148 from Patent WO03000905.
ACCESSION AX756409
VERSION AX756409.1 GI:32168540
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 Zhu, T., Cheng, W., Briggs, S., Cooper, B., Goff, S.A., Moughamer, T.,
Glazebrook, K., Katagiri, F., Kreps, J., Provart, N. and Rieke, D.
Identification and characterization of plant genes
Patent: WO 03000905-A 1148 03-JAN-2003;
JOURNAL Syngenta Participations AG (CH)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 7.5e-90;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 258 GCCGAGGGAACCCCTCTCGAGCTCTCGGCTCCGCGAGGAGGCGATGTCGCGCG 195

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QY 287 CACGAGCTCAGCGCTCAGCACTCAGCTCTCGAGTACCTCCGCTTCAAGAGAGAGTT 346
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QY 347 GTCCAGGCGCA 357
DB 78 GTCCAGGCGCA 68

RESULT 5

AR246503
LOCUS AR246503 265 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1862 from patent US 6476212.
ACCESSION AR246503
VERSION AR246503.1 GI:27294377
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 265)
Lajudi, R.V., Ito, L.Y. and Sherman, B.K.
Polynucleotides and polypeptides derived from corn ear
Patent: US 6476212-A 1862 05-NOV-2002;
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Best Local Similarity 100.0%; Pred. No. 4.3e-53;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 624 TGTCAAGCTCCCTGCTGACACACCAATCTACAAATTTGCTATTAATTCAAGAGTGG 683
DB 170 TGTCAAGCTCCCTGCTGACACACCAATCTACAAATTTGCTATTAATTCAAGAGTGG 229

QY 684 GC 685
DB 230 GC 231

RESULT 6
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LOCUS BV079817
DEFINITION sc1180_p3 Mol17 Zea mays Mol17 Zea mays SRS genomic, sequence tagged
site.
ACCESSION BV079817
VERSION BV079817.1 GI:37051474
KEYWORDS SRS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 221)
McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
MP2-UCI Joint SNP Discovery
Unpublished (2003)

COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGCGCTACCTGAGATGTCGA
Primer B: ATTATCAGCACTTACCACTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: RedTag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with amplified DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

FEATURES

PHRED/PHRAP Quality Scores 62 53 60 59 86 86 80 80 82 80 82 82 82
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Best Local Similarity 100.0%; Pred. No. 5.6e-43;
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119 GGCGAAGACCGTGGCGCTTGCATTGACCAACCGAGTAGCTTGGCAACTGGACTGCG 178

2431 TAGCACTTGTTCAGACCTGAAACCTGAAAGGACCTTCACTAAT 2473

179 TAGCACTTGTTCAGACCTGAAACCTGAAAGGACCTTCACTAAT 221

RESULT 7

LOCUS BV079815 225 bp DNA linear STS 30-SEP-2003

DEFINITION sc1180.p3 CML322 Zea mays CML322 Zea mays STS genomic, sequence

ACCESSION BV079815

VERSION BV079815.1 GI:37051472

KEYWORDS STS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 225)
McMillen,M.D., Vroth Bi,I., Schroeder,S.S. and Gaut,B.S.

AUTHORS MP2-UCI Joint SNP Discovery

TITLE Unpublished (2003)

JOURNAL

COMMENT

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Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: GAGGCGTACCTTGAGATGTTCTA

Primer B: ATTATACGACCTTACCAAGTGGC

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Tag Polymerase: Redtag (Sigma)

Total Vol: 10 uL

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

Sequencing ready reaction with amplified DNA polymerase FS

Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

FEATURES

PHRED/PHRAP Quality Scores 47 44 40 34 66 61 63 63 82 82 80 82 82
87 81 85 85 81 77 76 81 84 80 73 73 88 90 90 82 70 73 85 81 90
81 90 83 79 79 84 81 88 83 86 90 90 90 79 82 88 90 82 82 90 84
83 79 81 81 81 74 83 83 82 8.
Location/Qualifiers
1..225
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CML322"
/db_xref="taxon:4577"
/clone_lib="Zea mays CML322"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1..>225

ORIGIN

Query Match 3.8%; Score 103; DB 11; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2371 GGCGAAGACCGTGGCGCTTGCATTGACCAACCGAGTAGCTTGGCAACTGGACTGCG 2430

123 GGCGAAGACCGTGGCGCTTGCATTGACCAACCGAGTAGCTTGGCAACTGGACTGCG 182

2431 TAGCACTTGTTCAGACCTGAAACCTGAAAGGACCTTCACTAAT 2473

183 TAGCACTTGTTCAGACCTGAAACCTGAAAGGACCTTCACTAAT 225

RESULT 8

LOCUS BV079813 234 bp DNA linear STS 30-SEP-2003

DEFINITION sc1180.p3 CML333 Zea mays CML333 Zea mays STS genomic, sequence

ACCESSION BV079813

VERSION BV079813.1 GI:37051470

KEYWORDS STS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 234)
McMillen,M.D., Vroth Bi,I., Schroeder,S.S. and Gaut,B.S.

AUTHORS MP2-UCI Joint SNP Discovery

TITLE Unpublished (2003)

JOURNAL

COMMENT

Contact: Brandon S. Gaut

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Tel: (949) 824-2564

Fax: (949) 824-2181

Email: bgaut@uci.edu

Primer A: GAGGCGTACCTTGAGATGTTCTA

Primer B: ATTATACGACCTTACCAAGTGGC

Protocol:

PCR amplification of genomic DNA

Template: 50 ng

Primer: each 0.5 uM

dNTPs: each 200 uM

Tag Polymerase: Redtag (Sigma)

Total Vol: 10 uL

Amplicon sequencing

ABI protocol - using d-Rhodamine terminator cycle

ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 37 44 40 29 29 29 42 42 44 77 73 60
55 51 58 58 82 82 82 82 82 82 85 85 80 76 77 77 77 75 73 90
90 90 83 63 63 62 71 83 90 77 81 87 82 84 81 81 83 86 81 90 90
90 79 79 86 84 79 79 84 81 83 76 79 77 77 60 65.

FEATURES

Location/Qualifiers
1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="CML333"
/db_xref="taxon:4577"
/clone_lib="Zea mays CML333"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>234

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 234;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTGGCACTGCGACTGCG 2430

Db 132 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTGGCACTGCGACTGCG 191

QY 2431 TAGCACTTGTACAGACTGAACCTGAAGACCTTCAGTAAT 2473

Db 192 TAGCACTTGTACAGACTGAACCTGAAGACCTTCAGTAAT 234

RESULT 9
BV079812 239 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Kull11 Zea mays STS genomic, sequence
DEFINITION tagged site.

ACCESSION BV079812 GI:37051469
VERSION BV079812.1
KEYWORDS STS.

SOURCE
ORGANISM Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 239)
AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)

COMMENT
Contact: Brandon S. Gaut
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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCATTCCACAGTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL

Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 32 32 28 28 56 70 74 67 67 63 75 61
75 81 77 76 62 60 54 67 62 90 88 84 82 82 90 81 90 87 82 81 76 81
81 77 77 77 83 90 79 71 71 79 83 79 90 90 89 84 84 89 84
80 80 80 86 90 87 87 87 90 79 79 87 86 82 90 90 81 81 7.

FEATURES

Location/Qualifiers
1. .239
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Kull11"
/db_xref="taxon:4577"
/clone_lib="Zea mays Kull11"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"
<1. .>239

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTGGCACTGCGACTGCG 2430

Db 137 GGGGAGACCGTGGCGCTTGCAATTGACCAACCGCAGTAGCTTGGCACTGCGACTGCG 196

QY 2431 TAGCACTTGTACAGACTGAACCTGAAGACCTTCAGTAAT 2473

Db 197 TAGCACTTGTACAGACTGAACCTGAAGACCTTCAGTAAT 239

RESULT 10
BV079814 239 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Oh43 Zea mays Oh43 Zea mays STS genomic, sequence tagged
DEFINITION site.

ACCESSION BV079814
VERSION BV079814.1
KEYWORDS STS.

SOURCE
ORGANISM Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 239)
AUTHORS McMullen, M.D., Vroh Bi, I., Schroeder, S.S. and Gaut, B.S.
TITLE MP2-UCI Joint SNP Discovery
JOURNAL Unpublished (2003)

COMMENT
Contact: Brandon S. Gaut
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321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCATTCCACAGTGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)

Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:

Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 32 29 34 33 48 37 33 28 44 33 37
44 48 48 46 42 34 25 33 31 42 42 44 42 42 44 48 48 35 35 35
13 13 13 13 42 35 66 73 58 68 71 77 73 79 82 76 73 76 73 76 76
75 75 75 80 85 82 90 88 92 90 79 90 90 78 88 88 73 73 6.

FEATURES

source

1..239
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Oh43"
/db_xref="taxon:4577"
/clone_1ib="Zea mays Oh43"
/dev_stage="seedling"
/note="Organ: Leaf; genomic DNA from inbred line"
<1..>239

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGCGAGACCGTGGCCCTTGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGCG 2430
DB 137 GGCGAGACCGTGGCCCTTGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGCG 196
QY 2431 TAGCACTTGTACAGACCTGAAGACCTTCACTAAT 2473
DB 197 TAGCACTTGTACAGACCTGAAGACCTTCACTAAT 239

RESULT 11
LOCUS BV079819 239 bp DNA linear STS 30-SEP-2003
DEFINITION sc1180_p3 M37W Zea mays M37W Zea mays STS genomic, sequence tagged
site.
ACCESSION BV079819
VERSION BV079819.1 GI:37051476
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
Muller,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 239)
Muller,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

COMMENT

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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATACAGACTTCACCGATGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM
dNTPs: each 200 uM

Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
Sequencing ready reaction with ampliTaq DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 40 37 31 28 28 52 66 59 59 57 52 63 57
75 77 73 75 75 67 61 67 65 82 82 84 84 82 90 90 86 86 82 81 82
90 80 76 76 76 87 89 90 90 82 88 84 90 82 83 90 82 77 74 75 80
85 80 80 82 79 79 77 80 86 84 82 82 90 87 83 79 81 81 81 7.

FEATURES

source

1..239
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="M37W"
/db_xref="taxon:4577"
/clone_1ib="Zea mays M37W"
/dev_stage="seedling"
/note="Organ: Leaf; genomic DNA from inbred line"
<1..>239

ORIGIN

STS

Query Match 3.8%; Score 103; DB 11; Length 239;
Best Local Similarity 100.0%; Pred. No. 5.6e-43;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2371 GGCGAGACCGTGGCCCTTGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGCG 2430
DB 137 GGCGAGACCGTGGCCCTTGCAATTGACCAACCGCAGTGGCTGGCACTGGCACTGGCG 196
QY 2431 TAGCACTTGTACAGACCTGAAGACCTTCACTAAT 2473
DB 197 TAGCACTTGTACAGACCTGAAGACCTTCACTAAT 239

RESULT 12
LOCUS BV079818 240 bp DNA linear STS 30-SEP-2003
DEFINITION sc1180_p3 Ky21 Zea mays Ky21 Zea mays STS genomic, sequence tagged
site.
ACCESSION BV079818
VERSION BV079818.1 GI:37051475
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 240)
Muller,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 240)
Muller,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
MPZ-UCI Joint SNP Discovery
Unpublished (2003)

COMMENT

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Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGCTACCTTGAGATGTTCTA
Primer B: ATTATACAGACTTCACCGATGCC
Protocol:
PCR amplification of genomic DNA
Template: 50 ng
Primer: each 0.5 uM

Primer: each 200 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliflag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 46 42 34 34 56 73 64 63 61 71 61 66
67 75 74 66 74 76 85 73 90 90 90 82 77 90 87 87 81 80
82 80 73 73 88 90 90 82 82 71 85 85 74 90 90 84 84 77 75
77 72 77 85 80 79 81 84 86 90 85 85 84 84 85 90 90 87 7.

FEATURES
source
1. .240
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Ky21"
/db_xref="taxon:4577"
/clone_lib="Zea mays Ky21"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"

STS
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 72; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

2.6%; Score 72; DB 11; Length 240;
2402 CCGAGTAGCTTGCGCACTGCGACTGCTGACCTTGTTCACAACTGAAACCTGAAGG 2461
169 CCGAGTAGCTTGCGCACTGCGACTGCTGACCTTGTTCACAACTGAAACCTGAAGG 228
QY 2462 ACCTTCAGTAAT 2473
DB 229 ACCTTCAGTAAT 240

RESULT 13
BV079820 234 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 Hp301 Zea mays Hp301 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079820
VERSION BV079820.1 GI:37051477
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 234)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
REFERENCE MPZ-UTi Joint SNP Discovery
TITLE Unpublished (2003)
JOURNAL
AUTHORS
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAAGTGC
Protocol: PCR amplification of genomic DNA
Template: 50 ng

Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: Redtag (Sigma)
Total Vol: 10 uL
Amplicon sequencing
ABI protocol - using d-Rhodamine terminator cycle
sequencing ready reaction with ampliflag DNA polymerase FS
Sequence ran on ABI 3700 sequencer.

Buffer:
Genomic DNA amplification
Redtag (Sigma)
Sequencing buffer
d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 52 66 62 61 67 65 61 61 61 69 71 73 63
66 64 72 72 87 87 88 84 80 80 80 85 84 81 76 77 80 71 73 84
79 79 79 78 78 67 81 85 90 81 85 83 77 72 69 69 77 75 85 80
79 90 90 90 90 81 81 84 84 82 90 79 77 70 75.

FEATURES
source
1. .234
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="Hp301"
/db_xref="taxon:4577"
/clone_lib="Zea mays Hp301"
/dev_stage="seedling"
/note="Organ: leaf; genomic DNA from inbred line"

STS
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 7.2e-25;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2.5%; Score 69; DB 11; Length 234;
2405 CAGTAGCTTGCGCACTGCGACTGCTGACCTTGTTCACAACTGAAACCTGAAGACC 2464
166 CAGTAGCTTGCGCACTGCGACTGCTGACCTTGTTCACAACTGAAACCTGAAGACC 225
QY 2465 TTTCAGTAAT 2473
DB 226 TTTCAGTAAT 234

RESULT 14
BV079821 246 bp DNA linear STS 30-SEP-2003
LOCUS sc1180_p3 CM247 Zea mays CM247 Zea mays STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV079821
VERSION BV079821.1 GI:37051478
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 246)
McMullen,M.D., Vroh Bi,I., Schroeder,S.S. and Gaut,B.S.
REFERENCE MPZ-UTi Joint SNP Discovery
TITLE Unpublished (2003)
JOURNAL
AUTHORS
COMMENT
Contact: Brandon S. Gaut
Dept. Ecology and Evolutionary Biology
U.C. Irvine
321 Steinhaus Hall, Irvine, CA 92697-2525, USA
Tel: (949) 824-2564
Fax: (949) 824-2181
Email: bgaut@uci.edu
Primer A: GAGGCGTACCTTGAGATGTTCTA
Primer B: ATTATCAGCACTTCACCAAGTGC
Protocol: PCR amplification of genomic DNA
Template: 50 ng

Template: 50 ng
 Primer: each 0.5 μ M
 dNTPs: each 200 μ M
 Taq Polymerase: Redtaq (Sigma)
 Total Vol: 10 μ l
 Amplicon sequencing
 ABI protocol - using d-Rhodamine terminator cycle
 sequencing ready reaction with amplitaq DNA polymerase FS
 Sequence ran on ABI 3700 sequencer.

Buffer:
 Genomic DNA amplification
 Redtaq (Sigma)
 Sequencing buffer
 d-Rhodamine kit (ABI)

PHRED/PHRAP Quality Scores 42 37 34 34 42 42 42 42 42 42 26 26 26
 26 37 35 34 34 52 50 61 57 82 73 78 71 71 77 70 82 82 79 66 58 58
 58 55 63 63 80 84 75 70 66 61 56 61 61 67 67 84 84 79 79 90 83
 81 87 77 81 81 79 82 82 87 77 82 90 82 82 84 79 77 77 83 81 71
 83 83 71 66 60.

FEATURES

Location/Qualifiers
 1..246
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="CML247"
 /db_xref="taxon:4577"
 /clone_lib="Zea mays CML247"
 /dev_stage="seedling"
 /note="Organ: leaf; genomic DNA from inbred line"
 <1..>246

ORIGIN

Query Match 2.5%; Score 69; DB 11; Length 246;
 Best Local Similarity 100.0%; Pred.No. 7.2e-25;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2405 CAGTAGCTGCGCACTGCGACTGCGTACACTTGGTACAGACTGAACTGAGGACC 2464
 DB 178 CAGTAGCTGCGCACTGCGACTGCGTACACTTGGTACAGACTGAACTGAGGACC 237
 QY 2465 TTCACTAAT 2473
 DB 238 TTCACTAAT 246

Search completed: May 26, 2004, 06:45:30
 Job time : 7016.39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 53.7325 Seconds
(without alignments)
4254.056 Million cell updates/sec

Title: US-10-080-114A-12

Perfect score: 4247
Sequence: 1 MAAKRNRASTRDRVDTL.....YIAKFEAKTYZALIDPQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 segs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4247	100.0	809	5	AAE28502 Corn suc3
2	4177	98.4	802	5	AAE28499 Corn suc3
3	3485	82.1	809	5	ABB92810 Herbicida
4	3158	74.4	766	2	AAE66222 Sucrose-s
5	3129	73.7	797	6	ABR39586 A. thalia
6	3108.5	73.2	805	5	ABD93752 Herbicida
7	3108.5	73.2	805	6	ABR39585 A. thalia
8	3060.5	72.1	773	5	AAE28503 Maize suc
9	3011.5	70.9	802	5	AAE28500 Corn suc3
10	3006.5	70.8	808	3	AAE28501 Corn suc3
11	2997	70.6	816	5	AAE28502 Corn suc3
12	2985	70.3	816	7	ADC07856 Rice prot
13	2985	70.3	816	7	ADC08209 Rice prot
14	2976.5	70.1	815	7	ADC68460 Lolium pe
15	2972	70.0	806	5	AAU97898 Cotton su
16	2972	70.0	814	7	ADC68366 Lolium pe
17	2947	69.4	816	7	ADC68367 S. arundi
18	2942.5	69.3	808	7	ADC68459 Lolium pe
19	2938.5	69.2	808	7	ADC68364 Lolium pe
20	2934.5	69.1	809	5	ABG69063 Amino aci
21	2934.5	68.9	808	7	ADC68365 S. arundi
22	2914.5	68.6	771	7	AAE85666 PSS3 prot
23	2905.5	68.4	808	5	ABE92501 Herbicida
24	2892.5	68.1	805	3	AAE16282 Eucalyptu
25	2892.5	68.1	805	3	AAE16336 Eucalyptu

26	2892.5	68.1	805	3	AAE28141 Sucrose s
27	2892.5	68.1	805	5	AAU80759 Eucalyptu
28	2867.5	67.5	808	5	ABE93562 Herbicida
29	2763.5	65.1	777	7	ADC08297 Rice prot
30	2763.5	65.1	777	7	ADC07858 Rice prot
31	2353.5	55.4	942	5	ABE91573 Herbicida
32	2319.5	54.6	786	7	ADC07862 Rice prot
33	2295	54.0	843	5	ABE93633 Herbicida
34	2260.5	53.2	798	7	ADC07860 Rice prot
35	2005	47.2	514	7	ADC07854 Rice prot
36	1833	43.2	806	2	AAW53103 Andoena
37	1692.5	39.9	395	5	ABG69054 Amino aci
38	1212	28.5	348	3	AAE16313 Pinus rad
39	802.5	18.9	225	5	ABG69052 Amino aci
40	709	16.7	149	3	AAE16309 Eucalyptu
41	651	15.3	217	3	AAE16312 Pinus rad
42	639	15.0	198	3	AAE85667 Plant col
43	633	14.9	204	7	ABW73686 DNA clone
44	622	14.6	158	3	AAE16284 Pinus rad
45	587	13.8	139	3	AAE16314 Pinus rad

ALIGNMENTS

RESULT 1

AAE28502 standard; protein; 809 AA.

AAE28502;

29-AUG-2003 (revised)
27-DEC-2002 (first entry)

Corn Sus3-Sorghum EST chimeric protein.

Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1; transgenic plant; plant breeding; grain breakage; grain strength; enzyme; cellulose; corn; Sus3; chimeric.

Zea mays.
Sorghum propinquum.
Chimeric.

Key location/Qualifiers

Region 1..13 /note= "Sorghum propinquum EST DNA encoded peptide"
FT 14..809 /note= "Corn Sus3 protein"

MO200267662-AL.

06-SEP-2002.

21-FEB-2002; 2002MO-US005137.

22-FEB-2001; 2001US-0270777P.

(PTON-) PIONEER HI-BRED INT INC.

Dhuga KS, Helentjaris TG, Niu X;

WPI; 2002-691625/74.

N-PSDB; AAD45856.

New polynucleotide and its encoded sucrose synthase, useful for modulating the level of sucrose synthase in transgenic plants (e.g. maize or soybean) to improve stalk length, reduce grain breakage, or improving plant or grain strength.

Claim 12; Page 120-121; 125pp; English.

The invention relates to two sucrose synthases, shrunken-1 (Sh1) and

CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 CC acids. The polynucleotide, or its encoded protein, is useful for
 CC modulating the level of sucrose synthase in a transgenic plant,
 CC increasing cellulose production in the stalk tissue of a transgenic
 CC plant, or increasing the concentration of cellulose in the tissues of a
 CC seed of a transgenic plant. This is particularly useful in plant (e.g.
 CC maize or soybean) breeding, especially for e.g. improving stalk length in
 CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is Corn Sus3-Sorghum Bst1 chimeric protein. (Updated on 29-AUG-2003 to
 CC standardise OS field)

XX Sequence 809 AA;

Query Match 100.0%; Score 4247; DB 5; Length 809;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSAPPLANRNASIRDEVEITLHAHRNEELVALSKYNNKGKGLQPHHIDALDEVQSGVR 60
 Db 1 MSAPPLANRNASIRDEVEITLHAHRNEELVALSKYNNKGKGLQPHHIDALDEVQSGVR 60
 QY 61 ALAEGPFLDVNSAQEALVLPPEVALAVRPRGWEYVAVNVNHELSEVQLTVSEYLAREKE 120
 Db 61 ALAEGPFLDVNSAQEALVLPPEVALAVRPRGWEYVAVNVNHELSEVQLTVSEYLAREKE 120
 QY 121 ELYVQGNHDPVYLELDEPEFNVSVPRRNSSISGVGVPLNRHLSIMFRNDCLEPPLD 180
 Db 121 ELYVQGNHDPVYLELDEPEFNVSVPRRNSSISGVGVPLNRHLSIMFRNDCLEPPLD 180
 QY 181 FLRGHRHGHVWMLNDRIQSLGRLQSLVLTKEAEHLSKLEPADPYPSQFAKFOEMGLEKGM 240
 Db 181 FLRGHRHGHVWMLNDRIQSLGRLQSLVLTKEAEHLSKLEPADPYPSQFAKFOEMGLEKGM 240
 QY 241 GDTAGHLEMHLLDIIQAPDSTLEKEFLGRIPIPIFNVVVVSHPGFCQANVLGLPDTG 300
 Db 241 GDTAGHLEMHLLDIIQAPDSTLEKEFLGRIPIPIFNVVVVSHPGFCQANVLGLPDTG 300
 QY 301 GQIVVILDOVRALNEMVTALTKQCHDVSFKLITVTRILPDAKGTSCNQRLEKISTQHT 360
 Db 301 GQIVVILDOVRALNEMVTALTKQCHDVSFKLITVTRILPDAKGTSCNQRLEKISTQHT 360
 QY 361 YLLARPERENGILKKKISRFDVWFLFTEPAEDAGEIAAEIQGTFPIIGVNSDGNLVA 420
 Db 361 YLLARPERENGILKKKISRFDVWFLFTEPAEDAGEIAAEIQGTFPIIGVNSDGNLVA 420
 QY 421 SLLSYKMGITQCNIAHLEKITYEPDSDFWKNPDEKRYHSCQFTADIIAMNNADFTITST 480
 Db 421 SLLSYKMGITQCNIAHLEKITYEPDSDFWKNPDEKRYHSCQFTADIIAMNNADFTITST 480
 QY 481 YGEIAGSKRTVQYSEETAFPLGLYRVVHGIDVPRKNIVTSRGADMSTYEPHEKAR 540
 Db 481 YGEIAGSKRTVQYSEETAFPLGLYRVVHGIDVPRKNIVTSRGADMSTYEPHEKAR 540
 QY 541 LNSLGSISINLLYDPQNDENHGLDNRKPLIFSMARADRYKNIIGLYEARPAKCKARE 600
 Db 541 LNSLGSISINLLYDPQNDENHGLDNRKPLIFSMARADRYKNIIGLYEARPAKCKARE 600
 QY 601 LVNLYVAVAGYDYNVSKDREELIAEIRKMEELIKTNHLFQGFWMISAQINRAENGELVRYI 660
 Db 601 LVNLYVAVAGYDYNVSKDREELIAEIRKMEELIKTNHLFQGFWMISAQINRAENGELVRYI 660
 QY 661 AOTGAFVCPALYEAGLTVVEMTGLTFANLHGPAEILIEHGVSGHIDIDYHDEQAV 720
 Db 661 AOTGAFVCPALYEAGLTVVEMTGLTFANLHGPAEILIEHGVSGHIDIDYHDEQAV 720
 QY 721 NLMADPFRCODPDHWNVISGAGLQRIYEKTYTWKISERLMTLAGVGFWXYSLERL 780
 Db 721 NLMADPFRCODPDHWNVISGAGLQRIYEKTYTWKISERLMTLAGVGFWXYSLERL 780
 QY 781 ETRRYLEMFYIILKRELAKTVPLADIPQ 809
 Db 781 ETRRYLEMFYIILKRELAKTVPLADIPQ 809

RESULT 2
 AAE28499
 ID AAE28499 standard; protein; 802 AA.

XX AAE28499;

AC 27-DEC-2002 (first entry)

XX Corn sucrose synthase (Sus3).

XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;

XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;

XX cellulose; corn; Sus3.

XX Zea mays.

XX WO200267662-A1.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US005137.

XX 22-FEB-2001; 2001US-0270777P.

XX (PION-) PIONEER HI-BRED INT INC.

XX Dhurga KS, Helentjaris TG, Ninu X;

XX MPI: 2002-691625/74.

XX N-PSDB; AAD45849.

XX New polynucleotide and its encoded sucrose synthase, useful for

XX modulating the level of sucrose synthase in transgenic plants (e.g. maize

XX or soybean) to improve stalk length, reduce grain breakage, or improving

XX plant or grain strength.

XX Claim 12; Page 103-104; 125pp; English.

XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and

XX constitutive sucrose synthase (Sus1) and their corresponding nucleic

XX acids. The polynucleotide, or its encoded protein, is useful for

XX modulating the level of sucrose synthase in a transgenic plant,

XX increasing cellulose production in the stalk tissue of a transgenic

XX plant, or increasing the concentration of cellulose in the tissues of a

XX seed of a transgenic plant. This is particularly useful in plant (e.g.

XX maize or soybean) breeding, especially for e.g. improving stalk length in

XX maize, reducing grain breakage during combining, transport or movement

XX into storage, or improving plant or grain strength. The present sequence

XX is corn Sus3 protein

XX Sequence 802 AA;

Query Match 98.4%; Score 4177; DB 5; Length 802;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 795; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 DREVEITLHAHRNEELVALSKYNNKGKGLQPHHIDALDEVQSGGRALABGFLDVLR 73
 Db 7 DREVEITLHAHRNEELVALSKYNNKGKGLQPHHIDALDEVQSGGRALABGFLDVLR 73
 QY 74 AOEALVLPPEVALAVRPRGWEYVAVNVNHELSEVQLTVSEYLRFKRELVDGQHNDEYVL 133
 Db 67 AOEALVLPPEVALAVRPRGWEYVAVNVNHELSEVQLTVSEYLRFKRELVDGQHNDEYVL 126
 QY 134 ELDFEFPNVSVPRRNSSISGVGVPLNRHLSIMFRNDCLEPPLDLFLGHRKHYMM 193
 Db 127 ELDFEFPNVSVPRRNSSISGVGVPLNRHLSIMFRNDCLEPPLDLFLGHRKHYMM 186
 QY 194 LNDRIQSLGRLQSLVLTKEAEHLSKLEPADPYPSQFAKFOEMGLEKMGDTAGVLEMIHL 253
 Db 187 LNDRIQSLGRLQSLVLTKEAEHLSKLEPADPYPSQFAKFOEMGLEKMGDTAGVLEMIHL 246

QY 254 LLDIIQAPPSTSEKFLGRIPMIENNVVVSPhGYFGQAVNLGPPYGGQIVYLLDQVRAL 313
 XX |||||
 Db 247 LLDIIQAPPSTSEKFLGRIPMIENNVVVSPhGYFGQAVNLGPPYGGQIVYLLDQVRAL 306
 QY 314 ENKMWIRLRKQGLDVSPPKILVTRLIPDAKGTSCNOLERISGTQHTYILRVPRNENGI 373
 XX |||||
 Db 307 ENKMWIRLRKQGLDVSPPKILVTRLIPDAKGTSCNOLERISGTQHTYILRVPRNENGI 366
 QY 374 LKKWIRFDPVWPLTEFPAEPAAGEIAAELOSTPDPIIGNSDGNVVASLSTYMGITQCN 433
 Db 367 LKKWIRFDPVWPLTEFPAEPAAGEIAAELOSTPDPIIGNSDGNVVASLSTYMGITQCN 426
 QY 434 IAALEKTKYPPSDIFMNKPFDEKYHSCOPTADIIAMNNADFIITTSYOGIAGSKNTVGO 493
 Db 427 IAALEKTKYPPSDIFMNKPFDEKYHSCOPTADIIAMNNADFIITTSYOGIAGSKNTVGO 486
 QY 494 YESHTAFPLPGLYRVVHGIDVDPKXENIVSPGADMSIYPPEHTEKAKRLTSLHGSINLILY 553
 Db 487 YESHTAFPLPGLYRVVHGIDVDPKXENIVSPGADMSIYPPEHTEKAKRLTSLHGSINLILY 546
 QY 554 DEQONDEHGHLDDBRSKPIIFSMARLDRYKNTGLVZAPAKKAKRELNVLVVYAGYNDV 613
 Db 547 DEQONDEHGHLDDBRSKPIIFSMARLDRYKNTGLVZAPAKKAKRELNVLVVYAGYNDV 606
 QY 614 NKSCKRESEIAIEKMHKELIKTNLFGQEFWISAQTRNARNGELYRYTIADTHGAFVOPALY 673
 Db 607 NKSCKRESEIAIEKMHKELIKTNLFGQEFWISAQTRNARNGELYRYTIADTHGAFVOPALY 666
 QY 674 EAPGLTVBAMTCGLTFPATLHGSPAEIIEHGVSGPHIDYHBEQAVNIMADFFDCKOD 733
 Db 667 EAPGLTVBAMTCGLTFPATLHGSPAEIIEHGVSGPHIDYHBEQAVNIMADFFDCKOD 726
 QY 734 PSHWVVISAGAGLORITEKTYMTKISERLMTLAVGYGPMKVSGLERLETRRYILEMYILK 793
 Db 727 PSHWVVISAGAGLORITEKTYMTKISERLMTLAVGYGPMKVSGLERLETRRYILEMYILK 786
 QY 794 FRELAKEVPLADPOQ 809
 Db 787 FRELAKEVPLADPOQ 802

RESULT 3
 ABB92810
 ID ABB92810 standard; protein; 809 AA.
 XX
 AC ABB92810;
 XX
 DT 31-MAY-2002 (first entry)
 XX
 DB Herbicidally active polypeptide SEQ ID NO 2021.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN MO200210210-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 28-AUG-2001; 2001MO-EP009892.
 XX
 PR 28-AUG-2001; 2001MO-EP009892.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Tietjen K, Weidler M;
 XX
 DR WPI; 2002-26310/11.
 XX
 PT Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant

PT organisms.
 XX
 PS Claim 5; SEQ ID NO 2021; 261pp + Sequence Listing: English.
 XX
 CC The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 CC
 XX
 SQ Sequence 809 AA;
 Query Match 82.1%; Score 3485; DB 5; Length 809;
 Best Local Similarity 79.5%; Pred. No. 4.ee-304;
 Matches 642; Conservative 90; Mismatches 74; Indels 2; Gaps 1;

QY 1 MSAPKLNKASIRDRVEDTAAHNEVALLSKYVNGKGLIOPHHLLDADEVQSGS- 58
 Db 1 MANPKTRVLTSDRVQDTLSARHNEVALLSRVVDQKGLIOPHHLLDEHESVIGDET 60
 QY 59 VRLAEGPELDVLRSAQEAIVLPFPVALAVRPPGVMEYRVNVHELVSQLTYSYLRF 118
 Db 61 KSLISGPEGEILKSMAMEAIVRPPFVALAVRPPGVMEYRVNVFELSVEGLTYSYLRF 120
 QY 119 KEELVDSQNDPVYELDEFPENVSVPNRSSISGVGFQFLNHLISIMFRDCLPEL 178
 Db 121 KEELVDSQNDPVYELDEFPENVSVPNRSSISGVGFQFLNHLISIMFRDCLPEL 180
 QY 179 LDFLRGHRHGHMMINDRIOSLGRLOSVLTKAEHSKLPADPIYSGFAFKPEMGLEK 238
 Db 181 LDFLRHAKYGHPLMNDRIQSISRLQIJSKADHISKSQEPFSFBSYALQMGREK 240
 QY 239 GWDGTAGHVLNEMHLLDIIQAPPSTSEKFLGRIPMIENNVVVSPhGYFGQAVNLGPPD 298
 Db 241 GWDGTAGHVLNEMHLLDIIQAPPSTSEKFLGRIPMIENNVVVSPhGYFGQAVNLGPPD 300
 QY 299 TGGQIVYLLDQVRALENEMVLRKQGLDVSPPKILVTRLIPDAKGTSCNOLERISGTQ 358
 Db 301 TGGQIVYLLDQVRALENEMVLRKQGLDVSPPKILVTRLIPDAKGTSCNOLERISGTQ 360
 QY 359 HTYILRVPRNENGIKMKISRFQVWPLYETFPADAGEIAAELOSTPDPIIGNSDGNL 418
 Db 361 HTYILRVPRNENGIKMKISRFQVWPLYETFPADAGEIAAELOSTPDPIIGNSDGNL 420
 QY 419 VASLISYKMGITQONTAALEKTKYPPSDIFMNKPFDEKYHSCOPTADIIAMNNADFIIT 478
 Db 421 VASLISYKMGITQONTAALEKTKYPPSDIFMNKPFDEKYHSCOPTADIIAMNNADFIIT 480
 QY 479 STYOGIAGSKNTVGOYESHTAFPLPGLYRVVHGIDVDPKXENIVSPGADMSIYPPEHTEK 538
 Db 481 STYOGIAGSKNTVGOYESHTAFPLPGLYRVVHGIDVDPKXENIVSPGADMSIYPPEHTEK 540
 QY 539 KRFTSLHGSTENLIYDEQONDEHGHLDDBRSKPIIFSMARLDRYKNTGLVZAPAKKAKYL 598
 Db 541 KRFTSLHGSTENLIYDEQONDEHGHLDDBRSKPIIFSMARLDRYKNTGLVZAPAKKAKYL 600
 QY 599 RELVNVLVVAGYNDVVKSKDRESEIAIEKMHKELIKTNLFGQEFWISAQTRNARNGELYR 658
 Db 601 RELVNVLVVAGYNDVVKSKDRESEIAIEKMHKELIKTNLFGQEFWISAQTRNARNGELYR 660
 QY 659 YIADTHGAFVOPALYAEFGLTVEAMTCGLTFPATLHGSPAEIIEHGVSGPHIDPYHEQ 718
 Db 661 YIADTHGAFVOPALYAEFGLTVEAMTCGLTFPATLHGSPAEIIEHGVSGPHIDPYHEQ 720
 QY 719 AVNIMADFFDCKODPDHWNVISAGAGLORITEKTYMTKISERLMTLAVGYGPMKVSGLER 778
 Db 721 AVNIMADFFDCKODPDHWNVISAGAGLORITEKTYMTKISERLMTLAVGYGPMKVSGLER 780
 QY 779 RLETRRYILEMYILKPRELAKEVPLAD 806

Db 781 RRETRRYLEMFTYILKFRDLVNTVPSIAD 808

RESULT 4

AA066222 standard; protein: 766 AA.

AA066222;

25-MAR-2003 (revised)

05-AUG-1995 (first entry)

Sucrose synthase.

Sucrose synthase; sugarbeet; sucrose; crop improvement.

Beta vulgaris.

DB4317596-A1.

01-DEC-1994.

24-MAY-1993; 33DE-04317596.

24-MAY-1993; 33DE-04317596.

(SCHED) SCHEERING AG.

Hesse H, Mueller-Roeber B;

WPI, 1995-007485/02.

N-PSDB; AA080005.

New DNA sequences encoding sucrose regulating enzymes of sugar beet - for regulating sucrose concn. specifically ADP glucose pyrophosphorylase, sucrose phosphatase and sucrose synthase.

Claim 4; Page 72-78; 78pp; German.

cDNA encoding sugarbeet sucrose-synthase was isolated from a cDNA library in phage lambda Zap. Alterations to the coding sequence may be designed to by-pass the plant's regulatory mechanisms, allowing manipulation of the sucrose content of sugarbeet. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 766 AA;

Query Match 74.4%; Score 3158; DB 2; Length 766;

Best Local Similarity 79.2%; Pred. No. 1,1e-274; Mismatches 81; Indels 2; Gaps 2;

Matches 595; Conservative 73; Mismatches 81; Indels 2; Gaps 2;

58 GVRALAEQPFIDVLSAQEAIVCPPEFVAIAVRPRGWEYRVVNHLSVQLTVSEYLR 117

3 GKQIISDGPFESEVLRSAGEALIVPFPFVAIAVRPRGWEYRVVNHLSVQLTVSEYLR 62

118 FKESLVDSQNDPVLLEDPFEPENYSVPRPNRSSISGNGQFQFNHLSISIMPRNDCELP 177

63 FKESLVDSQNDPVLLEDPFEPENYSVPRPNRSSISGNGQFQFNHLSISIMPRNDCELP 122

178 LLDPLRGHKGHWMMNDRIQSLQSVLTAKESHSKLPALCPYQSAFVKFQEMGLE 237

123 LLDPLRGHKGHWMMNDRIQSLQSVLTAKESHSKLPALCPYQSAFVKFQEMGLE 182

238 KGMGDTAGHVLMIHLJDIIOAPDPSTLEKFLGRIPMI FNVVVSHPGYQGANVGLP 297

183 KGMGDTAGHVLMIHLJDIIOAPDPSTLEKFLGRIPMI FNVVVSHPGYQGANVGLP 242

298 DTGGQIVITLDOVRLNEMVRLKKGQDVSPTLITRILIPDKKGSNORLERISGT 357

243 DTGGQIVITLDOVRLNEMVRLKKGQDVSPTLITRILIPDKKGSNORLERISGT 302

358 QHTYILIRVPFENENGILKKMISREPWVPLETFEADAGELIAELQGTPTDPIIGVNSDGN 417

Db 303 EHASILKVPFSEKGIILKRWISRFDPWVPLETFEADAGELIIGELQGRPDILIGVNSDGN 362

418 LVASLISYKMGITQCNIAHALEKTKYDPSDIFMKNFDEKHFSCQETADIIAMNADPII 477

363 IVASLISYKMGITQCNIAHALEKTKYDPSDIFMKNFDEKHFSCQETADIIAMNADPII 422

478 TSTVOETAGSKNTGQVSESHAFLLPGLYRVVHGDVDPKFNYSQADMSIYEPHTEK 537

423 TSTVOETAGSKNTGQVSESHAFLLPGLYRVVHGDVDPKFNYSQADMSIYEPHTEK 482

538 AKRLTSHGSIEMLIYDPEQNDENHIGLIDRSKPIIFSMARLDRVKNITGLVEAFACKA 596

483 DYTCLTSHRLIEBOLKRPBNEBHIIGLIDTSKPIIFSMARLDRVKNITGLVEAFACKA 542

597 KLRBLVNLVVAGYNDVKSQREELAEIKEMELIKTNLFGQFRMISAQTNRANSEL 656

543 KLRBLVNLVVAGYNDVKSQREELAEIKEMELIKTNLFGQFRMISAQTNRANSEL 602

657 YRYIADCHGAFVOPALVEAFGLTVVEAMTGLPTFATLHGGPAEIEHVSQGFHIDPYHP 716

603 YRYIADCHGAFVOPALVEAFGLTVVEAMTGLPTFATLHGGPAEIEHVSQGFHIDPYHP 662

717 EQAVNLADPFDRCKODPDHWNISGAGLQRIYERYTWKISERLMTLAGVYGFVKYYSK 776

663 DQA-EKCTBRPVKREDPNWTKISAGGLTKIKERYTQKYSERLMTLAGVYGFVKYYSK 721

777 LERLSTRYLEMFTYILKFRDLVNTVPSIAD 807

722 LERLSTRYLEMFTYILKFRDLVNTVPSIAD 752

RESULT 5

ABR39586 standard; protein: 797 AA.

ABR39586;

12-JUN-2003 (first entry)

A. thaliana lipid metabolism protein (LMP)-clone ID PK118-1.

Lipid metabolism protein; LMP; seed storage; plant; transgenic.

Arabidopsis thaliana.

W02003014376-A2.

20-FEB-2003.

12-AUG-2002; 2002MO-US025586.

10-AUG-2001; 2001US-0311414P.

(BADI) BASF PLANT SCI GMBH.

Mittendorf V, Haerfel H, Cirpus P;

WPI, 2003-256595/25.

N-PSDB; AB276372.

New nucleic acid molecule encoding lipid metabolism protein, useful for producing transgenic plants, for modulating seed storage compounds, e.g. lipid or fatty acid, in plants, and for evolutionary and protein structural studies.

Claim 2; Fig 12D; 108pp; English.

The invention relates to isolated lipid metabolism proteins (LMP) and polynucleotides. The LMP functions as a modulator of seed storage compound in a plant. The LMP nucleic acid and protein are useful in producing transgenic plants and in modulating the levels of seed storage compounds. These are used to modify or increase lipids and fatty acids,


```

De 386 TEAEDASNEISAELOGVENLIGNYSIDGNLVASLLASKLGVIOCNIAHALEKTKYPSDI 445
QY 449 EFKNDEKXHSOCOTADIIAMNADFIITSTYOEIAGSKNVGVQESTATLLEGLRV 508
Db 446 YWRNEDKXHSOCOTADIIAMNADFIITSTYOEIAGSKNVGVQESTATLLEGLRV 505
QY 509 VHGIVFDPKFNIVSPGADMSIYFPPTKAKRLTSLHGSIMLIVDPEONDEHIGLDDR 568
Db 506 VHGIVFDPKFNIVSPGADMSIYFPPTKAKRLTSLHGSIMLIVDPEONDEHIGLDDR 565
QY 569 SKPIIFSMARLDKRVKNTITGLVEAFKACAKLRELVLNVVAGYNDVNSKDRBEIAIEKM 628
Db 566 SKPIIFSMARLDKRVKNTITGLVEAFKACAKLRELVLNVVAGYNDVNSKDRBEIAIEKM 625
QY 629 HELIKTHNLFGQFRWISAQTNARANGELYRYTADTHGAFVQPALYEAFGITVYEANTCG 688
Db 626 HSLIEQYDLHGFRWISAQTNARANGELYRYTADTHGAFVQPALYEAFGITVYEANTCG 685
QY 689 PFEATLHGAPAEIIEHVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 748
Db 686 PFEATLHGAPAEIIEHVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 745
QY 749 YERYTWKXYSERLTLAGVYGFVKVYSKLELETRRYLEMFIYILKPRELAKTVPLAIDQ 807
Db 746 YERYTWKXYSERLTLAGVYGFVKVYSKLELETRRYLEMFIYILKPRELAKTVPLAIDQ 804

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RESULT 7

ABR39585

ID ABR39585 standard; protein; 805 AA.

AC ABR39585;

DT 12-UN-2003 (first entry)

DE A. thaliana lipid metabolism protein (LMP)-clone ID PK118.

KM Lipid metabolism protein; LMP; seed storage; plant; transgenic.

OS Arabidopsis thaliana.

PN W0203014376-A2.

PD 20-FEB-2003.

PF 12-AUG-2002; 2002WC-US025586.

PR 10-AUG-2001; 2001US-0311414P.

PA (BADI) BASF PLANT SCI GMBH.

PI Miltendorf V, Haertel H, Cirsus P;

DR WPI, 2003-256595/25.

N-PSDB; A3276371.

XX New nucleic acid molecule encoding lipid metabolism protein, useful for
 XX producing transgenic plants, for modulating seed storage compounds, e.g.
 PT lipid or fatty acid, in plants, and for evolutionary and protein
 PT structural studies.

PS Claim 2; Fig 12B; 108pp; English.

XX The invention relates to isolated lipid metabolism proteins (LMP) and
 XX polynucleotides. The LMP functions as a modulator of seed storage
 CC compound in a plant. The LMP nucleic acid and protein are useful in
 CC producing transgenic plants and in modulating the levels of seed storage
 CC compounds. These are used to modify or increase lipids and fatty acids,
 CC cofactors, and enzymes in microorganisms and plants. Additionally, the
 CC LMP nucleic acid and protein may be used in identifying an organism as
 CC being Arabidopsis thaliana, as markers for specific regions of the
 CC genome, and in evolutionary and protein structural studies. Sequences
 CC ABR39572-587 represent A. thaliana LMP sequences

XX Sequence 805 AA;
 SQ

Query Match 73.2%; Score 3108.5; DB 6; Length 805;
 Best Local Similarity 74.3%; Pred. No. 3.6e-270;
 Matches 579; Conservative 98; Mismatches 97; Indels 5; Gaps 3;

```

QY 31 LSKYNNKKGKIGIOPHHILDA-LDEVQSG-VALLAEGPLDYLRSQKAVIYPPFAIIV 88
Db 29 LVRIYAQKGIQSQHLDLBEFLKTVKVDLTDLAKSPFMKVL--QELVLPFFALAI 85
QY 89 RRRPGVMEYVRVNVHLSVEQLTVSEYLRFKEELVDGQNDPVLDELFPNVSVPRN 148
Db 86 RRRPGVMEYVRVNVHLSVEQLTVSEYLRFKEELVDGQNDPVLDELFPNVSVPRN 145
QY 149 RSSSTGNGVQFANRLHSSIMFERNRCLBLDFLAGHNRKGVNMLNDISQSLGRQSLV 208
Db 146 RSSSTGNGVQFANRLHSSIMFERNRCLBLDFLAGHNRKGVNMLNDISQSLGRQSLV 205
QY 209 TKAEBHLKLPADPTYSOPAYKFOEMGLEKMGDTRAGHVLMLHLLDIIQAPDPSTLAK 268
Db 206 TKAEBHLKLPADPTYSOPAYKFOEMGLEKMGDTRAGHVLMLHLLDIIQAPDPSTLAK 265
QY 269 FLGRIPMLTENVVVSPPHGYFGQANYLGAPDTGQIVYILDQVRA-ENEMVRLKKQGLDY 328
Db 266 FLGRIPMLTENVVVSPPHGYFGQANYLGAPDTGQIVYILDQVRA-ENEMVRLKKQGLDY 325
QY 329 SPKIIIVTRLIPDAKSTCONRLERISGQHTYILRVPRNNGILKKMISRPDWPYLE 388
Db 326 IPKIIIVTRLIPDAKSTCONRLERISGQHTYILRVPRNNGILKKMISRPDWPYLE 385
QY 389 TEADDAAGRIAAELQSTPDIIGNYSIDGNLVASLLASYKMGITQCNIAHALEKTKYPSDI 448
Db 386 TEADDAAGRIAAELQSTPDIIGNYSIDGNLVASLLASYKMGITQCNIAHALEKTKYPSDI 445
QY 449 EFKNDEKXHSOCOTADIIAMNADFIITSTYOEIAGSKNTVGVQESTATLLEGLRV 508
Db 446 YWRNEDKXHSOCOTADIIAMNADFIITSTYOEIAGSKNTVGVQESTATLLEGLRV 505
QY 509 VHGIVFDPKFNIVSPGADMSIYFPPTKAKRLTSLHGSIMLIVDPEONDEHIGLDDR 568
Db 506 VHGIVFDPKFNIVSPGADMSIYFPPTKAKRLTSLHGSIMLIVDPEONDEHIGLDDR 565
QY 569 SKPIIFSMARLDKRVKNTITGLVEAFKACAKLRELVLNVVAGYNDVNSKDRBEIAIEKM 628
Db 566 SKPIIFSMARLDKRVKNTITGLVEAFKACAKLRELVLNVVAGYNDVNSKDRBEIAIEKM 625
QY 629 HELIKTHNLFGQFRWISAQTNARANGELYRYTADTHGAFVQPALYEAFGITVYEANTCG 688
Db 626 HSLIEQYDLHGFRWISAQTNARANGELYRYTADTHGAFVQPALYEAFGITVYEANTCG 685
QY 689 PFEATLHGAPAEIIEHVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 748
Db 686 PFEATLHGAPAEIIEHVSGFHIDPYHPPEQAVNLMADEFDRCKODPDHWNISGAGLORI 745
QY 749 YERYTWKXYSERLTLAGVYGFVKVYSKLELETRRYLEMFIYILKPRELAKTVPLAIDQ 807
Db 746 YERYTWKXYSERLTLAGVYGFVKVYSKLELETRRYLEMFIYILKPRELAKTVPLAIDQ 804

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RESULT 8

AAE28503

ID AAE28503 standard; protein; 773 AA.

AC AAE28503;

DT 27-DEC-2002 (first entry)

DE Maize sucrose synthase consensus protein.

XX Sucrose synthase; shrunken-1; SHL; constitutive sucrose synthase; Suel;
 KM transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 KM cellulose; maize.

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XX Zea mays.
OS
XX MO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helemtjaris TG, Nin X;
XX WPI; 2002-691625/74.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Example 9; Fig 8; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Susi) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement
XX into storage, or improving plant or grain strength. The present sequence
XX is maize sucrose synthase consensus protein
XX
XX Sequence 773 AA;
XX
XX Query Match 72.1%; Score 3060.5; DB 5; Length 773;
XX Best Local Similarity 76.7%; Pred. No. 7e-266;
XX Matches 614; Conservative 72; Mismatches 86; Indels 29; Gaps 21;
XX
XX 6 LNRNASTGRDVEPTLHAHRELVATLSKYVNGKGLIOPHHILDALDEVGSGVRLAAG 65
XX 1 LSRHLSLRERIGDGLSAHPRELVATLSRYN-CKGMLOPHQILAEPDAIDAC--KSLKDG 57
XX
XX 66 PFLDVLRSAGQEAIVLPPFAIAVPRPGWYVYVNVHLSVQTLVSEYLRKEELVDG 125
XX 58 PFEDVLRAGQEAIVLPPWALAIRPRGWYVYVNVHLSVSEYLRKEELVDG 116
XX
XX 126 QHNDPVYLEIDFPEVNSVPRNKSISNGVGFARHLSLTFNRKDLCEPLDPLRGH 185
XX 117 QNN--FVLEIDFPEVNASPPRPSLSKISNGVGFARHLSLTFNRKDLCEPLDPLRGH 173
XX
XX 186 RHKGWMMNDRIGSLQSVLTAKAEHLSKLPADPYSGAPYKPOEMLEKMGDPTAG 245
XX 174 NIMG-TMMLMDRIQSLA-LQSALRKAEHLSLPAOTYSEF-HRQELGLEKMGDPTAK 230
XX
XX 246 HYLEMTHLLDIIQADDPSTLEKFLGRIPMIFNVVNSPPRGYGAQANVLGPDTCQIVY 305
XX 231 RYLETHLLDLEADDPSTLEKFLGRIPMIFNVVNSPPRGYGAQANVLGPDTCQIVY 290
XX
XX 306 ILDCYALNEMVRLAKGQIDVSPKILITRLIPDAKGSQORLERISGTHYTLK 365
XX 291 ILDCYALNEMVRLAKGQIDVSPKILITRLIPDA-GTTCORLEKVGTHYTLK 349
XX
XX 366 PPKENGLIKKWSRFVWPLYLTFADAGELAAELQGPDPFLIGYSQGNVSLASY 425
XX 350 PPKENGLIKKWSRFVWPLYLTFADAGELAAELQGPDPFLIGYSQGNVSLASY 407
XX
XX 426 KMGITQCNIAALEKTKYPSDIFMKNFDEKYPHSCQFTADITAMNADPITSTYQELA 485
XX 408 KMGITQCNIAALEKTKYPSDIFMKNFDEKYPHSCQFTADITAMNADPITSTYQELA 466

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XX 486 GSKMTGYGVESHAFITLPGLYRVVHGIWDEPKENIVSPGADMSIYEPHTEKARLTSLH 545
XX 467 GSKDTVGQYESHAFITLPGLYRVVHGIWDEPKENIVSPGADMSIYEPHTEKARLTSLH 525
XX
XX 546 GSIEENLYDPEONDEHIGLIDRSKPLFSMARLDKVNITGLVEAFKAKDLBELVNLV 605
XX 526 PATEHILY--SENSEKFLVD--RKPIIFSMARLDKVNITGLVEAFKAKDLBELVNLV 581
XX
XX 606 VVAGINDVNSKORKEETAEIKKHELIKTHNLFGQFRMISAQTRNANGELRYIAOTGK 665
XX 582 VVAGIDHG--SKDREHQAERKQKHDLI-DYNL-GHIRMISAQTRNANGELRYIAOTGK 636
XX
XX 666 AFVQPAFYEAFLGTLVEAMTCGLPTFAT-HQGPBELLVHVGSGFHDPIYHDKAA--LLVD 725
XX 637 AFVQPAFYEAFLGTLVEAMTCGLPTFAT-HQGPBELLVHVGSGFHDPIYHDKAA--LLVD 693
XX
XX 726 FPDRCQDDPDHWNISGAGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTY 785
XX 694 FPDRCQDDPDHWNISGAGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTY 751
XX
XX 786 LEMFYLLKREELAKTYVPLAID 806
XX 752 LEMFYLLKREELAKTYVPLAID 772
XX
XX RESULT 9
XX AAE28500 standard; protein; 802 AA.
XX
XX AAE28500;
XX
XX 21-DEC-2002 (first entry)
XX
XX Corn sucrose synthase shrunken-1 (Sh1) protein.
XX
XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
XX transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
XX cellulose; corn; chromosome 9.
XX
XX Zea mays.
XX
XX MO200267662-A1.
XX
XX 06-SEP-2002.
XX
XX 21-FEB-2002; 2002MO-US005137.
XX
XX 22-FEB-2001; 2001US-0270777P.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Dhuga KS, Helemtjaris TG, Nin X;
XX
XX WPI; 2002-691625/74.
XX
XX N-PSDB; AAD45851.
XX
XX New polynucleotide and its encoded sucrose synthase, useful for
XX modulating the level of sucrose synthase in transgenic plants (e.g. maize
XX or soybean) to improve stalk length, reduce grain breakage, or improving
XX plant or grain strength.
XX
XX Example 9; Page 108-110; 125pp; English.
XX
XX The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
XX constitutive sucrose synthase (Susi) and their corresponding nucleic
XX acids. The polynucleotide, or its encoded protein, is useful for
XX modulating the level of sucrose synthase in a transgenic plant,
XX increasing cellulose production in the stalk tissue of a transgenic
XX plant, or increasing the concentration of cellulose in the tissues of a
XX seed of a transgenic plant. This is particularly useful in plant (e.g.
XX maize or soybean) breeding, especially for e.g. improving stalk length in
XX maize, reducing grain breakage during combining, transport or movement

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CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sh1 protein. Corn Sh1 gene is located at chromosome 9
 XX
 SQ Sequence 802 AA;

Query Match 70.9%; Score 3011.5; DB 5; Length 802;
 Best Local Similarity 70.0%; Pred. No. 1,9e-261;
 Matches 563; Conservative 105; Mismatches 133; Indels 3; Gaps 2;

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QY 3 APLNNASIRDRVEDTTHAHRELVALLSKYNNKKGILLPHHLLDALDEVQSGVRL 62
DB 2 AAKLTHSLRLRGATFSSHPNELIALPSRYVHQKMLQHRQLAEFDALFDSKEXX 61
QY 63 AAGPLDVRSAQEAIVLPPVLAIAVRPPGWVYRVNVVHLSVEQLVSEYLRKEEL 122
DB 62 A--PEEDILRAQEAIVLPPVLAIAVRPPGWVYRVNVVHLSVEQLVSEYLRKEEL 119
QY 123 VDGQNDPYVLELDEPFNVSVPRPSSSIGNGVOFLNRHLSIIFNRNDCLEPLDPL 182
DB 120 VDGQNSNRYVLELDEPFNVASFPSPMSISIGNGVOFLNRHLSKLFQKESLYPLNLT 179
QY 183 RGRHKGHWMLNDRIQSLGRLQSVITKAEHLSKLPADTPYSQPAKYKQEMGLEKMGD 242
DB 180 KAHNYKGTMTMNDRIQSLRGLQSSLRKAEYLLSVPODTPYSEFNRHFOELGLEKMGD 239
QY 243 TAGHVLMTHTLDDIQAADPSTLEKLGRIPIEVNVVSVSPHYGQANVLGLPTGGQ 302
DB 240 TAKRVLDTHLDDLEAPDPANLEKFLGTPPMFNVLVLSHGIRYQSVLGYPTGGQ 299
QY 303 IYVILDOVRALNEMVLRKKGGLDVSPKILVTRLLIPDAKTSQNRERISGTOHTYI 362
DB 300 VYIILDOVRALNEMVLRKKGGLDTPKILVTRLLIPDAKTCGQRLKXVIGTHETDI 359
QY 363 IAVPRNENKILKMWISRPDVPVYLETFAEDAAGETIAELQSTPDPIIGNYSDGNIYAS 422
DB 360 IAVPRNENKILKMWISRPDVPVYLETEDVSEIMKEMQAKPDILLIGYSDGNVATL 419
QY 423 LSYKMGITGCTAHAALEKTKYPSDIPMNPFDEKVFSCQFADIIAMNADPIITSTQ 482
DB 420 LAKRGVTOCTTAHALEKTKYPSDILYDKFSDYFSCQFADIIAMNADPIITSTQ 479
QY 483 ELASGNVYQYSESHATFLPGLYRVVHGIDVDPKYNIVSPGADMSIYFPHTEKAKRL 542
DB 480 ELASGNVYQYSESHATFLPGLYRVVHGIDVDPKYNIVSPGADMSIYFPHTEKAKRL 539
QY 543 SHSGISTENLIYDEQNDERTGHLDRSKPLTESMAULDYKNTGIVYAPAKCAKIRELY 602
DB 540 AFEPEIEELIYSDVENSEHEKFLVLDKXKPKPIIFSMARLDYKNTGIVYAPAKCAKIRELY 599
QY 603 NIVVAVGVYDVNKSXDRREIAZIERKHELIKTNLFGQSPMISAQTNRAANGELYRIAD 662
DB 600 NIVVAVGVYDVNKSXDRREIAZIERKHELIKTNLFGQSPMISAQTNRAANGELYRIAD 658
QY 663 TGAFAVQAPALYEAFTLVVEAMTGLPTATLHGGPAEIIIEHVSQPHIIDPYHEQAVNL 722
DB 659 TGAFAVQAPALYEAFTLVVEAMTGLPTATLHGGPAEIIIVDVGSLHIDPYHSDAADI 718
QY 723 MADPFRCKQDPDRHVNITSGAGIQRIYKXTWKIYSESLMTLAGVIGPMKYYSKLERLE 782
DB 719 LVVFFPKCKADPDPYWEISQGGIQRIYKXTWKIYSESLMTLAGVIGPMKYYSKLERLE 778
QY 783 RRYLEMFYILKPEELAKTVPLAID 806
DB 779 RRYLEMFYILKPEELAKTVPLAID 802

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RESULT 10

AA85664
 AA85664 standard; protein; 808 AA.

AC AA85664;
 XX
 DT 13-FEB-2001 (first entry)

XX Rice sucrose synthase amino acid sequence.
 XX Cold resistance; transgenic plant; sucrose decomposition; rice;
 XX sucrose synthase.

XX Oryza sativa.

XX JP2000245279-A.

XX 12-SEP-2000.

XX 01-MAR-1999; 99JP-00052102.

XX 01-MAR-1999; 99JP-00052102.

XX (MITA) MITSUI CHEM INC.

XX WPI; 2000-675173/66.

XX N-PSDB; AAC66090.

PT Novel method for the reinforcement of cold resistance in a plant
 PT comprising introducing a vector encoding an enzyme that decomposes
 PT sucrose into the plant.

PS Disclosure; Page 8-11; 22pp; Japanese.

CC This invention relates to a method for the reinforcement of cold
 CC resistance in a plant, comprising introducing an expression vector having
 CC a DNA encoding an enzyme for decomposing sucrose connected downstream to
 CC a promoter expressible in the plant, and expressing the enzyme in the
 CC plant body. Included in the invention are an expression vector used in
 CC the method; a transformed plant carrying the expression vector; and a
 CC transformed rice carrying the above expression vector. The method is used
 CC for reinforcing cold resistance in a plant. The present sequence
 CC represents a sucrose synthase protein used in the method

XX
 SQ Sequence 808 AA;

Query Match 70.8%; Score 3006.5; DB 3; Length 808;
 Best Local Similarity 69.8%; Pred. No. 5,5e-261;
 Matches 565; Conservative 103; Mismatches 127; Indels 15; Gaps 3;

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QY 3 APLNNASIRDRVEDTTHAHRELVALLSKYNNKKGILLPHHLLDALDEVQSGVRL 62
DB 2 AAKLTHSLRLRGATFSSHPNELIALPSRYVHQKMLQHRQLAEFD-----AL 53
QY 63 AAE-----GPILDVRSQAQEAIVLPPVLAIAVRPPGWVYRVNVVHLSVEQLVSEYLR 116
DB 54 IEADKKEVAPFEDILRAQEAIVLPPVLAIAVRPPGWVYRVNVVHLSVEQLVSEYLR 113
QY 117 RPKKEELVDQNDHPVYLELDEPFNVSVPRPSSSIGNGVOFLNRHLSIIFNRNDCLE 176
DB 114 AFEQQLVDGHTNSFVLELDEPFNVASFPSPMSKISIGNGVOFLNRHLSIIFNRNDCLE 173
QY 177 PLIDPLRGRHKGHWMLNDRIQSLGRLQSVITKAEHLSKLPADTPYSQPAKYKQEMGLE 236
DB 174 PLINFLKANHKGITMMNDRIQSLGRLQSVITKAEHYLMGICQDTPYSEHNRFOELGL 233
QY 237 EKGWGDAGHYLEMTHTLDDIQAADPSTLEKLGRIPIEVNVVSVSPHYGQANVLGL 296
DB 234 EKGWGDCAKAVLDTHLDDLEAPDPANLEKFLGTPPMFNVLVLSHGIRYQSVLGY 293
QY 297 PDTGGQVYIILDOVRALNEMVLRKKGGLDVSPKILVTRLLIPDAKTSQNRERISG 356
DB 294 PDTGGQVYIILDOVRALNEMVLRKKGGLDTPKILVTRLLIPDAKTCGQRLKXVIG 353
QY 357 TQHTYILRVPRNENKILKMWISRPDVPVYLETFAEDAAGETIAELQSTPDPIIGNYSDG 416
DB 354 TQHTDILRVPRNENKILKMWISRPDVPVYLETEDVSEIMKEMQAKPDILLIGYSDG 413
QY 417 NIVASLSTYKMGITGCTAHAALEKTKYPSDIPMNPFDEKVFSCQFADIIAMNADPI 476

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Db 414 KVAATLAAHLGVTQCTIAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNATDFI 473
 QY 477 TSTVOELGSKNTWGQYSHTAFTPLGLYRVVHGIDVDPKNTYSPGADMSIYPHPE 536
 Db 474 IYSTOELGSKNTWGQYSHTAFTPLGLYRVVHGIDVDPKNTYSPGADMSIYPHPE 533
 QY 537 KAKRLTSLGSIENLYDPEONDEHIGLDDRSKPLTFPMARLDRYKNTGTVEAFKCA 596
 Db 534 AKKRLTAFPELBEILYSVEENDEHIFVLKDKNKPLTFPMARLDRYKNTGTVEAFKCA 593
 QY 597 KLEELYNLVAVGYNDVYKSKDREELAEIEKHELIKTNLFGQFPMISAGQTRANGEL 656
 Db 594 HIRDLANIVYVG-DHGNSKOREBAEFKKMYGLIDQYKMKHINMISAQNMRYANGEL 652
 QY 657 YRIADTGAFTQPALYEAFGLTVVEAMTCGLPTFTLHGCPAETIEHVSGFHIDPHYE 716
 Db 653 YRICITKTVFVQPAYEAFGLTVVEAMTCGLPTFTLHGCPAETIEHVSGFHIDPHYE 712
 QY 717 EDAVNLMADEPDRCKDDPHWVNISGAGLQRIYEKTYKTIYSRLMTLAGVYGFMYKYSK 776
 Db 713 DKAADILVNFPECKODSTYMDNISQGLQRIYEKTYKTIYSRLMTLAGVYGFMYKYSK 772
 QY 777 LRLLETRRYLMEFYLIKEREELAKTVPLAID 806
 Db 773 LRRERTRRYLMEFYLIKEREELAKTVPLAID 802

RESULT 11
 AAE28501
 ID AAE28501 standard; protein; 816 AA.

AC AAE28501;

DT 27-DEC-2002 (first entry)

DE Corn sucrose synthase (Sus1).

KM Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 cellulose; corn; chromosome 9.

OS Zea mays.

PN MO200267662-A1.

PD 06-SEP-2002.

PF 21-FEB-2002; 2002WC-TS005137.

PR 22-FEB-2001; 2001US-0270777P.

PA (PION-) PIONEER HI-BRED INT INC.

PI Dhuga KS, Helentjaris TG, Niu X;

DR WPI; 2002-691625/74.

N-PSDB; AAD45852.

PT New polynucleotide and its encoded sucrose synthase, useful for
 modulating the level of sucrose synthase in transgenic plants (e.g. maize
 or soybean) to improve stalk length, reduce grain breakage, or improving
 plant or grain strength.

PS Example 9; Page 114-115; 125pp; English.

CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 constitutive sucrose synthase (Sus1) and their corresponding nucleic
 acids. The polynucleotide, or its encoded protein, is useful for
 modulating the level of sucrose synthase in a transgenic plant,
 increasing cellulose production in the stalk tissue of a transgenic
 plant, or increasing the concentration of cellulose in the tissues of a
 seed of a transgenic plant. This is particularly useful in plant (e.g.
 maize or soybean) breeding, especially for e.g. improving stalk length in

CC maize, reducing grain breakage during combining, transport or movement
 CC into storage, or improving plant or grain strength. The present sequence
 CC is corn Sus1 protein. Corn Sus1 gene is located at chromosome 9
 CC
 SQ Sequence 816 AA;

Query Match 70.6%; Score 2997; DB 5; Length 816;
 Best local similarity 69.8%; Pred. No. 4e-260;
 Matches 562; Conservative 107; Mismatches 128; Indels 8; Gaps 3;

QY 6 LKRNASIRDRVEDTTLAHNRNELVALISKYNNKSGILQPHHIL---DALDEVQSGVRA 61
 Db 10 LSRHSVRRIIGDSLASHPELVAAVFTRLKNLKGMLQPHQIIAEYNNALPEAER---EK 66
 QY 62 LAGPFLDYLRSGQEAIVLPFVALAVRPPGWEYRVNVVHLSVQGLVSEYKREEK 121
 Db 67 LKGAEDVYLRAGQEAIVLPFWALAIRPPGWEYRVNVVHLSVQGLVSEYKREEK 126
 QY 122 LVDSQNDPYYVLELDEPEFNVSVPRPSSISNGVQFLNRHLSIMFRNRDCLPELDF 181
 Db 127 LVDSQNDPYYVLELDEPEFNVSVPRPSSISNGVQFLNRHLSIMFRNRDCLPELDF 186
 QY 182 LRGRHKGVMMLNDRISQISGLQSVITKAEELSKLPADTPYSQPAKYQEWGLKGMG 241
 Db 187 LRANHYKGMVMMLNDRISLSALQALRKABEHLSTLQADTPYSSEFHRREFGLKGMG 246
 QY 242 DTNGHYLMLHLLDIIQADPSTLEKEGRIMIENVVSVSPHGYGQANVGLPPTGG 301
 Db 247 DCKRAQETHLLDLEAPDPSTLEKEGLTIPWVNVLLSPGHYQANVGLPPTGG 306
 QY 302 QIVYILDQVRLNEMWLRKQGLDVSFKILVTRLLIPAKGTSNQRERISGTOHTY 361
 Db 307 QVYIILDQVRLNEMWLRKQGLDVSFKILVTRLLIPAKGTSNQRERISGTOHTY 366
 QY 362 ILRVPRNENGILKKWISRPDVPYLTFABDAAAGETAAELQSTPDPILGYSNGNLVAS 421
 Db 367 ILRVPRNENGILKKWISRPDVPYLTFABDAAAGETAAELQSTPDPILGYSNGNLVAS 426
 QY 422 LLSYKMITQCNLAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNADFIITSTY 481
 Db 427 LLAHKMGVTHCTIAHALEKTKYPSNDIYLDKFDSDQVHFSQFTADLIAMNADFIITSTY 486
 QY 482 QELAGSKNTVGOYESHTAFTPLGLYRVVHGIDVDPKNTYSPGADMSIYPHPEKAKRL 541
 Db 487 QELAGSKNTVGOYESHTAFTPLGLYRVVHGIDVDPKNTYSPGADMSIYPHPEKAKRL 546
 QY 542 TSLHGSIENTLYDPEONDEHIGLDDRSKPLTFPMARLDRYKNTGTVEAFKCAKAREL 601
 Db 547 TSLHGSIENTLYDPEONDEHIGLDDRSKPLTFPMARLDRYKNTGTVEAFKCAKAREL 606
 QY 602 VNLVVAVGYNDVYKSKDREELAEIEKHELIKTNLFGQFPMISAGQTRANGELYRYIA 661
 Db 607 VNLVVAVGYNDVYKSKDREELAEIEKHELIKTNLFGQFPMISAGQTRANGELYRYIA 665
 QY 666 DTGCAFTQPALYEAFGLTVVEAMTCGLPTFTLHGCPAETIEHVSGFHIDPHYEQAKASA 725
 Db 722 LMADEPDRCKDDPHWVNISGAGLQRIYEKTYKTIYSRLMTLAGVYGFMYKYSKLEPLE 781
 QY 726 LMADEPDRCKDDPHWVNISGAGLQRIYEKTYKTIYSRLMTLAGVYGFMYKYSKLEPLE 785
 Db 782 TRRYLMEFYLIKEREELAKTVPLAID 806
 QY 786 TRRYLMEFYLIKEREELAKTVPLAID 810

RESULT 12
 ADC07856
 ID ADC07856 standard; protein; 816 AA.

AC ADC07856;

18-DEC-2003 (first entry)
Rice protein sequence Seq ID122 related to grain filling.
plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
gene; ds; plant.
Oryza sativa.
MO200300905-A2.
03-JAN-2003.
21-JUN-2002; 2002MO-IB002450.
22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
(SYGN) SYNGENTA PARTICIPATIONS AG.
Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T,
Gizebrook U, Katagiri F, Kreps J, Provart N, Ricke D,
WPI; 2003-229341/22.
N-PSDB; ADC07855.
New plant genes encoding polypeptides having an activity involved in or
associated with the synthesis, metabolism or degradation of carbohydrates
in the plant grain useful in generating plants having improved
nutritional properties.
Claim 1; SEQ ID NO 122; 130bp; English.
This invention, in the area of plant biotechnology, relates to novel
polynucleotides comprising a nucleotide sequence encoding a protein which
is involved in or associated with the synthesis, metabolism or
degradation of carbohydrates in the plant grain and the expression of
which is up-regulated during grain filling. The plant is selected from
corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
sugarbeet, wheat, and rice. The invention may be useful for the
improvement of protein, oil, starch, fibre and moisture content of the
cereal grains. In addition, carbohydrate levels may be modified to a more
desirable level using the present invention. The present sequence is the
amino acid sequence of a rice protein of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/pubishedpct_sequences.
Sequence 8-6 AA;
Query Match 70.3%; Score 2985; DB 7; Length 816;
Best Local Similarity 69.7%; Pred. No. 4.8e-259;
Matches 561; Conservative 107; Mismatches 129; Indels 8; Gaps 3;
6 INRNASIRDRVEDTTHAHNELVALISKVKKGLQPHHL---DALDEVQSSGVA 61
10 LSRHSVRERIGDSJSAHNELVAVPTRLVNLGKMLQAOHIAEYNNMISEDR--EK 66
62 LAGPPLDYLRSNOEALVPPFAIVRRPGWVEYRVNVHLSYEOLTVSEYLFKES 121
67 LKQGAEDVLRSGQESVTSFWALAIRPPGYEYRVNVSLANELLTVEPYLQPKQ 126
122 LVDGQHNDPYVLELDEPPNVSVPRDNRSSISNGVQFLNRHLSIMFNRDCLPLDF 181
127 LVEEGNNKNEVLEIDEPFNASPPRSLSKSIGNGVQFLNRHLSKLPFDKESMPLMF 186
182 LSGHRKHGVNMLNDRIGSLGRQSVLTAAEHLSTLPDTPYSSQAVYKQEWGLKMG 241
187 LRAHNYKGMTMLNDRISLISALQGLRRAEHLISGLSDTPYSSEPHHRFQELGKMG 246

242 DTAGVLEMIHLIDLIQAPDPSTLEKFLGRIPMIFNVVVS PHGFGQAVNLGPDFTG 301
247 DCAKRSQETIHLIDLIABPDPSTLEKFLGTPMVENNVIMS PHGFAQAVNLGYDPTGG 306
302 QIVYILDVRALEMBVIRLKKQGLDPSKLLITRLIPDAKGSNCNRLRISTORTY 361
307 QVVYILDVRALEMBVIRLKKQGLDPSKLLITRLIPDAKGSNCNRLRISTORTY 366
362 ILRVPERENGILIKKTSIRFPVWPLTEFADAGEIAAELOQTPDFTIGNSDGNLVAS 421
367 ILRVPERENGILIKKTSIRFPVWPLTEFADAGEIAAELOQTPDFTIGNSDGNLVAS 426
422 LLSYMGITQCNIAHALEKTKYPSDIPWKFDEKHSQCTADILAMNADPFIITSTY 481
427 LIAHMGVTHCTIALALEKTKYPSDILWKFEDHYHSCQCTDILAMNADPFIITSTY 486
482 QEIASKNTVQGVESHYVFTPLGLYRVHGDVPPPKNVISRGADMSTYPPHTEAKRL 541
487 QEIASKNTVQGVESHYVFTPLGLYRVHGDVPPPKNVISRGADMSTYPPHTEAKRL 546
542 TSLHGSINLTYDPEQNDHEIGHLDPSKPLDPSMARLDKRVNITGLVEAFKACALREL 601
547 TSLHGSINLTYDPEQNDHEIGHLDPSKPLDPSMARLDKRVNITGLVEAFKACALREL 606
602 VNLVAVAGYNDVNSKREBEIAIEKHEILKTHNLSCQFEMI SAQTNBARNGELYRYIA 661
607 VNLVAVAGYNDVNSKREBEIAIEKHEILKTHNLSCQFEMI SAQTNBARNGELYRYIA 665
662 LTRGAPVOPALYBAAGLYVYEAAMTGLPPFALHGGRAFIIEHSGVGHIDPHPEQAVN 721
666 DTKGAFVOPALYBAAGLYVYEAAMTGLPPFALHGGRAFIIEHSGVGHIDPHPEQAVN 725
722 LMADEPDSCKOPDPMVNINISGAGLQRIYKTYKLYSERLMTLAGYGFWRKYSKLER 781
726 LIVERFEKQEDPSMTKISOGGLQRIEKTMYKLYSERLMTLAGYGFWRKYSKLER 785
782 TRRYLEMFYIIKRELAKTVPDAID 806
786 TRRYLEMFYIIKRELAKTVPDAID 810
RESULT 13
ID ADC08209 standard; protein; 816 AA.
AC ADC08203;
DT 18-DEC-2003 (first entry)
DB Rice protein sequence Seq ID514 related to grain filling.
XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
XX tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
XX wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
XX gene; ds; plant.
OS Oryza sativa.
XX MO200300905-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002MO-IB002450.
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0325277P.
XX 20-DEC-2001; 2001US-0342327P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;

PI Glazebrook J, Karagiri F, Kreps J, Provart N, Riecke D;
 XX
 DR WPI, 2003-229341/22.
 DR N-PSDB; ADC684208.
 XX
 XX New plant genes encoding polypeptides having an activity involved in or
 27 associated with the synthesis, metabolism or degradation of carbohydrates
 27 in the plant grain useful in generating plants having improved
 27 nutritional properties.
 XX
 XX Claim 34; SEQ ID NO 514; 130bp; English.
 XX
 CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, sorghum, peanut, tobacco,
 CC sugarcane, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at ftp.wipo.int/pub/publishepct_sequences.
 CC
 XX
 XX Sequence 816 AA;
 SQ
 Query Match 70.3%; Score 2985; DB 7; Length 816;
 Best Local Similarity 69.7%; Pred. No. 4.8e-259;
 Matches 561; Conservative 107; Mismatches 129; Indels 8; Gaps 3;
 QY 6 LNBNASTRDRVETTLTAHRENEVALSKYKNGKGLIOPHIL---DAIDVQSGSRA 61
 DB 10 ISRLHSVRERIGDLSAHFVELVAVFTRVLNLSKGMLOAHQIIAENNAISEADR--EK 66
 QY 62 LAEGPELDVRSNOBALVLPFVAIAVRPVGWEYVYRVVHLSYEQLVSEYLRPKEE 121
 DB 67 LKQGAEDVRSKQEGIVLSPFWALAIRPVGWEYVYRVVHLSYEQLVSEYLRPKEE 126
 QY 122 LVDSQNDPVLBLDEPFVSVPRPSSSISGNGVQFLNRHLSIFRRDCLEPLIDF 181
 DB 127 LVDSQNDPVLBLDEPFVSVPRPSSSISGNGVQFLNRHLSIFRRDCLEPLIDF 186
 QY 182 LRGHRKGVVMTNDRISQSLQSVLTAKBHHLSKLPADTPYSQAFYKQWGLKGMG 241
 DB 187 LRAHNYKGMTMTNDRISQSLQSVLTAKBHHLSKLPADTPYSQAFYKQWGLKGMG 246
 QY 242 DTAGHLEMTHTLIDITQADPSTLEKEIGRIPIFVNVVSVPGVSGQANVGLPTTG 301
 DB 247 DCAKRSOETHTLIDLEADPSTLEKEIGRIPIFVNVVSVPGVSGQANVGLPTTG 306
 QY 302 QIVYIILDQVATLENEMVLRLKQGLDVSPKILIVTRILIPDAKTSQNRERISGTQHTY 361
 DB 307 QVYVYIILDQVATLENEMVLRLKQGLDVSPKILIVTRILIPDAKTSQNRERISGTQHTY 366
 QY 362 ILVPPFENGLIKKMTSRDVPVPIETPAEDAAIGTAELQSTPPITIGNISDGNIVAS 421
 DB 367 ILVPPFENGLIKKMTSRDVPVPIETPAEDAAIGTAELQSTPPITIGNISDGNIVAS 426
 QY 422 LLSYKMGICCCNLAHLEKTRPSDIFEMKPFDEKHFSCOPTADIIAANNADPIINSTY 481
 DB 427 LLSYKMGICCCNLAHLEKTRPSDIFEMKPFDEKHFSCOPTADIIAANNADPIINSTY 486
 QY 482 QEAGSKNTVQGYESHATFTLPGLYRVVHSDIVDPKENVISPGADMSIYFPHTEKAKRL 541
 DB 487 QEAGSKNTVQGYESHATFTLPGLYRVVHSDIVDPKENVISPGADMSIYFPHTEKAKRL 546
 QY 542 TSLHGSTENTLYPEQNDHEIGHIDRSKPILSMAALDVKNITGTGVEAPAKAKAREL 601
 DB 547 TSLHGSTENTLYPEQNDHEIGHIDRSKPILSMAALDVKNITGTGVEAPAKAKAREL 606

QY 602 VNLVYAVYDVNKKOREIABEKHELIKTHNLFGOPRMTSAQNNRANGLYRIA 661
 DB 607 VNLVYAVYDVNKKOREIABEKHELIKTHNLFGOPRMTSAQNNRANGLYRIA 665
 QY 662 DTGAFAVQALYFAFGLTVVAMTCGLPTEATLHGGPABIIENGVSGPHIDPYRBOAVN 721
 DB 666 DTGAFAVQALYFAFGLTVVAMTCGLPTEATLHGGPABIIENGVSGPHIDPYRBOAVN 725
 QY 722 LMADPEKCKADPDHWNINISAGLQRIYKTYTWIYSEBRLMTLAGVYGFMYSTLELE 781
 DB 726 LMADPEKCKADPDHWNINISAGLQRIYKTYTWIYSEBRLMTLAGVYGFMYSTLELE 785
 QY 782 TRRYLEKFTLKRFELAKTVPLAID 806
 DB 786 TRRYLEKFTLKRFELAKTVPLAID 810
 RESULT 14
 ID ADC68460 standard; protein; 815 AA.
 XX
 AC ADC68460;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Lolium perenne fructan biosynthesis protein SEQ ID NO:170.
 XX
 KM Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
 XX
 KM Biosynthetic pathway; plant.
 XX
 XX Lolium perenne.
 XX
 PN NO2003040306-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002MO-NZ000239.
 XX
 PR 07-NOV-2001; 2001US-0337703P.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PA (WRIG-) WRIGHTSON SEEDS LTD.
 XX
 PI Demmer J, Forster RL, Gibson JB, Shenk MA, Norris MG, Glenn M;
 XX
 XX Saulsbury KM, Hall C;
 XX
 DR WPI, 2003-441544/41.
 DR N-PSDB; ADC68424.
 XX
 PT New polynucleotide encoding polypeptides from Lolium perenne or Festuca
 PT arundinacea, useful for modulating the biosynthesis of lignin, fructan or
 FT tannin in a plant.
 XX
 XX
 PS Claim 18; SEQ ID NO 170; 240bp; English.
 XX
 XX The present invention describes isolated polynucleotides (I) encoding
 CC proteins (II) from Lolium perenne and Festuca arundinacea which are
 CC active in lignin, fructan and tannin biosynthetic pathways. Also
 CC described: (1) an isolated oligonucleotide probe or primer comprising at
 CC least 10 contiguous residues complementary to 10 contiguous residues of
 CC (1); (2) a kit comprising the oligonucleotide probe or primer; (3) a
 CC genetic construct comprising (1); (4) a transgenic plant cell comprising
 CC the genetic construct of (3); (5) a plant or its seed, fruit or progeny
 CC comprising the transgenic plant cell of (4); (6) modulating one or more
 CC of the lignin, fructan or tannin compositions of a plant; (7) producing a
 CC plant having one or more of the lignin, fructan or tannin compositions;
 CC and (8) modifying the activity of (II) involved in a lignin, fructan or
 CC tannin biosynthetic pathway in a plant. (I) can be used for modulating
 CC the biosynthesis of lignin, fructan or tannin in a plant. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 815 AA;

Db 361 DLRVPPREKGIYRKNIISREKRWPIYLETEDVAHEISKELHGTPLLIGNXSDGNTY 420
QY 420 ASILSYKMGITQCNIAHALEKTYPPDSDFWKNFDEKYNHSCQFTADIIAMNNADEIITS 479
Db 421 ASILAKRLGVTOCTIAHALEKTYPPDSDIYWKLEBKYNHSCQFTADLFAMNHTDFIITS 480
QY 480 TYQELAGSKNTVQGYSHHTAFILPGIYRVVHGSDVPDEKNIYVSGADMSIYPPHTEKAK 539
Db 481 TFOELIAGSKDITVQGYSHHTAFILPGIYRVVHGSDVPDEKNIYVSGADMEIYPPYTEEKR 540
QY 540 RLTSLSHGSJENLIYDPEONDEHIGLDDRSKZILFSMARLDRYKNITGLVEAFACAKLR 599
Db 541 RLKHFPELBDLTYKVENEBHLCVLDRKZILFTMPRLDRYKXNLGLVWCGKNPKLR 600
QY 600 EIVNLVYVAGYNDVNSKXDRBIEAIEKMHLEIKTNLFGQFRWISAQTNRANGELIYRY 659
Db 601 ELANLVVVGSDRRKSKOLEEKAEMKMPBELIDKYNLNGQFRWISSQMRIRNVELIYRY 659
QY 660 IADTHGAFVQPALYEAFGLTVVEAMTCGLPTFATLHGGPAEITEHGVSGFHIDPYHBCA 719
Db 660 ICDTKGAFVQPALYEAFGLTVVEAMTCGLPTFATLHGGPAEITEHGVSGFNIDPYHBCA 719
QY 720 VNLMAJFPRCKODPDHMTNISGALQRIYEKTYMKIYSERLMTLAGVYGFMYKYSKLER 779
Db 720 ADLIVDFEKKCKODPSHMDKISQGLRIEKTWKIYSERLMTLAGVYGFMYKYSNLER 779
QY 780 IETRYLEMEFYILKPREIAKTVPLA 804
Db 780 RESRYLEMEFYALKRYKIAESVPLA 804

Search completed: May 24, 2004, 11:27:21

Cod time : 55.7325 secs

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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 19.5847 seconds
2132.550 Million cell updates/sec

Title: US-10-080-114A-12
Perfect score: 4247
Sequence: 1 MSAPKLNKNNASIRDRVEDTL.....YIKKRELAKTVPLAIDPQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 3%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3158	74.4	766	2	US-08-553-436A-8
2	2892.5	68.1	806	4	US-09-598-401C-77
3	1833	43.2	806	4	US-08-684-305-2
4	467.5	11.0	720	4	US-09-394-272-14
5	466.5	11.0	1083	4	US-09-394-272-11
6	450	10.6	1056	4	US-09-394-272-12
7	447.5	10.5	963	4	US-09-394-272-13
8	447.5	10.5	963	4	US-09-394-272-13
9	445	10.5	1059	4	US-09-394-272-5
10	444	10.5	1068	2	US-08-429-054A-11
11	444	10.5	1068	2	US-08-718-777-7
12	444	10.5	1068	3	US-09-051-341-7
13	444	10.5	1068	4	US-09-394-272-8
14	441.5	10.4	1045	2	US-08-553-436A-6
15	441.5	10.4	1045	4	US-09-394-272-7
16	438	10.3	1054	1	US-08-356-354-4
17	438	10.3	1054	2	US-08-778-656-4
18	436.5	10.3	1053	4	US-09-394-272-6
19	425	10.0	1054	4	US-09-394-272-3
20	420	9.9	1059	4	US-09-697-367-16
21	414	9.7	1057	4	US-09-697-367-23
22	414	9.7	1057	3	US-09-394-272-2
23	411	9.7	1057	3	US-08-853-948B-2
24	408.5	9.6	1081	4	US-09-394-272-4
25	401.5	9.5	1084	4	US-09-394-272-9
26	396	9.3	846	1	US-08-356-354-2
27	396	9.3	846	2	US-08-778-656-2

28	355	8.4	125	4	US-09-598-401C-76	Sequence 76, Appl
29	351	8.3	1049	4	US-09-394-272-10	Sequence 10, Appl
30	307	7.2	908	1	US-08-356-354-6	Sequence 6, Appl
31	307	7.2	908	2	US-08-778-656-6	Sequence 2, Appl
32	280	6.6	668	4	US-09-697-367-2	Sequence 2, Appl
33	262.5	6.2	343	3	US-09-697-367-24	Sequence 10, Appl
34	256	6.0	343	3	US-08-853-948B-10	Sequence 4, Appl
35	251	5.9	341	3	US-08-853-948B-4	Sequence 8, Appl
36	233.5	5.5	365	4	US-09-697-367-8	Sequence 20, Appl
37	222	5.2	343	3	US-08-853-948B-3	Sequence 3, Appl
38	221	5.2	348	3	US-08-853-948B-5	Sequence 5, Appl
39	186	4.4	59	3	US-09-125-984-2	Sequence 2, Appl
40	172	4.0	210	4	US-09-697-367-10	Sequence 19, Appl
41	161	3.8	507	4	US-09-134-031C-3978	Sequence 3978, Ap
42	160.5	3.8	358	4	US-09-697-367-20	Sequence 20, Appl
43	152.5	3.6	502	4	US-09-134-031C-4511	Sequence 4511, Ap
44	149.5	3.5	369	4	US-09-543-681A-7514	Sequence 7514, Ap
45	148	3.5	393	4	US-09-252-991A-19043	Sequence 19043, A

ALIGNMENTS

RESULT 1
US-08-553-436A-8
Sequence 8, Application US/08553436A
Patent No. 5866730
GENERAL INFORMATION:
APPLICANT: HESSE, Holger
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,436A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4317596.1
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-117
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 766 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-553-436A-8
Query Match 74.4% Score 3158, DB 2; Length 766;

Best Local Similarity 79.2%; Pred. No. 6.7e-286;
Matches 595; Conservative 73; Mismatches 81; Indels 2; Gaps 2;

QY 58 GVALAEGPELDVRSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLR 117
DB 3 SKQLSDGPSESEVARSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLR 62
QY 118 FKEELVDSQNDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEP 177
DB 63 FKEELVDSQNDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEP 122
QY 178 LIDPELRGHRKHGVMMLNDRIQSLQSLVLTAKAEHLSKLPATPYSPQAFKQEWGLE 237
DB 123 LIDPELRGHRKHGVMMLNDRIQSLQSLVLTAKAEHLSKLPATPYSPQAFKQEWGLE 182
QY 238 KGMWDTAGVLEMLHLLDITIQAPDPSTLEKFLGRIPIFNVVVSPPHGYQGANVGLP 297
DB 183 KGMWDTAGVLEMLHLLDITIQAPDPSTLEKFLGRIPIFNVVVSPPHGYQGANVGLP 242
QY 298 DTGGQIVVILDOVRLEHEMVLRIKKQGLDVTPLRILVSLIPDAKGTINQKMKVSGT 357
DB 243 DTGGQIVVILDOVRLEHEMVLRIKKQGLDVTPLRILVSLIPDAKGTINQKMKVSGT 302
QY 358 QHTVILRVPFRNENGLKKKISRFDVWYLETFAEDAGELAAELQGTDPDPIGNYSDGN 417
DB 303 QHTVILRVPFRNENGLKKKISRFDVWYLETFAEDAGELAAELQGTDPDPIGNYSDGN 362
QY 418 LVASLSTRMGITTCNIAHALEKTYPPSDIPKMFDEKTHSCQFTADITAMNADFTII 477
DB 363 LVASLSTRMGITTCNIAHALEKTYPPSDIPKMFDEKTHSCQFTADITAMNADFTII 422
QY 478 TSTVDELGSKTVQYQESHHTAFTLPGLYRVVHGIDVPKFNIVSPGADMSIYPPHTEK 537
DB 423 TSTVDELGSKTVQYQESHHTAFTLPGLYRVVHGIDVPKFNIVSPGADMSIYPPHTEK 482
QY 538 AKRSTLSHGSIEHLIYDPEQNDHILGHLDKSKPLFSMARLDKYNITGLVEAFKAKA 596
DB 483 AKRSTLSHGSIEHLIYDPEQNDHILGHLDKSKPLFSMARLDKYNITGLVEAFKAKA 542
QY 557 KLESLVNLVAVAGNDVNSKQREBELAEKMHLEIKTNLFGQRFNISAQNTNRRANGL 656
DB 543 KLESLVNLVAVAGNDVNSKQREBELAEKMHLEIKTNLFGQRFNISAQNTNRRANGL 602
QY 653 YRYINDTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHP 716
DB 603 YRYINDTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHP 662
QY 717 EQAVNIMADFPDRCKODPDHWNISGAGLQRIYKTYKTYSERLMTLTAAGVYGFMYKYSK 776
DB 663 EQAVNIMADFPDRCKODPDHWNISGAGLQRIYKTYKTYSERLMTLTAAGVYGFMYKYSK 721
QY 777 LERLETRRLMEFYLLKRELAQTVPLADQ 807
DB 722 LERLETRRLMEFYLLKRELAQTVPLADQ 752

RESULT 2
US-09-598-401C-77
Sequence 77, Application US/09598401C
Patent No. 6596925
GENERAL INFORMATION:
APPLICANT: Patera, J. Ganjan
APPLICANT: Eagleton, Clare
APPLICANT: Rice, Stephen U.
TITLE OF INVENTION: Compositions and Methods for the
File Reference: 11000.1036c2
CURRENT APPLICATION NUMBER: US/09/598.401C
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: PCT/NZ00/00018
PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 805
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-598-401C-77

Query Match 68.1%; Score 2892.5; DB 4; Length 805;
Best Local Similarity 66.9%; Pred. No. 4.7e-261;
Matches 540; Conservative 120; Mismatches 144; Indels 3; Gaps 2;

QY 1 MSAPLNANASIRDOVEETLHAHREHVALLSKYVKKGGIIPHHIIDLALBEVQSGVVR 60
DB 1 MSAPLNANASIRDOVEETLHAHREHVALLSKYVKKGGIIPHHIIDLALBEVQSGVVR 60
QY 61 ALAEGPFLDVRSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLRPEK 120
DB 61 ALAEGPFLDVRSAGEAIVLPFVAIAVRPRGWEYVRVNVHLSVEQLVSEYLRPEK 120
QY 121 ELVDQENDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEPLD 180
DB 121 ELVDQENDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEPLD 180
QY 181 ELVDQENDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEPLD 180
DB 181 ELVDQENDPVYLELDPEEPNVSVPRNRSISGNGVQFLNHLSSIMERNDCLEPLD 180
QY 241 GDTAGVLEMLHLLDITIQAPDPSTLEKFLGRIPIFNVVVSPPHGYQGANVGLPDTG 300
DB 241 GDTAGVLEMLHLLDITIQAPDPSTLEKFLGRIPIFNVVVSPPHGYQGANVGLPDTG 300
QY 301 GQIVVILDOVRLEHEMVLRIKKQGLDVTPLRILVSLIPDAKGTINQKMKVSGT 360
DB 301 GQIVVILDOVRLEHEMVLRIKKQGLDVTPLRILVSLIPDAKGTINQKMKVSGT 360
QY 361 YRYINDTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHP 420
DB 361 YRYINDTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHP 420
QY 421 SLLSYKMSITQCNIAHALEKTYPPSDIPKMFDEKTHSCQFTADITAMNADFTII 480
DB 421 SLLSYKMSITQCNIAHALEKTYPPSDIPKMFDEKTHSCQFTADITAMNADFTII 480
QY 481 YOEIAGSKTVQYQESHHTAFTLPGLYRVVHGIDVPKFNIVSPGADMSIYPPHTEKAKR 540
DB 481 YOEIAGSKTVQYQESHHTAFTLPGLYRVVHGIDVPKFNIVSPGADMSIYPPHTEKAKR 540
QY 541 LYSINGSIENLIYDPEQNDHILGHLDKSKPLFSMARLDKYNITGLVEAFKAKALRE 600
DB 541 LYSINGSIENLIYDPEQNDHILGHLDKSKPLFSMARLDKYNITGLVEAFKAKALRE 600
QY 601 LYNLVVAVAGNDVNSKQREBELAEKMHLEIKTNLFGQRFNISAQNTNRRANGLERY 659
DB 601 LYNLVVAVAGNDVNSKQREBELAEKMHLEIKTNLFGQRFNISAQNTNRRANGLERY 659
QY 659 LADTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHPDQA 719
DB 659 LADTGAFQOPALYEAFFGLTVVEAMTCGLPTFATLHGPAEIIIEHGVSGHIDPYHPDQA 719
QY 719 LERLETRRLMEFYLLKRELAQTVPLADQ 806
DB 719 LERLETRRLMEFYLLKRELAQTVPLADQ 806
QY 805 RRSRRRLMEFYLLKRELAQTVPLADQ 805
DB 805 RRSRRRLMEFYLLKRELAQTVPLADQ 805

RESULT 3
US-08-684-005-2

```

Sequence 2 Application US/08684005
Patent No. 6682918
GENERAL INFORMATION:
APPLICANT: Haseelkorn, Robert
APPLICANT: Bulkema, William J.
APPLICANT: Bauer, Christopher C.
TITLE OF INVENTION: BACTERIAL SUCROSE SYNTHASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,005
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARSB:508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 806 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-684-005-2

Query Match: 43.2%; Score 1833; DR 4; Length 806;
Best Local Similarity 45.6%; Pred. No. 4,7e-162;
Matches 359; Conservative 163; Mismatches 251; Indels 14; Gaps 7

24 RNEIYALISKYVKNKGKGILOPHHILDALDEVQSGVRALAEQFLD--VIRSAGEAIVL 80
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
2b KHDRGFSSELRQDQKNTLRRDILNIVYAEVSCQKPEYTSYKFSNLKLYYTGEIIOE 73
14 KHDRGFSSELRQDQKNTLRRDILNIVYAEVSCQKPEYTSYKFSNLKLYYTGEIIOE 73

81 PEFVALIAKRPKGVWEYRVAVNHESVQGLTYSEITFKREELVYDQNDPY---VLEIDF 137
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
74 DSNFCFIIIRPKIAAEVVRILTA-DLDVEMTVQELIDLRDRIVNKF--PYGDIIEIDF 130
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

138 EPEVNVSVRPRNRSSISGVQVOLFNEHLSIMFR-NRDCLEPIIDFLRGHREKHYMMIND 196
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
131 GPFIYTTPTIRDPKRIKGVQVOLFNIYLSKLTQDSQOMLESFPHFKLHNYGIGLIINH 190
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

197 R-QSIGRLQSVLYTKAEELSKLPADTPYSQFAYKQEMGLEKMGEDTACIVLEMIHLLID 256
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
191 QIQSQGQLSQCKRNALNLFSDRPNDEPYQFLQIQTFEPQMGNTASRVADTLNIDLE 250
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

257 ITQADPSTLEKFLGILPMIENVVNVVSPKGYGQANVGLPTGGQIYVYIDQVAALENE 316
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
251 LIDSPDPQTLAEFAPISRIPIWIFRIVVASAHGMFGQEGVIGRPDTGGVVVVLDAQNLEKQ 310
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

317 M---VLRLLKQGLDVSPKILYTRILIPDAKGTSCNQRLEISGTOBTYILRVPFNNEN-G 372
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
311 IQEDAILAGLEAVLNQPKYTLIRLLIPNSDGLCNQRLKXYGTETMAATLLRPDIRFENK 370
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

373 IIKKWIREDVWPYUETFAEDAAGEITAEILQSTPDFIIGNYSDGNIVASILSYKMGITOC 432
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
371 MGNWNISREFPYLETFAIDSERELLAEFGQRPDIAGVYTDGNIVAEILTRRMKVTOC 430
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

433 N-AHALKTKKYDSDILFWKRPDEKHFSCQFTNDIIMNMADEFTITSYQELTAGSKNTYG 492
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

Db	431	NIHAHLEKRYLFSNLYMOLBEKHFSJQFTADLIAMAAANFVISTQELVGTGDSIG	490
Qy	493	QYESHTAFTLPGLYRVVHGIDVPDEKFNIVSPGADMSIYFPHTEKAKRLTSLHGSIENLI	552
Db	491	QVBSYKCFMPELXHVNGIELFSPKFNVPVPGVNSNSYFPYQJONRIEESDRDREEMLI	550
Qy	553	YDPEDONDEHIGHLDMSKPLPSMALDVRKNTGLVEAFKAKRELVINLVVAGYND	612
Db	551	FTLEDSQSJEGKXLDHNNKRPISFMALDRKNTGLAECCGSGOSJQERNCLLIWAKLR	610
Qy	613	VNKSQRREEFAIEKKHMLIKTNLFEGCFRMSIAQTNRAKNGELVYIADTHGAFYOPAL	672
Db	611	IRSESDNEEDLIVKLYRIIDEINLHGKIRWLGVRSLSKSDSGIYIVICRQSIGFYOPAL	670
Qy	673	YEAFTGLVVEAMTQGPTEATLHGFAEIIHSGVSGFHIDPYHPEQAVNIMADPDRCKQ	732
Db	671	FEAFGLTIRESMISGLPTFATQGGPLEIIOQKINGFIYIPTHLEBATYKILDFVTKCEQ	730
Qy	733	DPEHWNISAGJQRIYKXTKMLIYSEKRLMTAGVYGFMYKVSKELETRRYLEMFYIL	792
Db	731	NPYWNIISEKALDRVYSTYWKIHTTKLLTLARIYGFNFTSKERKEDILRYLESFLYL	790
Qy	793	KFRBLAK 799	
Db	791	ITYKRAQ 797	
RESULT 4			
US-09-394-272-14			
Sequence 14: Application US/09394272			
Patent No. 6472588			
GENERAL INFORMATION:			
APPLICANT: Haigler, Candace H.			
APPLICANT: Holaday, A. Scott			
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED			
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE			
FILE REFERENCE: 201304/1000			
CURRENT APPLICATION NUMBER: US/09/394,272			
CURRENT FILING DATE: 1999-09-10			
NUMBER OF SEQ ID NOS: 14			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO: 14			
LENGTH: 720			
TYPE: PRT			
ORGANISM: Synecchocystis sp.			
US-09-394-272-14			
Query Match 11.0%; Score 467.5; DB 4; Length 720;			
Best Local Similarity 27.5%; Pred. No. 1.6e-34;			
Matches 145; Conservative 108; Mismatches 190; Indels 85; Gaps 20			
Qy	279	VVVVSPHVEFGQANV-IQL-PTGSGQIVYIILDVYAL-ENEMVLRLLKKQGLDVSFKILIV	335
Db	8	ILLISVHLLINGENLEIGRADDTGGQTKVLELALATVKNPQVARVD-----LL	56
Qy	336	TRLLPDAGKGTSCNQLERISGTQRTYILRVPPRNENGLKKMISFDVWPYLETFAADAA	395
Db	57	TRLIDPQVDVADYAPRELIG-DRAQIVRIEGGPEEYIAKENVL-----WDYIDNFA-DHA	109
Qy	396	GEIAAELOGTPTFIIIGNYSDGNLVASLSTYKMGILQCNIAHAL-----EKTYVPSDIWMKN	452
Db	110	LDYLKEQPELDPVHSHYADAGYVTRLSHQGILGVYTHSGLSGSKTRRLLSGIXDDE	169
Qy	453	FDEKTHFSQCFADIIAMNADFIITSTGYOETJASKNVQGYESHSTAFTLPGLYRVVHGI	512
Db	170	IESRYNMARRINAAEETIGSARAVITSTHGEIA-----EYAAQY-----	208
Qy	513	DYFDE-KRNIYSPGADMSIYFPHTEKAKRLTSLHSGSIENLIYDPQONDEHIGHLDKSRP	571
Db	209	DYQGDQMLVIPPQGTLEKFPY-PKGNEMETPTVOELQFLNHR-----KP	254
Qy	572	ILFSAR-EDRVKNITGLVEAFKAKRELVINLVVAGYNDVYKSKDREELAEI-----E	626

Db 255 LIALSLSPDRKRNHKLIAVAGSPQ:QAQANLTVAG-----NRDITLDDQPRE 306
Qy 627 KMEHLKT---HNIFGQFRMISAQTNBARN-GEIYRIADTHGAFVOPALYEAGLTVYE 682
Db 307 VLTLTLITDRYDLYGKAAV--PKONQAEVYALFRLTALSQGVFINPALTEPGLTLIB 364
Qy 683 AMTCGLPFLTHGCPHEIIEHVSGFHIDPYHEQAVNMADPFDCCKODPDHVMVNSG 742
Db 365 AAAGGVIVATEDGGPVDIILKNCGYLINELSDV---LADKLIVANDKQOMQPLSE 420
Qy 743 AGLORIEKTYWKIYSERIMTLAGVGFWMKYVSKLEBLETREYLEMPY 790
Db 421 SGLBGVNRHISMESHVESY--LBAINALTQOTSLVAKSDLKRRTIVY 466

RESULT 5
US-09-394-272-11
; Sequence 11, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-394-272-11

Query Match 11.0%; Score 466.5; DB 4; Length 1083;
Best Local Similarity 24.3%; Pred. No. 3.8e-34;
Matches 184; Conservative 130; Mismatches 285; Indels 159; Gaps 32;
Qy 118 EKEELVDG-QHNDPVLELDEPPENVSVPRNRSSST-----GNGVOPL 160
Db 67 FVEEVENSPDESDDYKTIKVIATATNTERESNRLENIQRIWHLARKKQIYWDGVLIS 126
Qy 161 NRHLSSINFRRDCEPLIDEL-RGRHKGHWMLNDRISQSLRQSVLTAEHLSKLP 219
Db 127 KRRIREGGRM-DAEEDLISLSEBKDK-----NDGKESVYVTLIAPRDMPIR 179
Qy 220 ADTPYSQPAFKQEWLEKGMGDTAGHVLMIHLIDIIQAPDPSLTKFLGRIMFINV 279
Db 180 SE-----VQIMSED-----DKSR-----NLVIILRVEIGPSDLF-----VVFNM 216
Qy 280 VV-----VSPHGYF-GQANVLGL-PTGGQIYIILDOVALNEMLRLKK 323
Db 217 LVGLTMCYLYVPCFTNCSWGLVGRBNMELGRDSDTGQVKKVVALARMAN-----T 269
Qy 324 QGLDVSFKLIYTRLIIPDAK-GTSCNQLERIS-----GTQH--TYILKVPFNENGILKK 376
Db 270 EGVH--RVDLITRQISPEVDVSYGEPEVEMLSCEPSSDSGSGIIRIPC-----GSRBK 322
Qy 377 WISREVPVYLETFAEDAGRIAA-----ELQG-----TPDFIIGNYSQNLVASLSLY 425
Db 323 YIPKESLWPHIPEFDGALNHIVSLARSLGEQVNGKXP:WYVYIGHVADAGEVAHLAG 382
Qy 426 KMGITQCNIAHLEKTKY---PDSDIYKQNDKDEKHSQCTADIIAMNNADFIITSY 481
Db 383 ALNVPMVLTHGSLGNKKEQQLDQGRITREDIDRTYKIMRIEABEQSLDAAEYVVTSTR 442
Qy 482 QELIASKYTVQGVESHATFLPGLYVYHGIDV-----FDPKFNIV 522
Db 443 QSID-----AQM-----GLY-----LGFIDIKLEKRIYRRKRGVSLGIVPMYVI 484
Qy 523 SPGADMSIYFPH--TEKARLTLSHGSIENLIYDPEQN--DEHIGLDRSKPILFSMAR 578

Db 485 PRGMDPSYVLTODSQEODGDLKSLIGDRNQIKKPEVPIWSEIRPFSPNPKPTLLALSR 544
Qy 579 LCRVKNITGLVEAFKCAK:RELVNLVWVAGYDVNSKQEEIAIEKMBLITKTNLF 638
Db 545 PBEKKNVTLTKAGCEQOPLRELANVLIIQNRDIEHMRSSSVLMNVKLTIDQYLY 604
Qy 639 GQFRMISAQTNBARNGEIYRIADTHGAFVOPALYEAGLTVEMTCGLPFLTHGCP 698
Db 605 QGVAV-PKHNGSEVPRIYRLAAKTKGVFINPALVEPGLTLIBAAAGLPIVATRNQSP 663
Qy 699 AEITHEGVSGFHIDPYHEQAVNMADPFDCCKODPDHVMVNSAGLORIEKTYWKIYS 758
Db 664 VDIYKALNNGILYDP-HDQQA:--SDALJLKVANKHLMACRKGKLNH-RFSWPEHC 718
Qy 759 ERLMTLAGVGFWMKYVSKLEBLETREYLEMPYILKPRE 796
Db 719 R-----NYLSHVEHCRNRHPTSSIDIKKYPE 744

RESULT 6
US-09-394-272-1
; Sequence 1, Application US/09394272
; Patent No. 6472588
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/09/394,272
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-394-272-1

Query Match 10.6%; Score 450; DB 4; Length 1056;
Best Local Similarity 26.4%; Pred. No. 1.3e-32;
Matches 145; Conservative 97; Mismatches 218; Indels 90; Gaps 18;
Qy 279 VVWVSPHGYF-GQANVLGL-PTGGQIYIILDOVALNE-----MVLRIKQGLDV 328
Db 176 VVLSIHGILNGENNELGRDSDTGQVKKVVELARLGSMPGVYRVDLITRQVSAQVDM 235
Qy 329 S---PKIIVTRLIIPDAKGTSCNQLERISGTQHTYIIRVPRNENGILKKWISREDPVP 385
Db 236 SYGEP-----TEMLSSRSENSTEQIGSSG--AYIIRIP--GPKQKYAKELLP 283
Qy 386 YLETFADNAG-----EIAELQGTDPDFIIGNYSQNLVASLSYNGITQCN 434
Db 284 YIPEFVDGLSHITKQMSKVLGQIGGLPWYASVHGHAADGSDAALLSGALNVPMVFT 343
Qy 435 AVALERTK---YPPSDIFWKNFDEKHYSCQFTADIIAMNNADFIITSYQELIASKY 490
Db 344 GHSIRGDKLDQQLKQGRLSREVDATYKIMRIEABELCLDASRIYITSTRDIEBQ--- 400
Qy 491 VQGYRSHATFLPGLYVYHGIDV-----FDPKFNIVSPGADMSIY 531
Db 401 -----WQYHGFVLTERKLARMRGRVSCHGRTFMRAKIPGMEFNHI 445
Qy 532 PFTEKAKLTLSHGIS-ELIYDPQNDHEIHLDRSKPILFSNARLDVKNITGLVE 590
Db 446 AP--EDALMDTQIDHKKESNANPDVYIWEIRFENGKRPMTALARPCKNLTLLVX 503
Qy 591 AFAKCAKRELVNLVWVAGYDVNSKQEEIAIEKMBLITKTNLFQGFPMISAQTN 650
Db 504 AFGECEPFLRELANLTIIQNRDIDEMSTSSSVLSIKLTDKDYLGQVAV-PKHNGK 562
Qy 651 ARNGELYRIADTHGAFVOPALYEAGLTVEMTCGLPFLTHGCPAEIIEHVSQGH 710

Db 608 -NALADALYKLSIDKQMSRCRENGLTNIHQ-FSPHECKNYLRILTL 654

RESULT 9
US-03-394-272-5
Sequence 5, Application US/09394272
Patent No. 6472588
GENERAL INFORMATION:
APPLICANT: Haigler, Cardace H.
APPLICANT: Holaday, A. Scott
TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: 201304/1000
CURRENT APPLICATION NUMBER: US/09/394,272
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentia Ver. 2.0
SEQ ID NO 5
LENGTH: 1059
TYPE: PRT
ORGANISM: Vicia faba
US-09-394-272-5

Query Match 10.5%; Score 445; DB 4; Length 1059;
Best Local Similarity 27.4%; Pred. No. 3.7e-32;
Matches 148; Conservative 92; Mismatches 222; Indels 78; Gaps 22;

QY 279 VVVVSPHGYF-GQANVLGL-PDTGGQIVYILDVRALENEM-----VLRKKQGLDVP 330
Db 169 IVLISHLIGENNELGRSDTGGQVKKVVELARLGSMPGVYVDLITRQVSSPDVDM 228
QY 331 KILIVTRILPAKSGSCNORLERISGQHTYILRPFRNENGLKKWISRPVWYLETPE 390
Db 229 SYGPEPTMLAPRNTDFDQDMSGSG--AYIRLPGFRN--KYLPEKELMPYIPEE 281
QY 391 AEDAGEI-----AAELQGT-----PDLIGNYSDGNLVASLSTYKMGITQCNIAHLE 439
Db 282 VDGANGHILQMSKALGEQIGSHAWPVALHGHYADAGSALLGALNVPIPLFGHSIG 341
QY 440 KTK---YPSDIEFWKDFEKYHFSQFTADIIAMNADFIITSTYQEIAGSKNTVGQYE 495
Db 342 RDKLEQLKQGRSLSTDEINSTYKIMRIEAEELALDGTETVITSTRQIE-----EQWR 395
QY 446 SHTATTLGLYRVVHG-----IDVDPKFNIVSPGADMSIYEPHTEKAKRLTSLHS 547
Db 396 LYNQFD-PVLERKIPARIRRNVSQYGRVPMVSVIPGME-----FHH-----IAPLDGD 444
QY 548 I-----ENLIYDEQND-----EHLGLDPRSXPILFSMARLDPRKNTGLVAFAKACAL 598
Db 445 IETPEGLDHPAPQDPPIMSEIMPFSPKPKFVILALARPDKXITTLVAKAFGECPRL 504
QY 599 RELVNVVVAGYNDVYKSKREELAEIEKHEHLIKTHNIFGQFRWISAGTNFARNGEILYR 658
Db 505 RELANLITLMGRDQIDEMSTSSSVLSTVLKIDKIDYQVAV--FKHKKSSDPVDIYR 563
QY 653 YIADTHGAFVQALYEAEGILVVEAMTCGLPPFALHGGPAILIEGV--SGPHIDPYR 716
Db 564 IAAKTKGVFINPAFIEPGLTLEAAAYGLPMVATKNGSPVDI--HRVVDNGLLDP--HD 620
QY 717 EOVAVIMADPFPRCKQDPDHWNVISGAGHQRIYEKTY-----KIYSERLMTLAGYGVFK 772
Db 621 EKSI---ADALLKIVSNKQMAKCRONGKXNH-LFSWPEHCKTYLSKATQPRHPQMG 676

RESULT 10
US-08-429-054A-11
Sequence 11, Application US/08429054A
Patent No. 597126
GENERAL INFORMATION:
APPLICANT: JEAN ASSCHE, CHARLES LANDO, DANIELLE BRUHEAU,
APPLICANT: VAN VOELKER, TONI GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),

TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 842,337
FILING DATE: 20-MARCH-1992
APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-JULY-1991
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-JULY-1990
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Charles A. Muserlian
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146,1137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-429-054A-11

Query Match 10.5%; Score 444; DB 2; Length 1068;
Best Local Similarity 25.2%; Pred. No. 4.7e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGVLEMIHLIDIIQAPDPSTLEKFLGRIPMI-----FNVVVSPHGYF- 288
Db 141 GDTIGEL-----APVETTKKQFRNFSDLTWSDDKEKKYIVLISVHGLVR 188
QY 289 GQANVLGL-PDTGGQIVYILDVRALENEMVRLKKQGLDVP--KILIVRELI--PD- 341
Db 189 GENMEIGRSDTGGQVKKVVELARA-----MSMGEYRVVDFTRQVSSPDV 235
QY 342 -----AKGTSONORLERISGQHTYILRPFRNENGLKKWISRPVWYLETPE 390
Db 236 DMSYGPETMLCAISDGEKMSGSG--AYIRLPGFRN--KYLPEKELMPYIPEE 281
QY 391 AEDAGEI-----AAELQGT-----PDLIGNYSDGNLVASLSTYKMGITQCNIAHLE 439
Db 289 VDGANGHILQMSKALGEQIGSHAWPVALHGHYADAGSALLGALNVPIPLFGHSIG 341
QY 440 KTK---YPSDIEFWKDFEKYHFSQFTADIIAMNADFIITSTYQEIAGSKNTVGQYE 495
Db 342 RDKLEQLKQGRSLSTDEINSTYKIMRIEAEELALDGTETVITSTRQIE-----EQWR 395
QY 446 SHTATTLGLYRVVHG-----IDVDPKFNIVSPGADMSIYEPHTEKAKRLTSLHS 547
Db 396 LYNQFD-PVLERKIPARIRRNVSQYGRVPMVSVIPGME-----FHH-----IAPLDGD 444

QY 537 KAKRLTSLHSGSIENLTYDEQNDHEIG-----HLDKSKPLFSMAR 578
DB 449 -----EDDGDGVKDDIVLGASPKSMPTIWAELVFLTNPHKPMIALSR 496
QY 579 LDRVKNITGLVEAFKACAKLRELVLNVVAGYDVNKSXDRBELAEIKHEMLKTHNLF 638
DB 497 PDKKNITTLVAFKPCREPLRELANTLLMGNRDIDDMSAGNASVLTTLKLIKIDKDYDLY 556
QY 639 GCFRWSAOTNRARNGELRYIADTHGAFVOPALYEAGLTVEAMTGLPTFATLHGSP 698
DB 557 GSVAF-PKHNGQADVETIYRLAKKMGVFINPALVEPFGTLLEAAHGLPIVATKNGSP 615
QY 699 AEIIEHVSGFHIDYHPHQAIVNLADFPDRCKODPDHWNISGAGLQRIYKTYKTXS 758
DB 616 VDTNALNGLVDPHDQ-----NAIADALKLVADKNLMQBCRRNGRLNTH-LYSWPHC 670
QY 759 ERLMT-LAGVYGFWMKYSKLELETRRYLE 787
DB 671 RYTLTRVAGC-----RLRNPRLK 689

RESULT 11
US-08-718-777-7
; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Vekker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: SYNTHASE IN PLANTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,777
; FILING DATE: NOT YET ASSIGNED
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,471
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GANE.072.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-777-7

Query Match 10.5%; Score 444; DB 2; Length 1068;
Best Local Similarity 25.2%; Pred. No. 4,7e-32;
Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGHVLTEMLHLLDIIQADPSTLEKFLGRIEMI-----ENVVVSPEHYF- 288
DB 141 GDTIEL-----APVETTKKFKQSNFSDLTWSDDNKEKLYIVLISVGLVR 188
QY 289 GQANVLGL-PTGGQIVILLDOVRALNEMVLRLKQGLDVP-----KILIVRELI--PD- 341
DB 189 GENMEIGRSDSDGGGVKKVVELARA-----MSMGGVYRVDLFTQVSSPDV 235
QY 342 -----AKGTSQNRLEISGTOHTYLLRVFRNENGLIKKWSRFDVWPLYLET 390
DB 236 DMSYSEPTMLCAGSNDGMBESG--AYIVRIC-----GRDYLKKEBALMPYLOEF 288
QY 391 AEDAGEI-----AAELQGT-----PDEIIGNSDGNIVASILSYRMGITQCNIAHAB 439
DB 289 VDGALAHILNMSKALGEGVGNRPLVPIYHGHYADAGVAAALSGALINVPWLTGHSIG 348
QY 440 KTK-----YDSDFIWMNPFDEKTHFSQCFADIIANNRPDITSTQELAGSNVYQYE 495
DB 349 RYKLSQLLKQGRMSKEIDSTYKIMRIRIGBELADASELVITSTQED-----EQW- 401
QY 496 SHTAFTLPLGLYRVHGIDY-----PDKENIYSGADMSIYPHTE 536
DB 402 -----GLY--DEEDVYKLEKYLARARAGVSGGRVMPRVVPIPGMDFSNVVH-- 448
QY 537 KAKRLTSLHSGSIENLTYDEQNDHEIG-----HLDKSKPLFSMAR 578
DB 449 -----EDDGDGVKDDIVLGASPKSMPTIWAELVFLTNPHKPMIALSR 496
QY 579 LDRVKNITGLVEAFKACAKLRELVLNVVAGYDVNKSXDRBELAEIKHEMLKTHNLF 638
DB 497 PDKKNITTLVAFKPCREPLRELANTLLMGNRDIDDMSAGNASVLTTLKLIKIDKDYDLY 556
QY 639 GCFRWSAOTNRARNGELRYIADTHGAFVOPALYEAGLTVEAMTGLPTFATLHGSP 698
DB 557 GSVAF-PKHNGQADVETIYRLAKKMGVFINPALVEPFGTLLEAAHGLPIVATKNGSP 615
QY 699 AEIIEHVSGFHIDYHPHQAIVNLADFPDRCKODPDHWNISGAGLQRIYKTYKTXS 758
DB 616 VDTNALNGLVDPHDQ-----NAIADALKLVADKNLMQBCRRNGRLNTH-LYSWPHC 670
QY 759 ERLMT-LAGVYGFWMKYSKLELETRRYLE 787
DB 671 RYTLTRVAGC-----RLRNPRLK 689

RESULT 12
US-09-051-341-7
; Sequence 7, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17351
; FILING DATE: 25-OCT-1996

APPLICATION NUMBER: US 08/549,016
 FILING DATE: 27-OCT-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/372,200
 FILING DATE: 12-JAN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Barbara Rae-Venter, Ph.D.,
 REGISTRATION NUMBER: 32,750
 REFERENCE/DOCKET NUMBER: CGNE.110.0205
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415)328-4400
 TELEFAX: (415)328-4477
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1068 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-051-341-7

Query Match 10.5%; Score 444; DB 3; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 4.7e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGHVLMTLHLLDIQADPSTLEKELRIEMI-----FNVVVSPHGYF- 288
 DB 141 GDTIGEL-----APVETTKKFGQNNFSDLTWSDNKKKLYIVLSVHGLVR 188
 QY 289 GQANVLGL-PTGGQIVYILDQVRLNEMVRLKKGIDVSP--KLIYTRLI--PD- 341
 DB 189 GNNELGSDSDTGGQVYVVELARA-----MSMWPGVYRDLFTROVSSPDV 235
 QY 342 -----AKGSCNQRLERISGTOHTYTLRVPFNENGLKKWISRFVWPYLETF 390
 DB 236 DWSYGEPTMLCAGNDEGMGSSGQ--AYIVRLPC--GPRDKYLKEALNPLYLQEF 288
 QY 391 AEDAGEI-----AAELQGT-----PDFIIGNYSDGNLVAISLYKMGITOCNIAHALE 439
 DB 289 VDGLAHLILMSKALGEQVGNRPVLPYIHHGVADGVAALLSGALNVPMVLVGHSLG 348
 QY 440 KTK-----YPSDIEFNKNDKHYFSCQFTADIIANNADFIITSTYQELAGSKNTVGYQE 495
 DB 349 RNKLQLKQGMSEKIDSTYKIMRIEGEIALDASLVTSTQCEID-----EQW- 401
 QY 496 SHTATLPGLYRVNHGIDV-----FDPKFNIVSPGADMSIYPPHTE 536
 DB 402 -----GLY--DGFVKLEKVLRAARRGVSCGRIMPRVAVIPGMDPSNVVH-- 448
 QY 537 KAKRLTSLHSGIENLIYDEPQNDHIG-----HLDKSKPILEFSMAR 578
 DB 449 -----EDIDGDGDVMDIYGLEGASPKSMPTMAEVMRELTPHKKMILALSR 496
 QY 579 LDRVKNITGLVFAFAKCAKLRELVNLVVAGYNDVNSKSDREBIAIEKMHLEIKTHNLF 638
 DB 497 PDPKKNITTLVYAFGECREPLRELIANTLIMGNRDDIDMSAGNASVLTTLVKLIDKIDLY 556
 QY 639 GQFRTISAGTNARANELRYIADTHGAFOVALYEAFGITVVEAMTCGLPTFATLHGSP 698
 DB 557 GSVAF-PKHNDQADVEIYRLAAKMGVFINPLVPPFGITLLEAAHGLPIYATKNGP 615
 QY 699 AEIIEHGVSGFHIDPHYRPOAVNLADFPDRCKQDPDHWVNISGAGLQRIYEKTYTKIYS 758
 DB 616 VDIITNANLNGLLVDPHDQ-----NAIDALLKLVADKRLMQECCRNGRLNTH-LYSWPEHC 670
 QY 759 ERLMT-LAGYVGFYKVKYSLERLETTRYLE 787
 DB 671 RTYLITRVAGC-----RLRNPRWLK 689

RESULT 13
 US-09-394-272-8
 Sequence 8, Application US/09394272
 Patent No. 6472588

GENERAL INFORMATION:
 APPLICANT: Hatjeler, Candace H.
 APPLICANT: Holaday, A. Scott
 TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
 TITLE OF INVENTION: EXPRESSION OF SUCROSE PHOSPHATE SYNTHASE
 FILE REFERENCE: 201304/1000
 CURRENT APPLICATION NUMBER: US/09/394,272
 CURRENT FILING DATE: 1999-09-10
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 1068
 TYPE: PRT
 ORGANISM: Zea mays
 US-09-394-272-8

Query Match 10.5%; Score 444; DB 4; Length 1068;
 Best Local Similarity 25.2%; Pred. No. 4.7e-32;
 Matches 159; Conservative 96; Mismatches 211; Indels 164; Gaps 24;

QY 241 GDTAGHVLMTLHLLDIQADPSTLEKELRIEMI-----FNVVVSPHGYF- 288
 DB 141 GDTIGEL-----APVETTKKFGQNNFSDLTWSDNKKKLYIVLSVHGLVR 188
 QY 289 GQANVLGL-PTGGQIVYILDQVRLNEMVRLKKGIDVSP--KLIYTRLI--PD- 341
 DB 189 GNNELGSDSDTGGQVYVVELARA-----MSMWPGVYRDLFTROVSSPDV 235
 QY 342 -----AKGSCNQRLERISGTOHTYTLRVPFNENGLKKWISRFVWPYLETF 390
 DB 236 DWSYGEPTMLCAGNDEGMGSSGQ--AYIVRLPC--GPRDKYLKEALNPLYLQEF 288
 QY 391 AEDAGEI-----AAELQGT-----PDFIIGNYSDGNLVAISLYKMGITOCNIAHALE 439
 DB 289 VDGLAHLILMSKALGEQVGNRPVLPYIHHGVADGVAALLSGALNVPMVLVGHSLG 348
 QY 440 KTK-----YPSDIEFNKNDKHYFSCQFTADIIANNADFIITSTYQELAGSKNTVGYQE 495
 DB 349 RNKLQLKQGMSEKIDSTYKIMRIEGEIALDASLVTSTQCEID-----EQW- 401
 QY 496 SHTATLPGLYRVNHGIDV-----FDPKFNIVSPGADMSIYPPHTE 536
 DB 402 -----GLY--DGFVKLEKVLRAARRGVSCGRIMPRVAVIPGMDPSNVVH-- 448
 QY 537 KAKRLTSLHSGIENLIYDEPQNDHIG-----HLDKSKPILEFSMAR 578
 DB 449 -----EDIDGDGDVMDIYGLEGASPKSMPTMAEVMRELTPHKKMILALSR 496
 QY 579 LDRVKNITGLVFAFAKCAKLRELVNLVVAGYNDVNSKSDREBIAIEKMHLEIKTHNLF 638
 DB 497 PDPKKNITTLVYAFGECREPLRELIANTLIMGNRDDIDMSAGNASVLTTLVKLIDKIDLY 556
 QY 639 GQFRTISAGTNARANELRYIADTHGAFOVALYEAFGITVVEAMTCGLPTFATLHGSP 698
 DB 557 GSVAF-PKHNDQADVEIYRLAAKMGVFINPLVPPFGITLLEAAHGLPIYATKNGP 615
 QY 699 AEIIEHGVSGFHIDPHYRPOAVNLADFPDRCKQDPDHWVNISGAGLQRIYEKTYTKIYS 758
 DB 616 VDIITNANLNGLLVDPHDQ-----NAIDALLKLVADKRLMQECCRNGRLNTH-LYSWPEHC 670
 QY 759 ERLMT-LAGYVGFYKVKYSLERLETTRYLE 787
 DB 671 RTYLITRVAGC-----RLRNPRWLK 689

RESULT 14
 US-08-553-436A-6
 Sequence 6, Application US/08553436A
 Patent No. 5866790
 GENERAL INFORMATION:
 APPLICANT: HESSE, Holger
 APPLICANT: MULLER-ROBER, Bernd
 TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE

TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
 TITLE OF INVENTION: CONCENTRATION
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESS: Ostrolenk, Faber, Gerb & Soffen
 STREET: 1180 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: US
 ZIP: 10036-8403
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,436A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP94/01671
 FILING DATE: 20-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: DE P 4317596.1
 FILING DATE: 24-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Meliman, Edward
 REGISTRATION NUMBER: 24,735
 REFERENCE/DOCKET NUMBER: P/951-117
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 382-0700
 TELEFAX: (212) 382-0888
 TELETYPE: 236925
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1045 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-553-436A-6

Query Match 10.4%; Score 441.5; DB 2; Length 1045;
 Best Local Similarity 26.8%; Pred. No. 7,8e-32;
 Matches 146; Conservative 102; Mismatches 190; Indels 107; Gaps 24;

279 VVVVSPHGYF-GQANVLGL-PTGGQIVYILDOVRALENE-----MVALRLKKGGLDV 328
 163 LVLSLHGLIRGENNELGSDSTGGQVKKVVELARLGSMPGVYRVDLTRGVSSPDVDM 222
 329 S---PKLIVTRLIDPAKGTSCNQLERISGTOHTYILRVPPNENGILKKMISRPDVP 385
 223 SYGEPTKMLNPR---DSNGFDDDD--DEMGSSGAYIVRIPF---GPRDKYIAKEELWP 273
 386 YLETPADDAAGHIA-----AELQGT-----PDLIGNSDGNLVASLSYKMGITQCN 434
 274 YLPEFVDGALNHIYQMSKVLGEQISGETVWPVALHGHVADAGDSALLSGGLNVPMLLT 333
 435 AHAELEKTKYPD-----SDIFWKNPDEKHFSCQFADIIAMNNADPIITSTYQGEIA 485
 334 GHSLGDKLEQLLKGQMSKDI-----NNTYKIMRIABEELSDASEIVITSTQGEIE 388
 486 GSKNTVGQYESHHTAFLPGL-----YRVVHGIDV---FDPKFNIVSPGADMSYFPHTEK 537
 389 -----EQMHLVDGFD-PVLERKLRARMKRGVSCYGRFMRPMVAVIPGMEFNHIVP--- 438
 538 AKRLTSLHSGISIELIYDPRQNDH-----IGHLDKSKELPSMARLDRVKN 585
 439 -----EDMDG---ETETETEHPTSPDPPIWAEIMRPFPSKPKKPMILALARPDKNI 488
 586 TGLVEAFACAKLRELVNLVVAGYNDVKNKXOREIAIEKMHKELIKTNLFGQFRMIS 645
 489 TLLVYAFGCRPLRELANTLLIMGNBDGIDEMSSSTSSVLLSVLKLIIDQYDLYQVAV-P 547
 489 TLLVYAFGCRPLRELANTLLIMGNBDGIDEMSSSTSSVLLSVLKLIIDQYDLYQVAV-P 547

646 AOTNRARNGELRYTIADTHGAFVQALYEAFGLTVEAMTCGLPTPATLHGGPAELIEHG 705
 548 KHHKQADVPEIYRLAAKTVGFVFNPAFLIEPGLTILEAAHGLPMVATKMGCPVDIQRL 607
 706 VSGFHIDPYHPQAV-----NLMAD--FPDRKQDPDHVNINSAGLQRIYKTYKTIYS 758
 608 DMGLIYDP--HEQOSIATLALKLVADKQMLTKCOON-----GLKNH-LYSWEHES 655
 759 ERLMT 763
 656 KTYLS 660

Query Match 10.4%; Score 441.5; DB 4; Length 1045;
 Best Local Similarity 26.8%; Pred. No. 7,8e-32;
 Matches 146; Conservative 102; Mismatches 190; Indels 107; Gaps 24;

279 VVVVSPHGYF-GQANVLGL-PTGGQIVYILDOVRALENE-----MVALRLKKGGLDV 328
 163 LVLSLHGLIRGENNELGSDSTGGQVKKVVELARLGSMPGVYRVDLTRGVSSPDVDM 222
 329 S---PKLIVTRLIDPAKGTSCNQLERISGTOHTYILRVPPNENGILKKMISRPDVP 385
 223 SYGEPTKMLNPR---DSNGFDDDD--DEMGSSGAYIVRIPF---GPRDKYIAKEELWP 273
 386 YLETPADDAAGHIA-----AELQGT-----PDLIGNSDGNLVASLSYKMGITQCN 434
 274 YLPEFVDGALNHIYQMSKVLGEQISGETVWPVALHGHVADAGDSALLSGGLNVPMLLT 333
 435 AHAELEKTKYPD-----SDIFWKNPDEKHFSCQFADIIAMNNADPIITSTYQGEIA 485
 334 GHSLGDKLEQLLKGQMSKDI-----NNTYKIMRIABEELSDASEIVITSTQGEIE 388
 486 GSKNTVGQYESHHTAFLPGL-----YRVVHGIDV---FDPKFNIVSPGADMSYFPHTEK 537
 389 -----EQMHLVDGFD-PVLERKLRARMKRGVSCYGRFMRPMVAVIPGMEFNHIVP--- 438
 538 AKRLTSLHSGISIELIYDPRQNDH-----IGHLDKSKELPSMARLDRVKN 585
 439 -----EDMDG---ETETETEHPTSPDPPIWAEIMRPFPSKPKKPMILALARPDKNI 488
 586 TGLVEAFACAKLRELVNLVVAGYNDVKNKXOREIAIEKMHKELIKTNLFGQFRMIS 645
 489 TLLVYAFGCRPLRELANTLLIMGNBDGIDEMSSSTSSVLLSVLKLIIDQYDLYQVAV-P 547
 646 AOTNRARNGELRYTIADTHGAFVQALYEAFGLTVEAMTCGLPTPATLHGGPAELIEHG 705
 548 KHHKQADVPEIYRLAAKTVGFVFNPAFLIEPGLTILEAAHGLPMVATKMGCPVDIQRL 607
 706 VSGFHIDPYHPQAV-----NLMAD--FPDRKQDPDHVNINSAGLQRIYKTYKTIYS 758
 608 DMGLIYDP--HEQOSIATLALKLVADKQMLTKCOON-----GLKNH-LYSWEHES 655

QY 759 ERLMT 763
: : :
Db 656 KTYLS 660

Search completed: May 24, 2004, 11:28:53
Job time : 21.5847 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 15:32:41 ; Search time 4575.6 Seconds

(without alignments)
17993.290 Million cell updates/sec

Title: US-10-080-114a-11

Perfect score: 2757

Sequence: 1 atgcctgcctccgaagctgaa.....aaaaaaaaaagggcgccgcg 2757

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_escba:*
2: em_escbm:*
3: em_escbu:*
4: em_escbv:*
5: em_escpl:*
6: em_escro:*
7: em_escro:*
8: em_escro:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc4:*
13: gb_esc5:*
14: gb_esc5:*
15: em_escfm:*
16: em_escfm:*
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25: em_escfm:*
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27: em_escfm:*
28: gb_esc1:*
29: gb_esc2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2637.8	95.7	2705	AY104856 Zea mays
2	1174.6	42.6	3056	BT103683 SCGRZ100
3	1162.4	42.2	3140	AY103630 Zea mays
4	794.6	28.8	1005	BO619258 RNOS05F0

Result No.	Score	Query Match Length	ID	Description
5	793	28.8	938	BO619406
6	722	26.2	835	CA280212
7	704.8	25.6	888	CB662799
8	702.8	25.5	909	CB629313
9	688.6	25.0	841	CB648550
10	684.6	24.8	886	CB628458
11	676.2	24.5	745	CD426853
12	676	24.5	836	CB631982
13	664	24.1	690	CD442316
14	662.2	24.0	860	CB627276
15	655.6	23.8	808	CB651486
16	654.2	23.7	817	CB666247
17	647.6	23.5	797	CB647500
18	643.2	23.3	801	CB641607
19	641.2	23.3	836	CB635134
20	640.6	23.2	832	CB648734
21	639	23.2	839	CB645387
22	637.2	23.1	727	CA066428
23	636.8	23.1	824	CB668706
24	636.2	23.1	785	CB677314
25	636	23.1	833	CB631361
26	635.6	23.1	802	CB633383
27	635.2	23.1	836	CB631302
28	625.2	22.7	812	CB663333
29	623.6	22.6	807	CB6633104
30	622	22.6	767	CB682789
31	620	22.5	804	CB627329
32	618.8	22.4	806	CB627200
33	611.6	22.2	803	CB647961
34	607.8	22.0	779	CB635859
35	602.2	21.8	651	CF632182
36	599.2	21.7	800	CB628700
37	595.6	21.6	763	CB628938
38	594	21.5	700	CA195492
39	593.2	21.5	787	CB629315
40	592.8	21.5	756	CB628904
41	580.6	21.1	763	CB673208
42	560.6	20.3	727	CB632976
43	560	20.3	720	CA196779
44	545.4	19.8	628	CA283716
45	541.6	19.6	951	CF514627

ALIGNMENTS

RESULT 1
LOCUS AY104856
DEFINITION Zea mays PC0079420 mRNA sequence.
ACCESSION AY104856
VERSION AY104856.1 GI:21207934
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitlitt,M.S., Arthur,L.W., Hanatey,M., Korgante,M., and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE
AUTHORS Coe,B.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project. University of Missouri, Columbia, MO 65211, USA

COMMENT
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at www.zmdb.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

QY 1898 AGACCCACACTTGTTCGCGAGTTCCGCTGATCTCTGCCAGACAAAGGCCCTGA 1957
 DB 1861 AGACCCACAACTTGTTCGCGAGTTCCGCTGATCTCTGCCAGACAAAGGCCCTGA 1920
 QY 1958 AGCGGAGGCTATGCTGCTACATGCTGATACCAATGGTCTTTCGACAGCCGCTTGT 2017
 DB 1921 AGCGGAGGCTATGCTGCTACATGCTGATACCAATGGTCTTTCGACAGCCGCTTGT 1980
 QY 2018 ATGAAGCGTTCGCTGCTACCGTCTGAGGCTGAGCACTGTGGGCTTCTTACCTTTCGCA 2077
 DB 1981 ATGAAGCGTTCGCTGCTACCGTCTGAGGCTGAGCACTGTGGGCTTCTTACCTTTCGCA 2040
 QY 2078 CGCTCCATGAGAGTTCAGCTGAGATCTATGAGCATGGCTTTCGAGCTTCCATTTGACC 2137
 DB 2041 CGCTCCATGAGAGTTCAGCTGAGATCTATGAGCATGGCTTTCGAGCTTCCATTTGACC 2100
 QY 2138 CGTACACCCCGAAGCAGCTGTATATCTGATGGCCACTTCTTGACCGCTGACAGCAAG 2197
 DB 2101 CGTACACCCCGAAGCAGCTGTATATCTGATGGCCACTTCTTGACCGCTGACAGCAAG 2160
 QY 2198 ACCGAGATCACTGGTGTATATATCTGAGCAGGCTGACGCGCATATACGAGAGTACA 2257
 DB 2161 ACCGAGATCACTGGTGTATATATCTGAGCAGGCTGACGCGCATATACGAGAGTACA 2220
 QY 2258 CATGGAATATATCTGAGAGGTTGATGACACTGGCCGCGCTTACGCTTTCGAGAGT 2317
 DB 2221 CATGGAATATATCTGAGAGGTTGATGACACTGGCCGCGCTTACGCTTTCGAGAGT 2280
 QY 2318 AGCTGTGAAAGCTGCGAGAGGCTGAGACAGGCGCTGACCTTGATGATTTCTACATACTGA 2377
 DB 2281 AGCTGTGAAAGCTGCGAGAGGCTGAGACAGGCGCTGACCTTGATGATTTCTACATACTGA 2340
 QY 2378 AGTTCGCGAGCTGCGAGAGGCTGCGCTGCGCTTGAATGACCAACCGCAGTACTTGGCG 2437
 DB 2341 AGTTCGCGAGCTGCGAGAGGCTGCGCTGCGCTTGAATGACCAACCGCAGTACTTGGCG 2400
 QY 2438 AACTGTGATCTGCTGACACTTGTGTGACAACTGAAACCTGAAAGGACCTTCAATTTAG 2497
 DB 2401 AACTGTGATCTGCTGACACTTGTGTGACAACTGAAACCTGAAAGGACCTTCAATTTAG 2460
 QY 2498 GCGCGGAGAGGCTGACCAATTAATGTGCGGAGCTGAACTGTGTTTATATATGACA 2557
 DB 2461 GCGCGGAGAGGCTGACCAATTAATGTGCGGAGCTGAACTGTGTTTATATATGACA 2519
 QY 2558 TAAATGCAATTAACAAATTAATGAGAGGCTGAGTGTGTGTGTTACTG 2617
 DB 2520 TAAATGCAATTAACAAATTAATGAGAGGCTGAGTGTGTGTGTTACTG 2579
 QY 2618 TTATGCTGATTAATGAGAGTGTGTGCTCAATTTCTTGTGCGAAGCGGAGCACTG 2677
 DB 2580 TTATGCTGATTAATGAGAGTGTGTGCTCAATTTCTTGTGCGAAGCGGAGCACTG 2639
 QY 2678 GTGAAGTGTGATTAATGAGAGTGTGTGCTCAATTTCTTGTGCGAAGCGGAGCACTG 2730
 DB 2640 GTGAAGTGTGATTAATGAGAGTGTGTGCTCAATTTCTTGTGCGAAGCGGAGCACTG 2692

RESULT 2
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 DEFINITION Sacccharum officinarum cDNA, mRNA sequence.
 ACCESSION BUI03683
 VERSION BUI03683.1 GI:32815014
 KEYWORDS EST.
 SOURCE Sacccharum officinarum
 ORGANISM Sacccharum officinarum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Saccharum.
 1 (bases 1 to 3056)
 Nogueira, F.T.S., de Rosa, V.E. Jr., Menossi, M., Ulian, E.C. and

TITLE RNA expression profiles and data mining of sugarcane response to
 JOURNAL low temperature
 MEDLINE Plant Physiol. 132 (4), 1811-1824 (2003)
 PUBMED 22795309
 COMMENT Contact: Nogueira FTS
 Bioinformatics Lab
 Organization for Nucleotide Sequencing and Analysis
 C.P. 6176, Campinas, SP 13083-970, Brazil
 Tel: 55 19 37881101
 Fax: 55 19 37881089
 Email: tebaldi@unicamp.br

FEATURES
 source location/Qualifiers
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 /organism="Sacccharum officinarum"
 /mol_type="mRNA"
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ORIGIN
 Query Match 42.6%; Score 1174.6; DB 13; Length 3056;
 Best Local Similarity 68.5%; Pred. No. 2e-130;
 Matches 1653; Conservative 0; Mismatches 754; Indels 6; Gaps 2;

QY 16 CTGAGCGGAGGAGGAGCATCCGCGACCGCGTGAAGAGCACTCCACGCGACCGGAGC 75
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 QY 76 GAGCTGTGCGCTCTCTCTTCCAAATGATGTAACAAAGGAGGATCTGACCGGAC 135
 DB 2795 GAGCTGTGCGCTCTCTTCCAAAGGATGTAACAAAGGAGGATCTGACCGGAC 2736
 QY 136 CAATCTCTGAGCGCGCTGAGC---GAGTCCAGGCGTCCGCGGCGCGCGCGAG 192
 DB 2735 CAATCTCTGAGCGCGCTGAGC---GAGTCCAGGCGTCCGCGGCGCGCGCGAG 2676
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 DB 2675 GGAACCTCTCTGAGCGCT 2616
 QY 253 GCCATGCGGTGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 312
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 DB 2555 CTGAGCGTGAAGAGGAGCTCAAGTCTGAGAGTCTCTCTCTCTCTCTCTCTCTCTCT 2496
 QY 373 GGCAGAGCAATGATCT 432
 DB 2495 GGCAGAGCAATGATCT 2436
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 DB 2435 CCAAGCCCAATGGGTGATCATCTATTGGAACCGGTGCAAGTCTCTCAACCGACCTTG 2376
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 Db 1475 ACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1416
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Db 1055 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
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RESULT 3
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 ACCESSION
 AY103630
 VERSION
 AY103630.1 GI:21206708
 KEYWORDS
 SOURCE
 ORGANISM
 Zea mays
 Zea mays
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 3140)
 Hairey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M., and Tinsley, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 3140)
 Coe, E.H.
 DIRECT SUBMISSION
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 COMMENT
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:

FEATURES
Source

www.zmhd.iastate.edu.

Location/Qualifiers
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/mol_type="mRNA"
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/clone_lib="Maize Mapping Project/DuPont Consensus
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/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Query Match 42.2%; Score 1162.4; DB 11; Length 3140;
Best Local Similarity 68.3%; Pred. No. 5.4e-129;
Matches 1656; Conservative 0; Mismatches 761; Indels 7; Gaps 3;

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66 GCACGCGACAGAGCTGTCGCCCTCCCTCCAGATACGTGAACAAAGGAGGAGCTCT 125
240 CCACCCCATGAGCTTGTGCGCTTTCACAGGCTGAAACCTTGGAAAGGATGCT 299
126 GCAGCGGACCAATCTTCGACGCGCTGAC--GAGTTCAGAGGCTCCGGGCTCCGCG 182
300 GAGAGCCACCAAGATCATTTCCGAGACAAATGATGATCCCTGAGGCTGAGCGGAGAA 359
183 GCTGCGGAGGAGACCTTCTCTGACGCTCTCCGCTCCGCGAGAGAGGAGATGCTGCT 242
360 GCTCAAGATGATGCTTTTGAAGATGCTTGAAGGAGCTGAGGAGGAGGAGGAGGAGG 419
243 GCGGTTCCGCGCATTCGCGGCTGCGCGGCGCGGAGGAGTTGGAGATGATGCGGCTCA 302
420 CCATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
303 GCTTACGAGCTCAGCGTGCAGAGCTCAGAGCTCAGAGTCTCGAGTACCTCCGCTTCA 362
480 GCTCAGTATGCTGCTGCTTGAAGAGCTGAGAGTCTGAGTACCTCAGTTCAGAGAA 539
363 GCTTGTGAGCGGCGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 422
540 GCTTGTGAGAAAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 599
423 TGTCTCAGTCCAGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 482
600 TGTCTCTTCCCGGCTCTCTCTGCAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAG 659
483 CGGACACTGTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 542
660 GAGGACGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
543 CCTCGGTGCGACCGGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 602
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603 GGGGAGGCTTCACTGCTGCTGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662
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900 TGTATGCGTAAAGCGTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959

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DB 1080 CAGGTTGCTTACATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
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QY 1023 TGCAGAAAGAGATATG--CAATACGCGCTTGAAGAAATGATGAGACAGCATCTT 1081
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QY 1262 CATGCTATCTTAAGATGAGAAATGATGAGAAATGATGAGAAATGATGAGAAATGAT 1321
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QY 1382 GCCAGTTACTGCTGATATATATGATGATGATGATGATGATGATGATGATGATGAT 1441
DB 1560 GCGAGTTACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1619
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DB 1920 GTTGAAGAACTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1979
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DB 1980 TGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2036
QY 1862 AGATCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1921

Db	Accession	Source	Location/Qualifiers
Db	2037	AGCAGGCCGAGTTCAGAAAGATGTTTGAACCTTCATCGAGCAGTACACCTGAACGGGACCA	2095
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Db	2097	TCCGCTGGATCTCGGCCCAAGATGAACCGCGCTCCGCAACGCGAGCTCTACCCGTACATCT	2156
Qy	1982	CTGATGATCCCATGGGCGCTTTGGTATGACGCGCGCTTGATGAAGCGTTGCGTCAACCTCG	2041
Db	2157	GCGACACCAAGAGGCGCCTTCGTGTGAGCTGTCTTTCTACGAGGCTTTGGGCTGACGCTGG	2216
Qy	2042	TTGAGGCCATGACCTTGAGGCTTCTACTTTTCGGAACGCTTCATGAGGTTCAGCTGAGA	2101
Db	2217	TTGAGGCCATGACCTTGAGGCGCTTGCCCAAGTGTGCAACAGCTTACGCGCTCCGACGAGA	2276
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Db	2397	CCGAGGCGGGCTCCACAGTATCCAGAGAAAGTACACCTGGAACCTCTACTCGAGAGGC	2456
Qy	2282	TGATGACACTGACCGCGGCTTCAACGTTTCTGGAAGTACGTGTCCAAAGCTCGAGAGGCTGG	2341
Db	2457	TGATGACCTCTACCGCGCTGTACCGGTTCTGGAAGTATGTGTCCAACTGGAGAGGGCGG	2516
Qy	2342	AGACGAGGCGCTACCTTGAGATGTTCTACATATCTGAAGTTCCGAGCTGGCGAAGACCG	2401
Db	2517	AGACCCCGCGGCTACCTGGAGATGCTGTACGCGCTCAAGTACCGCACCATGGCGAGACCG	2576
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Db	2577	TGCCGCTGGCCGTGAGGAGAGGC	2600

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ORIGIN
/clone lib="Salt stressed Zea mays roots cDNA library"
/note="Vector: pBluescript SK+, Stressed 24 hours at 150
mM NaCl"

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	Query Match	Similarity	28.8%	Score	794.6	DB	13	Length	1005
	Best Local	Similarity	93.1%	Pred.	No. 3,56-85				
	Matches	885	Conservative	0	Mismatches	56	Indels	10	Gaps
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QY	1872	GATGAGAAAGATGATGATGATCTCAATCAAGACCCACAACTTGTTGCGGACAGTTCGCTGAT							1931
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QY	1932	CTCTGCCAGACAAACAGGCGCCGCTAAACGCGAGCTCTATGCTTACATCGCTGATACCA							1991
Db	133	CTCTGCCAGACAAACAGGCGCCGCTAAACGCGAGCTCTATGCTTACATCGCTGATACCA							191
QY	1992	TGAGGCTTGTGTAAGCGCGGCTGTATGAAAGCGTGGCTCAACCGCTGATGAGGCCAT							2051
Db	192	TGAGGCTTGTGTAAGCGCGGCTGTATGAAAGCGTGGCTCAACCGCTGATGAGGCCAT							251
QY	2052	GACCTGTGGGCTTCTACTTGTGCGAGCGCTTCATGAGGTCCAGCTGATCATAGACA							2111
Db	252	GACCTGTGGAATTCTCTACTTGTGCGAGCGCTTCATGAGGCGCAGCTGATCATAGACA							311
QY	2112	TGGGCTCTCGGCGCTTCCACATTTGACCGCTACACCCCGGACAGGCTGTAATCTATGAGC							2173
Db	312	TGGGCTCTCGGCGCTTCCACATTTGACCGCTACACCCCGGACAGGCTGTAATCTATGAGC							371
QY	2172	CGACTCTTCCACCGGCTCAAGACAAAGCCAGATCACTGGGTGGAATATATCTGAGACAG							223
Db	372	CGACTCTTCCACCGGCTCAAGACAAAGCCAGATCACTGGGTGGAATATATCTGAGACAG							431
QY	2232	GCTGAGAGCTATATACGAGAGTACACATGGAAGTATATCTCAGAGAGGTTGATGACACT							229
Db	432	GCTGAGAGCTATATACGAGAGTACACATGGAAGTATATCTCAGAGAGGTTGATGACACT							491
QY	2292	GACCGGCGCTCTACCGTCTTCTGGAAGTACGTTGCGAAGCTCGAAGGCTGAGAGCTGAGACGAGCG							235
Db	492	GACCGGCGCTCTACCGTCTTCTGGAAGTACGTTGCGAAGCTCGAAGGCTGAGAGCTGAGAGCG							551
QY	2352	CTACTTGAAGATGTTCTATACATACGAACTTCGCGAGCTGGGGAAGACCGTCCGCTTGC							241
Db	552	CTACTTGAAGATGTTCTATACATACGAACTTCGCGAGCTGGGGAAGACCGTCCGCTTGC							611
QY	2412	AATTGACCAACCGAGTAGCTTGCGCACTGCGACTGCGTAGCACTTGGTACAAAGCTGA							247
Db	612	AATTGACCAACCGAGTAGCTTGCGCACTGCGACTGCGTAGCACTTGGTACAAAGCTGA							671
QY	2472	AACCTGAAGACCTTCAGTAAATTATGAGCGCGGACACGCTGACCAATTAATGTGCGGGA							253
Db	672	AACCTGAAGACCTTCAGTAAATTATGAGCGCGGACACGCTGACCAATTAATGTGCGGGA							731
QY	2532	GCTGAACCGAGTTTATATATGATCATATGCACTATTAACAAATTACTGAAGCGAGGT							259
Db	732	GCTGAACCGAGTTTATATATGATCATATGCACTATTAACAAATTACTGAAGCGAGGT							791
QY	2592	GAGTT-----GCACTGTGTGTTCCTTACTCTTACTGT-ATTATGTCAAAGCTGTGCGT							2644
Db	792	GAGTTGTGCAAGTGTGGGGGTGCTGATTACTGTTACTGTAAATATGTCCAAAGCTGTGCGT							851
QY	2646	GCAATTTCTTTGCTGCGAAGCGCGACCTGTGT- AAGTCTGATTAATATCATCATAT							270
Db	852	GCAATTTCTTTGCTGCGAAGCGCGANGCTGGGTGAAGTCTGATTAATATCATCATAT							911
QY	2704	TCT- GTTGACTGTGTAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGCGCG							2753
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RESULT 5
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DEFINITION    mays cDNA clone RNOSEQ7D02.SK.ab1 similar to sucrose synthase [Zea
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ACCESSION     BO619406.1 GI:21621400
VERSION       BO619406.1
KEYWORDS      EST.
SOURCE        Zea mays
               Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
REFERENCE     Wang, H. and Bohnert, H.J.
               Genomics of plant stress tolerance
               Unpublished (2002)
AUTHORS       Contact: Mark Fredrickson
               Department of Plant Biology
               University of Illinois
               1201 W. Gregory Dr., Urbana, IL 61801, USA
               Tel: 2172655473
               Email: bohnertlab@life.uiuc.edu
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               mM NaCl"

ORIGIN
Query Match      28.8%; Score 793; DB 13; Length 938;
Best Local Similarity 95.0%; Pred. No. 5,5e-85;
Matches 881; Conservative 0; Mismatches 36; Indels 10; Gaps 6;

QY 1812 TGTGCTGCTGCGCGGAGACATGATGCAAGATGCAAGGAGAGAGATCGCGGA 1811
DB 13 TGTGCTGCTGCGCGGAGACATGATGCAAGATGCAAGGAGAGAGATCGCGGA 72
QY 1872 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1931
DB 73 GATAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 132
QY 1932 CTCTGCCAGACAAACAGGCGCGGTAAAGCGGAGCTTATGCTATCGCTGATCCCA 1991
DB 133 CTCTGCCAGACAAACAGGCGCGGTAAAGCGGAGCTTATGCTATCGCTGATCCCA 191
QY 1992 TGTGCTGCTGCGCGGAGACATGATGCAAGATGCAAGGAGAGATCGCGGA 2051
DB 192 TGTGCTGCTGCGCGGAGACATGATGCAAGATGCAAGGAGAGATCGCGGA 251
QY 2052 GACCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2111
DB 252 GACCTGTGAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 311
QY 2112 TGGCGCTTGGCGGCTTCCACATGACCCGTACACCCGAAAGAGCTGTATCTGATGCG 2171
DB 312 TGGCGCTTGGCGGCTTCCACATGACCCGTACACCCGAAAGAGCTGTATCTGATGCG 371
QY 2172 CGACTCTTCTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2231
DB 372 CGACTCTTCTGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
QY 2232 GCTGCAAGAGATATACAGAGAGATACAGATGAGAGATATACAGAGAGATGATGAC 2291

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DB 432 GCTGCAAGAGATATACAGAGAGATACAGATGAGAGATATACAGAGAGATGATGAC 491
QY 2292 GCTGCAAGAGATATACAGAGAGATACAGATGAGAGATATACAGAGAGATGATGAC 2351
DB 492 GCTGCAAGAGATATACAGAGAGATACAGATGAGAGATATACAGAGAGATGATGAC 551
QY 2352 CTACCTTGAAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 2411
DB 552 CTACCTTGAAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 611
QY 2412 AATTGACCAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 2471
DB 612 AATTGACCAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 671
QY 2472 AACCTGAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 2531
DB 672 AACCTGAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 731
QY 2532 GCTGAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 2591
DB 732 GCTGAAGAGATATACAGAGATATACAGAGATATACAGAGATATACAGAGATGAT 791
QY 2592 GGGTT---GCACTGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2645
DB 792 GGGTTGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 851
QY 2646 GCAATTTG---TTGCTGCGCAAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 2703
DB 852 GCAATTTGTTTGTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATGAT 911
QY 2704 TCT-GTTGACCTGTGAAAAA 2729
DB 912 TCTGTTGACCTGTGAAAAA 938

RESULT 6
CA280212      835 bp      mRNA      linear      EST 26-SEP-2003
LOCUS          SCVPLB2C05C09.g LB2 Saccharum officinarum cDNA clone SCVPLB2C05C09
DEFINITION    5', mRNA sequence.
ACCESSION     CA280212
VERSION       CA280212.1 GI:36007504
KEYWORDS      EST.
SOURCE        Saccharum officinarum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
               clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE     Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
               The libraries that made SUCFEST
               Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
AUTHORS       Contact: Arruda P
               Centro de Biologia Molecular e Engenharia Genetica
               Universidade Estadual de Campinas
               Caixa Postal 6010, 13083-970, Campinas SP, Brazil
               Tel: 55 19 3788 1137
               Fax: 55 19 3788 1089
               Email: parruda@unicamp.br
               Clone distribution information can be found
               through the Brazilian Clone Collection Center (BCCC) at
               http://www.bcccenter.fcav.unesp.br
               Plate: C05 row: C column: 09
               Seq primer: T7 Promoter Primer.
COMMENT       Location/Qualifiers
               1..835
               /organism="Saccharum officinarum"
               /mol_type="mRNA"
               /db_xref="taxon:4547"
               /clone="SCVPLB2C05C09"
               /lab_host="DH10B"
               /clone_lib="LB2"
               /note="Organ: Lateral buds from plants adult plants

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growing in greenhouse; Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from po-34+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at <http://sucess1.lad.ic.unlcamp.br/public>

ORIGIN

Query Match 26.2%; Score 722; DB 14; Length 835;

Best Local Similarity 92.5%; Pred. No. 1.5e-76; Indels 1; Gaps 1;

Matches 769; Conservative 0; Mismatches 61;

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Cy 781 CCAGACCCATCTACCCCTAGAGAAATCTTGGGAGAGATCCCATGATTTTAACTGTT 840
Db 1 CCAGACCCATCAACCCCTAGAGAAATCTTGGGAGAGATCCCATGATTTTAACTGTT 60
Cy 841 GTGGATCCCTCTATGATGATCTTTGCTCAAGTATATTTAGGCTTCCAGACAGGA 900
Db 61 GTGGATCCCTCTATGATGATCTTTGCTCAAGTATATTTAGGCTTCCAGACAGGA 120
Cy 901 GAGACGATCGTCTATATCTGAGACCAAGTCGCTGACATAGAAATGAGATGCTCCGT 960
Db 121 GAGACGATGCTCTATATCTGAGACCAAGTCGCTGACATAGAAATGAGATGCTCCGT 180
Cy 961 TTAAGGAAACAAGGCTTGAATGTTTCCCAAGATTTCTCATGTTTACTGCTGATACCA 1020
Db 181 TTAAGGAAACAAGGCTTGAATGTTTCCCAAGATTTCTCATGTTTACTGCTGATACCA 240
Cy 1021 GATGCAAAAAGGAAATCATGATGATCAAGGCTTGAAGATGAGGAAACAAGATCT 1080
Db 241 GATGCAAAAAGGAAATCATGATGATCAAGGCTTGAAGATGAGGAAACAAGATCT 300
Cy 1081 TACATATTAACAGATGCTCCCTTGAAGATGAAATGAGATGATGATGATGATGAT 1140
Db 301 TACATATTAACAGATGCTCCCTTGAAGATGAAATGAGATGATGATGATGATGATGAT 360
Cy 1141 TTTGATGTTGGCCATATCTGAGAAACATTTGCTGAGATGCTGCTGCTGCTGCT 1200
Db 361 TTTGATGTTGGCCATATCTGAGAAACATTTGCTGAGATGCTGCTGCTGCTGCTGCT 420
Cy 1201 GATTTACAGATGCTCCAGATCTCATATTTGAGAAATGAGATGAGATGAGATGAGAT 1260
Db 421 GATTTACAGATGCTCCAGATCTCATATTTGAGAAATGAGATGAGATGAGATGAGAT 480
Cy 1261 TCATGCTATCTTACAGATGAGATTTACCCAGTGCATGCTGCTGCTGCTGCTGCT 1320
Db 481 TCATGCTATCTTACAGATGAGATTTACCCAGTGCATGCTGCTGCTGCTGCTGCTGCT 540
Cy 1321 ACTAAGTATCCAGATTCAGATCATATTTTGGAGATTTGAGAGAGATGATGCTGCT 1380
Db 541 ACTAATATATCCAGATTCAGATCATATTTGAGAGATTTGAGAGAGATGATGCTGCT 600
Cy 1381 TGGCAGTATCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 601 TGGCAGTATCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Cy 1441 TACCAAGAAATTTGC-TGGAAGCAAAATATCTGTTGAGACAGTATGAGATGATGCT 1499
Db 661 TACCAAGAAATTTGCTGGAAGCAAAATATCTGTTGAGACAGTATGAGATGATGCT 720
Cy 1500 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1559
Db 721 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Cy 1560 TTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
Db 781 AATTAACCTCTTGAACCTGAGGCTGATATTTTCTTTTACCCCAA 831

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RESULT 7

CB662799 888 bp mRNA linear EST 09-APR-2003
LOCUS
DEFINITION
OSUNBD07C12 f OSUNBD Oryza sativa (japonica cultivar-group) cDNA
clone OSUNBD07C12 5', mRNA sequence.

ACCESSION
CB662799
VERSION
1 GI:29666524

KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukarjota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 888)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R., and Wang, G.

TITLE
JOURNAL
COMMENT
Unpublished (2003)
between rice and Magnaporthe oryzae
large-scale identification of ESTs involved in the interaction
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>

PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: C column: 12
Seq primer: gta aac cga cgg cca gtc
Location/Qualifiers
1..888
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultiar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSUNBD07C12"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSUNBD4"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES

source

ORIGIN
Query Match 25.6%; Score 704.8; DB 14; Length 888;
Best Local Similarity 87.8%; Pred. No. 1.6e-74; Indels 1; Gaps 1;
Matches 780; Conservative 0; Mismatches 107;

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Cy 711 GAAAGGTGGGATGATACAGACAGATGTTTGGAAATGATTCATCTCTTACAGAT 770
Db 1 GAAAGGTGGGATGATACAGACAGATGTTTGGAAATGATTCATCTCTTACAGAT 60
Cy 771 CATTCAGGCGCAGACCATCTACCTTACAGAAATCTTGGGAGAGATCCCATGATTT 830
Db 61 GCTTCAGGCGCAGACCATCTACCTTACAGAAATCTTGGGAGAGATCCCATGATTT 120
Cy 831 TTAAGTGTGTTGTTTCCCTCATGATGATGATGATGATGATGATGATGATGATGAT 890
Db 121 TTAAGTGTGTTGTTTCCCTCATGATGATGATGATGATGATGATGATGATGATGAT 180
Cy 891 AGACAGAGAGACAGATGCTATATCTGACCAAGTCCGTGACTAGAAAAATGAT 950
Db 181 AGATATCGAGAGAGACAGATGCTATATCTGACCAAGTCCGTGACTAGAAAAATGAT 240
Cy 951 GGTTCCTGTTTAAAGAAACAGGCTTATGTTTCCCAAAAGATCTCATGTTACTCG 1010
Db 241 GGTTCCTGTTTAAAGAAACAGGCTTATGTTTCCCAAAAGATCTCATGTTACTCG 300
Cy 1011 GCTGATACAGATGCAAAAGAAACATGATGATGATGATGATGATGATGATGATGAT 1070

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QY 1262 CATTGCTATCTTACAGATGGGAATTACCCAGTCGAACTATGCTCATGCT 1311
DB 859 CATTGCTATCTTACAGATGGGAATTACCCAGTCGAACTATGCTCATGCT 908

RESULT 9
LOCUS CB648550
DEFINITION OSJNEB11P18.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEB11P18 5', mRNA sequence.
ACCESSION CB648550
VERSION CB648550.1 GI:29643543
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 841)
Jantaauriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR primers
FORWARD: gta aac cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: P column: 18
Seq primer: gta aac cga cgg cca gtcg.
Location/Qualifiers
1..841
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEB11P18"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (Che
6061)."

ORIGIN
Query Match 25.0%; Score 688.6; DB 14; Length 841;
Best Local Similarity 88.8%; Pred. No. 1.4e-72;
Matches 745; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 943 AATTGAGATGTTCTCCGTTTAAAGAAAGAGGCTTGGTCCCAAGATTCAT 1002
DB 2 AATTGAGATGTTCTTAAAGTAAAGAAAGAGGCTTGGTCCCAAGATTCAT 61

QY 1003 GTTACTCGGCTATACAGATGCAAGAAAGAGATCATGCAATCAGCGCTTGAGAGATT 1062
DB 62 GTTACTCGGCTATACAGATGCAAGAAAGAGATCATGCAATCAGCGCTTGAGAGAA 121

QY 1063 AATGGAACACAGATCTTACATATTACAGATTCCTTCAAGAAATGAAATGGGATCTT 1122
DB 122 AATGGAACACAGATCTTACATATTACAGATTCCTTCAAGAAATGAAATGGGATCTT 181

QY 1123 AAGAAATGATATCAAGATTGATGATGATGATGATGATGATGATGATGATGATGAT 1182
DB 182 AAGAAATGATATCAAGATTGATGATGATGATGATGATGATGATGATGATGATGAT 241

QY 1183 GCTGTGAAATTTGCTGCTGATTTACAAAGTACTCCAGATTCATATTGGAACCTAC 1242
DB 242 GCTGTGAAATTTGCTGCTGATTTACAAAGTACTCCAGATTCATATTGGAACCTAC 301

QY 1243 GATGAAATCTTGTGGGCTCATTTGCTATCTTACAAAGATGGGAATTAACCAAGCAACT 1302
DB 302 GATGAAATCTTGTGGGCTCATTTGCTATCTTACAAAGATGGGAATTAACCAAGCAACT 361

QY 1303 GCTCATGCTGTGAAAGAAAGTAAAGTATTCAGATTCAGATATTTTGGAGAATTTGAT 1362
DB 362 GCTCATGCTGTGAAAGAAAGTAAAGTATTCAGATTCAGATATTTTGGAGAATTTGAT 421

QY 1363 GAGAATGACATTTCTCTGCGAGTTCACTGATATTAATTGTAAGCAATGCTAT 1422
DB 422 GAGAATGACATTTCTCTGCGAGTTCACTGATATTAATTGTAAGCAATGCTAT 481

QY 1423 TTTATCATACAGACATACCAAGAAATTTGCTGGAACCAAAATACGTGTGAGAGAT 1482
DB 482 TTTATCATACAGACATACCAAGAAATTTGCTGGAACCAAAATACGTGTGAGAGAT 541

QY 1483 GAGAGTCACTGCTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1542
DB 542 GAGAGTCACTGCTGCTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601

QY 1543 TTGATCCAAAGTTCAATATATGCTCTCTCTGAGCTGACATGCTCATATATCTTCCACAT 1602
DB 602 TTGATCCAAAGTTCAATATATGCTCTCTCTGAGCTGACATGCTCATATATCTTCCACAT 661

QY 1603 ACCGGAAGGCGCAAGCATGCTACCTCTCTTCAATGCTCAATGAAATTTGATTAAGC 1662
DB 662 ACTGAAAGGCGCAAGCATGCTACCTCTCTTCAATGCTCAATGAAATTTGATTAAGC 721

QY 1663 CCGAGCAAAACGATGAAACATATGAGCATGATGAGCGGCTCAAGGCTCATCTCTTC 1722
DB 722 CCGAGCAAAACGATGAAACATATGAGCATGATGAGCGGCTCATCTCTTC 781

QY 1723 TCCATGGAAGCTCTGAGAGGCTGAAAGCAATTAACAGGCTGCTGCAAGCTTTGCTAA 1781
DB 782 TCCATGGAAGCTCTGAGAGGCTGAAAGCAATTAACAGGCTGCTGCAAGCTTTGCTAA 840

RESULT 10
LOCUS CB628458 886 bp mRNA linear EST 08-APR-2003
DEFINITION OSIEB04A18.f OSIEB Oryza sativa (indica cultivar-group) cDNA
clone OSIEB04A18 5', mRNA sequence.
ACCESSION CB628458
VERSION CB628458.1 GI:29623447
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 886)
Jantaauriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu

PCR primers
FORWARD: gta aac cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: A column: 18
Seq primer: gta aac cga cgg cca gtcg.

FEATURES

Location/Qualifiers
1. 886
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="rRNA"
/cultivar="TR36"
/db_xref="taxon:39946"
/clone="OSIIE04A18"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIIEB"
/note="Vector: pBluescript II KS+; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (POB-6-3)"

ORIGIN

Query Match 24.8%; Score 684.6; DB 14; Length 886;
Best Local Similarity 86.5%; Pred. No. 4e-72;
Matches 767; Conservative 0; Mismatches 119; Indels 1; Gaps 1;

198 CTTCCTCGACGCTCTCCGCTCCGCGAGAGAGGAGATCGTCTGCGCGCTGCGCCAT 257
1 CTTCCTCGACGCTCTCCGCTCCGCGAGAGAGGAGATCGTCTGCGCGCTGCGCCAT 60
258 CGCGGTGCGCGCGCGCGCGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 317
61 CGCGGTGCGCGCGCGCGCGCGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 120
318 CGTCCAGAGCTCAGCTCCTCGAGTACCTCGCTCCAGAGAGAGAGAGAGAGAGAGAGAG 377
121 CGTCCAGAGCTCAGCTCCTCGAGTACCTCGCTCCAGAGAGAGAGAGAGAGAGAGAGAG 180
378 GACAAATGATCCCTTACGTTCTCGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 437
181 GTCAGAGAGCTCAGCTCCTCGAGTACCTCGCTCCAGAGAGAGAGAGAGAGAGAGAGAG 240
438 GACAAATGATCCCTTACGTTCTCGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 497
241 GTCAGAGAGCTCAGCTCCTCGAGTACCTCGCTCCAGAGAGAGAGAGAGAGAGAGAGAG 300
498 AATGATGTCGAG 557
301 GATCATGTCGAG 360
558 GACAAAGGAG 617
361 GATTAAGGAG 420
618 TGTGCTGACCAAGCTGAG 677
421 TGTGCTGACCAAGCTGAG 480
678 ATTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 737
481 GTTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
738 TATTTTGGAAATGATCAATCTCTCTGAGATCAATCAATCAATCAATCAATCAATCAATCT 797
541 TATCTTGGAAATGATCAATCTCTCTGAGATCAATCAATCAATCAATCAATCAATCAATCT 600
798 AGAGAAATTTGGAG 857
601 TGAAGATTTCTTGGAG 560
858 ATAATTTGCTGAT 917
661 ATAATTTGCTGAT 720
918 AATGAG 977
721 ACTGAG 780
978 TGAATTTTCCCAAGATTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1037

Db 781 TGAATTTTCCCAAGATTTCTTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 840
Oy 1038 ATGCATCAGCGGCTTGAAGAGATTTAGTGAGACAGACATCTTATCA 1084
Db 841 ATGCATCAGCGGCTTGAAGAGATTTAGTGAGACAGACATCTTATCA 886

RESULT 11
CD426853 745 bp mRNA linear EST 02-JUN-2003
LOCUS CD426853
DEFINITION Sal1 25 F05 g1 A002 Salicylic acid-treated seedlings Sorghum bicolor
CDNA clone Sal1 25 F05 A002 5', mRNA sequence.
ACCESSION CD426853
VERSION CD426853.1 GI:31333116
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 745)
Kleier, R.R., Liang, C., Sun, F., Sullivan, R., Shah, M., Salzman, R.,
Chua, R.N., Gonzalez, M., Lane, S., Miller, V., Nanda, P.,
Olaseinde, O., Bastman, A. and Pratt, L.H.
An EST database from Sorghum: salicylic acid-treated seedlings
Unpublished (2003)
Other ESTs: Sal1 25 F05 b1 A002
Contact: Cordomier-Pratt, M.
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpatt@uga.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University;
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug5 (CTTCTGCTTAAAGCTCG).
Location/Qualifiers
1. 745
/organism="Sorghum bicolor"
/mol_type="rRNA"
/cultivar="BRX623"
/db_xref="taxon:4558"
/clone="Sal1 25 F05 A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Salicylic acid-treated seedlings"
/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
library was prepared from polyA+ RNA from seedlings grown
in hydroponic culture. At 8 days of age, medium was
supplemented with 1 mM salicylic acid (SA). Roots and
shoots were harvested after 27 and 72 hr and material from
both time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
different DraIII sites of the pME18S-FL3 vector (5-prime
DraIII site is CACTGATG, 3-prime DraIII site is
CACCATG). XhoI excises the cDNA insert."

FEATURES

source

ORIGIN

Query Match 24.5%; Score 676.2; DB 14; Length 745;
Best Local Similarity 96.0%; Pred. No. 4.3e-71;
Matches 715; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

670 TACTCAATTTGCTTAAATTTCAAGAGTGGGCTCGAGAAAGTTGGGCTGATCA 729
1 TACCACAAATTGCTTAAATTTCAAGAGTGGGCTCGAGAAAGTTGGGCTGATCA 60

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Oy 730 GCAAGACATGTTTGGAAATGATCATCTCTCTTACAGATCATTCAGGCGCCAGACCA 789
Db 61 GCGAAACATGTTTGGAAATGATCATCTCTCTTACAGATCATTCAGGCGCCAGACCA 120
Oy 790 TCTAACCTTGAAGAAATCTTGGGAGATCCCAATGTTTTAAAGCTTTGTGTGTATCC 849
Db 121 TCAACCTTGAAGAAATCTTGGGAGATCCCAATGTTTTAAAGCTTTGTGTGTATCC 180
Oy 850 CCGCATGATATCTTGTGCAAGCTAATGATTAAGCTTGCAGACAGAGAGACAGATC 909
Db 181 CCGTATGATATCTTGTGCAAGCTAATGATTAAGCTTGCAGACAGAGAGAGATC 240
Oy 910 GCTATATATCTGACCAAGTCCGTGCACTAGAAAATGATGATGTTCCGTTTAAAGAA 969
Db 241 GCTATATATCTGACCAAGTCCGTGCACTAGAAAATGATGATGTTCCGTTTAAAGAA 300
Oy 970 CAAGGCTTGAATGTTTCCCAAGAAATCTCTGTTACTCGGCTGATACAGATGCAAA 1029
Db 301 CAAGGCTTGAATGTTTCCCAAGAAATCTCTGTTACTCGGCTGATACAGATGCAAA 360
Oy 1030 GGAACATCTGCAATCGAGGCTTGAAGATTAAGTGAACACAGACATCTACATTA 1089
Db 361 GGAACATCTGCAATCGAGGCTTGAAGATTAAGTGAACACAGACATCTACATTA 420
Oy 1090 CGAGTCCCTTCAAGAAATGAAATGGGATCTTAAGAAATGGAATCAAGATTGATGTG 1149
Db 421 CGAGTCCCTTCAAGAAATGAAATGGGATCTTAAGAAATGGAATCAAGATTGATGTG 480
Oy 1150 TGCGCATATCTGAAACATTTGCTGAGAGATGCTGTGTGAATGCTGCTGAATTA 1209
Db 481 TGCGCATATCTGAAACATTTGCTGAGAGATGCTGTGTGAATGCTGCTGAATTA 540
Oy 1210 GGTCTCCAGCTTCAATATGGAATACAGTGAATGGAATCTGTGCGCTGATGCTA 1269
Db 541 GGTCTCCAGCTTCAATATGGAATACAGTGAATGGAATCTGTGCGCTGATGCTA 600
Oy 1270 TCTTACAAAGATGGAATTAACCGATGCAACATTTGCTGCTGAAAAGATTAAT 1329
Db 601 TCTTACAAAGATGGAATTAACCGATGCAACATTTGCTGCTGAAAAGATTAAT 660
Oy 1330 CCAAGTTCAGACATTTTGGAGAAATTTGATGAGAAATGCAATTTCTCTGCCGCT 1387
Db 661 CCAAGTTCAGACATTTTGGAGAAATTTGATGAGAAATGCAATTTCTCTGCCGCT 720
Oy 1388 TCACGTGATATTAATGCTATGAA 1412
Db 721 TCACGTGATATTAATGCTATGAA 745

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RESULT 12
C9631982 836 bp mRNA linear EST 08-APR-2003
LOCUS OSIIIB09015.f OSIIIB Oryza sativa (indica cultivar-group) cDNA
DEFINITION OSIIIB09015 5', mRNA sequence.
ACCESSION CB631982
VERSION CB631982
KEYWORDS EST
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)

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REFERENCE
AUTHORS Jantseniyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA

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FEATURES
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Tel.: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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LOCUS ELUTIN0407HE37.b Endosperm_4 Zea mays cDNA, mRNA sequence.

DEFINITION CD442316

ACCESSION CD442316

VERSION CD442316.1 GI:31357959

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and Messing, J.

AUTHORS Sequencing of the maize endosperm ESTs

TITLE Unpublished (2002)

JOURNAL Contact: Lai, Jinsheng

COMMENT Dr. Joachim Messing's lab

Waksman Institute, Rutgers University

193 Frelinghuysen Rd., Piscataway, NJ 08854, USA

Tel: 732-445-5801

Fax: 732-445-5735

Email: jlai@waksman.rutgers.edu

Seq primer: T3.

FEATURES

source

Location/Qualifiers

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QY 1158 TCTGAGAAATCTTCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1217

Db 243 TCTGAGAAATCTTCTGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 302

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Db 363 GATGGGAATTACCGATGCAACATTCCTCATGCTGCAAAAAGACTAAGATACAGATTC 422

QY 1338 AGACATATTTTGGAAAGATTTTGATGAGAGTACCAATTTCTCTGCGCATGTTCACTGCTGA 1387

Db 423 AGACATATTTTGGAAAGATTTTGATGAGAGTACCAATTTCTCTGCGCATGTTCACTGCTGA 482

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RESULT 14

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LOCUS OS1IB02C04.f OS1IB Oryza sativa (indica cultivar-group) cDNA

DEFINITION OS1IB02C04.5', mRNA sequence.

ACCESSION CB627276

VERSION CB627276.1 GI:29622265

KEYWORDS EST.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS 1 (bases 1 to 860)

Jantasiyiyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

TITLE Unpublished (2003)

JOURNAL Contact: Rod Wing

COMMENT Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 02 row: C column: 04

Seq primer: gta aac cga cgg cca gtc.

FEATURES

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 2953838 seqs, 2272363821 residues

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Published Applications NA.*
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; Publication No. US20030005482A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080,114A
; PRIOR FILING DATE: 2002-04-30
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Qy 1741 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
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Qy 1801 CTGGTAAACCTTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Db 1801 CTGGTAAACCTTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
Qy 1861 GAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Db 1861 GAGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1920
Qy 1921 TTCCGCTGAGATCTTCCGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Db 1921 TTCCGCTGAGATCTTCCGCAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
Qy 1981 GCTGATACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Db 1981 GCTGATACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
Qy 2041 GTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Db 2041 GTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100
Qy 2101 ATCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Db 2101 ATCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160
Qy 2161 AATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220
Db 2161 AATCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2220

[illegible]

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RESULT 2
US-10-080-114A-1
; Sequence 1, Application US/10080114A
; Publication No. US2003005482A1
; GENERAL INFORMATION:
; APPLICANT: Dhesea, Karwarpal S.
; TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
; FILE REFERENCE: 1301P
; CURRENT APPLICATION NUMBER: US/10/080.114A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/270.777
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2737
; TYPE: DNA
; ORGANISM: Zea mays
US-10-080-114A-1

```

Query Match	98.4%;	Score 2714;	DB 15;	Length 2737;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 2717; Conservative	0;	Mismatches 5;	Indels 0;	Gaps 0

QY 36 CCGGACCGCGCCGACGACACCTTCAGCGGACGCAACAGAGCTCGTGACCTCTCTC 95

Db 16 CGGCACCGCGCGAGGACACCTTCAGCGGACGCAACAGAGCTCGTGACCTCTCTGTC 75

QY 96 CAAGTACGTGAACAAGGGGAGGGCATCTCTGACGCGGACCCATCTCTGACGCGCTGGA 155

Db 76 CAGTACGTGAACAAGGGGAGGGCATCTCTGACGCGGACCCATCTCTGACGCGCTGGA 135

QY 156 CAGGTCAAGGGATCCGGGGATCGGCGCTCGCCGAGGACCTTCTCTGAGGTCTCTCG 215

Db	136	CGAGGTCCAGGAGCTCCGGGGGGCCGGGCGTACGCGAGAGGAGCCCTTCTCCGACGTCCTCCG	196
Qy	216	CTCCGGCGAGAGGGCGATCTGTGTCTCCGCCGTTCTGTGGCATGCGGGTGGCCCGGCGCC	275
Db	196	CTCCGGCGAGAGGGCGATCTGTGTCTCCGCCGTTCTGTGGCATGCGGGTGGCCCGGCGCC	255
Qy	276	GGAGTTTGGAGTACGTCCGGCGTCAAGCTCAGCTCAGAGCGTGCAGAGAGCTCAAGGT	335
Db	256	GGAGTTTGGAGTACGTCCGGCGTCAAGCTCAGCTCAGAGAGCTCAAGGT	315
Qy	336	CTCGAGAGTCTCCGCTTCAAGAGAGAGCTGTGTGACGGGCCAGAGCAATGATCCCTACGT	395
Db	316	CTCGAGAGTCTCCGCTTCAAGAGAGAGCTGTGTGACGGGCCAGAGCAATGATCCCTACGT	375
Qy	396	TCTCGAGCTTGACTTCGAGCGCGTTCAATGTCTCAGTCCAGCGCCCAATGGTCAATC	455
Db	376	TCTCGAGCTTGACTTCGAGCGCGTTCAATGTCTCAGTCCAGCGCCCAATGGTCAATC	435
Qy	456	TATTGGAAACGGTGTGCAGTTCTCCAAACGCACTGTCTCCCATCATGTTCCGCAACAG	515
Db	436	TATTGGAAACGGTGTGCAGTTCTCCAAACGCACTGTCTCCCATCATGTTCCGCAACAG	495
Qy	516	GGATTGCTGGAGCCCGCTGTGATTTCTCCCGGGCCACCGGACAAAGGGACATGTAT	575
Db	496	GGATTGCTGGAGCCCGCTGTGATTTCTCCCGGGCCACCGGACAAAGGGACATGTAT	555
Qy	576	GATGCTTATATGATGAATACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACCAAGCTGA	635
Db	556	GATGCTTATATGATGAATACAAAGCTTGGGGAGGCTTCAGTCTGTGCTGACCAAGCTGA	615
Qy	636	GGAGCACTTGTCAAAAGCTCCCTGCTGACACACCATCACTCAATTTGCTATTAATTCA	695
Db	616	GGAGCACTTGTCAAAAGCTCCCTGCTGACACACCATCACTCAATTTGCTATTAATTCA	675
Qy	696	AGAGTGGGGCGCTGGAGGAAAGGTGGGGGTATACAGACAGACATGTTTGGAAATGATCA	755
Db	676	AGAGTGGGGCGCTGGAGGAAAGGTGGGGGTATACAGACAGACATGTTTGGAAATGATCA	735
Qy	756	TCTCCTTTAACAATCATTCAGGGGCCGACACCATCTACCTTAGAATAATCTTGGGAG	815
Db	736	TCTCCTTTAACAATCATTCAGGGGCCGACACCATCTACCTTAGAATAATCTTGGGAG	795
Qy	816	GATCCCATGATTTTAAAGTTGTGTGTGTATCCCTCATGAGATACCTTGGCAAGCTAA	875
Db	796	GATCCCATGATTTTAAAGTTGTGTGTGTATCCCTCATGAGATACCTTGGCAAGCTAA	855
Qy	876	TGTATTAGGCTGGCCAGACAGAGAGACATGCTCATATTACTGACCAAGTCCGTGC	935
Db	856	TGTATTAGGCTGGCCAGACAGAGAGACATGCTCATATTACTGACCAAGTCCGTGC	915
Qy	936	ACTAGAAATAGAGATGTTCTCTCTTTAAAGAAACAGAGCGCTGATGTTTCCCAAAAT	995
Db	916	ACTAGAAATAGAGATGTTCTCTCTTTAAAGAAACAGAGCGCTGATGTTTCCCAAAAT	975
Qy	996	TCTCATTTGTACTCGGCTGATACCGAGATGCAAAAGGAATCATCATGATCAAGCGCTTGA	1055
Db	976	TCTCATTTGTACTCGGCTGATACCGAGATGCAAAAGGAATCATCATGATCAAGCGCTTGA	1035
Qy	1056	GAGATTAGTGGAAACAGACATCTACTTACATATTACAGTTTCCCTTCAGAAATGAAATGG	1115
Db	1036	GAGATTAGTGGAAACAGACATCTACTTACATATTACAGTTTCCCTTCAGAAATGAAATGG	1095
Qy	1116	GATACCTTAAGAAATGATATCAAGATTTGATGTGTGGCATATCTCGGAAACATTTGCTGA	1175
Db	1096	GATACCTTAAGAAATGATATCAAGATTTGATGTGTGGCATATCTCGGAAACATTTGCTGA	1155
Qy	1176	GGATGCTGCTGGTGAATTTGCTGCTGAATTAACAGGTACTCCAGACTTCATATTGGAAA	1235
Db	1156	GGATGCTGCTGGTGAATTTGCTGCTGAATTAACAGGTACTCCAGACTTCATATTGGAAA	1215
Qy	1236	CTACAGTATGAAATCTTGTGGCTCATTTGCTATCTTACAGATGGAAATTAACCAAGTG	1295
Db	1216	CTACAGTATGAAATCTTGTGGCTCATTTGCTATCTTACAGATGGAAATTAACCAAGTG	1275

QY	1296	CAACATGCTCATTCTCTGAAAAGACTAGTATCCGATTCACACATATCTTTGGAAAG	1355
Db	1276	CAACATGCTCATTCTCTGAAAAGACTAGTATCCGATTCACACATATTTTGGAAAG	1335
QY	1356	TTTCGATGAGAAAGTACATTTCTCTCGCAGTTCACTGCTGATAAATTTGCTATGAACAA	1415
Db	1336	TTTTCGATGAGAAAGTACATTTCTCTCGCAGTTCACTGCTGATATAATTTGCTATGAACAA	1395
QY	1416	TGCTGATTTTATCATCAACACGACACATACCAAGAAATTGCTGGAAACAAAATACTTTGG	1475
Db	1396	TGCTGATTTTATCATCAACACGACACATACCAAGAAATTGCTGGAAACAAAATACTTTGG	1455
QY	1476	ACAGTATGAGGTATATCTACTGCTTTACTCTGCTCGTCTGACCGAGTGTCCATGGGAT	1535
Db	1456	ACAGTATGAGGTATATCTACTGCTTTACTCTGCTCGTCTGACCGAGTGTCCATGGGAT	1515
QY	1536	CGATGCTCTTGATCCAAAGTTCAATATATAGTCTCTCTGAGCCTGACATGTCCATATACTT	1595
Db	1516	CGATGCTCTTGATCCAAAGTTCAATATATAGTCTCTCTGAGCCTGACATGTCCATATACTT	1575
QY	1596	TCCCATATACCGAAGGCGAAGCGACATCACTCTCTCTCAAGTTCATTCGAAATTTGAT	1655
Db	1576	TCCCATATACCGAAGGCGAAGCGACATCACTCTCTCTCAAGTTCATTCGAAATTTGAT	1635
QY	1656	TTATGACCCGAGCAAAACGATGAAACATATGAGGCATCTGGATGACCGGTCAAAAGCCCAT	1715
Db	1636	TTATGACCCGAGCAAAACGATGAAACATATGAGGCATCTGGATGACCGGTCAAAAGCCCAT	1695
QY	1716	CCTCTTTCTCCATGCGCAACATCTCGACAGGCTTAAGAACATTAACAGGCTGTGTCAAGCTTT	1775
Db	1696	CCTCTTTCTCCATGCGCAACATCTCGACAGGCTTAAGAACATTAACAGGCTGTGTCAAGCTTT	1755
QY	1776	TGCTAAGTGCCTTAGCTGAGGAGAGCTGGTAAACCTTGTCTGCTGCTGGCCGAGTACATGA	1835
Db	1756	TGCTAAGTGCCTTAGCTGAGGAGAGCTGGTAAACCTTGTCTGCTGCTGGCCGAGTACATGA	1815
QY	1836	TGTCGAACAGTCCAGAGCAAGGAAAGAGATCCCGAGATAGAGAAAGATGATGAATCTCAT	1895
Db	1816	TGTCGAACAGTCCAGAGCAAGGAAAGAGATCCCGAGATAGAGAAAGATGATGAATCTCAT	1875
QY	1896	CAAGACCCCAACAATGTTCCGGGCAATTCGCGCTGATCTCTGCGCCAGCAAAACAAGGCCCG	1955
Db	1876	CAAGACCCCAACAATGTTCCGGGCAATTCGCGCTGATCTCTGCGCCAGCAAAACAAGGCCCG	1935
QY	1956	TAAACGGCAGCTCTATCTGCTACATCTGCTGATACCCATGAGTGTCTTTCTGTACAGCCGACCTT	2015
Db	1936	TAAACGGCAGCTCTATCTGCTACATCTGCTGATACCCATGAGTGTCTTTCTGTACAGCCGACCTT	1995
QY	2016	GTAATGAAGCTTCGGTCTTCAACGTTGTTGAAGCCCATGACCTGTGGGCTTTCCATCTTGGC	2075
Db	1996	GTAATGAAGCTTCGGTCTTCAACGTTGTTGAAGCCCATGACCTGTGGGCTTTCCATCTTGGC	2055
QY	2076	GACGCTCATGAGAGCTACAGCTGAGATCATAGAGCATGAGCGCTTCCGAGCTTCCACATTTGA	2135
Db	2056	GACGCTCATGAGAGCTTACAGCTGAGATCATAGAGCATGAGCGCTTCCGAGCTTCCACATTTGA	2115
QY	2136	CCCGTACACACCCCGAACAAGGCTGTTAATCTGAATGGCCCACTTTCTTGACCCGCTGACACA	2195
Db	2116	CCCGTACACACCCCGAACAAGGCTGTTAATCTGAATGGCCCACTTTCTTGACCCGCTGACACA	2175
QY	2196	AAGCCCAAGTACATCGAGGTGAATATATCTGGAGCAAGGCTGACAGCGCATATACAGAAAGTA	2255
Db	2176	AAGCCCAAGTACATCGAGGTGAATATATCTGGAGCAAGGCTGACAGCGCATATACAGAAAGTA	2235
QY	2256	CACATGAGAAATATATCTGAGAGGTTGATGACACTGGCCGGGACTTACGAGTTTCTGGAA	2315
Db	2236	CACATGAGAAATATATCTGAGAGGTTGATGACACTGGCCGGGACTTACGAGTTTCTGGAA	2295
QY	2316	GTAAGCTGTGAAGCTCGAGGCTGAGAGCTGAGACAGAGGCGTACCTTGAAGATTTCTACATCT	2375
Db	2296	GTAAGCTGTGAAGCTCGAGGCTGAGAGCTGAGAGGCGTACCTTGAAGATTTCTACATCT	2355

OY		2276	GAACTTCGCGAGCTGGCGGAACCCGGCCCTTGAATTGACCAACCGCAGTAGCTGC	2435
Db		2356	GAAGTTCGCGAGCTGGCGGAACCCGGCCCTTGCATTTAACCAACCGCAGTAGCTGC	2415
OY		2436	GCAACTCGCACTGGGTAGCACTTGATCAAGACTGAAACCTGAAAGACTTCAGTAATTT	2495
Db		2416	GCAACTCGCACTGGGTAGCACTTGATCAAGACTGAAACCTGAAAGACTTCAGTAATTT	2475
OY		2496	AGGCGCGCGACAGCGTAGCCAAATTAATATGTCGCCGAGCTGAACCTGTTTTATATATA	2555
Db		2476	AGGCGCGCGACAGCGTAGCCAAATTAATATGTCGCCGAGCTGAACCTGTTTTATATATA	2535
OY		2556	CATATAGCAGTATTAACAATAATTACTGAAAGCAGGTGGGTTGCACTGTGTGTGTTAC	2615
Db		2536	CATATAGCAGTATTAACAATAATTACTGAAAGCAGGTGGGTTGCACTGTGTGTGTTAC	2595
OY		2616	TGTTTACTGTATTAATGTCAAGCTGTGGCTGCAATTTCTTTGCTGGCAAGCGCAC	2675
Db		2596	TGTTTACTGTATTAATGTCAAGCTGTGGCTGCAATTTCTTTGCTGGCAAGCGCGCAC	2655
OY		2676	TGGGAAGTGTGATTAATTAATCATCATATCTGTGACCGCGAATAAAAAAAAAAAAAA	2735
Db		2656	TGGGAAGTGTGATTAATTAATCATCATATCTGTGACCGCGAATAAAAAAAAAAAAAA	2715
OY		2736	AAAAAAAAAAAAAGGCGCGCGCCG 2757	
Db		2716	AAAAAAAAAAAAAGGCGCGCGCCG 2737	
 RESULT 3 US-10-425-114-6036 ; Sequence 6036, Application US/10425114 ; Publication No. US2004003488BA1 ; GENERAL INFORMATION: APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 6036 LENGTH: 2275 TYPE: DNA ORGANISM: Zea mays FEATURE: OTHER INFORMATION: Clone ID: 700551647_FLI US-10-425-114-6036				
 Query Match 79.4%; Score 2189.2; DB 13; Length 2275; Best Local Similarity 98.9%; Pred No. 0; Matches 2225; Conservative 0; Mismatches 23; Indels 2; Gaps 2;				
OY		474	GTTCTCCAACCGCACTTGTCTCAATCAATCAATGTTCCGCAACAGGATTCCTTGAGCCCTT	533
Db		1	GTTCTCCAACCGCACTTGTCTCAATCAATGTTCCGCAACAGGATTCCTTGAGCCCTT	60
OY		534	GTTGATTTCTCCCGTGGCGACCGGCAAGGGGCAATGTAATGATGCTTAATGATAGAT	593
Db		61	GCTGATTTCTCCCGTGGCGACCGGCAAGGGGCAATGTAATGATGCTTAATGATAGAT	120
OY		594	ACAAAGCTTGGGAGGCTTCAGTCTGTGTGACCAAAGCTGAGAGCACTTGTCAAAGCT	653
Db		121	ACAAAGCTTGGGAGGCTTCAGTCTGTGTGACCAAAGCTGAGAGCACTTGTCAAAGCT	180
OY		654	CCCTGTGTGACAAACCATTCTCAAAATTTGCTTAATAATTCAAGAAGTGGGGCTGGAGAA	713
Db		181	CCCTGTGTGACAAACCATTCTCAAAATTTGCTTAATAATTCAAGAAGTGGGGCTGGAGAA	240

QY 714 AGTGTGGGGTGATACAGGAGGACGAAATGTTGGAAATGATCATCTCTTACAGACATCAT 773
 DB 241 AGGTTGGGGGTATATACAGGAGGACGAAATGTTGGAAATGATCATCTCTTACAGACATCAT 300
 QY 774 TCAGGCGCCAGAACCCATCTACCCCTAGAGAAATCTTGGGGAGGATCCCAATGATTTTAA 833
 DB 301 TCAGGCGCCAGAACCCATCTACCCCTAGAGAAATCTTGGGGAGGATCCCAATGATTTTAA 360
 QY 834 CGTTGTGTGTATCCCTCATGATCTTGTGTCAAGCTAATGTTATAGGCTTGCCAGA 893
 DB 361 CGTTGTGTGTATCCCTCATGATCTTGTGTCAAGCTAATGTTATAGGCTTGCCAGA 420
 QY 834 CACAGGAGGACGATGCTGTATATCTGAGCAATCCGTCGACATGAAATGAGATGAT 953
 DB 421 CACAGGAGGACGATGCTGTATATCTGAGCAATCCGTCGACATGAAATGAGATGAT 480
 QY 954 TCTCGGTTTAAAGAAACAGAGGCTGTATGTTCCCAAGATTCATGTTACTCGGCT 1013
 DB 481 TCTCGGTTTAAAGAAACAGAGGCTGTATGTTCCCAAGATTCATGTTACTCGGCT 540
 QY 1014 GATACCAAGTSCAAAGGAGACATCATGCAATCAGGCTTGAGAGAAATGATGAGACCA 1073
 DB 541 GATACCAAGTSCAAAGGAGACATCATGCAATCAGGCTTGAGAGAAATGATGAGACCA 600
 QY 1074 GCATPCTTACATATAGAGATGCTCCCTGAGAAATGAAATGAGATGATGATGAT 1133
 DB 601 GCATPCTTACATATAGAGATGCTCCCTGAGAAATGAAATGAGATGATGATGAT 660
 QY 1134 ATCAAGATTTGATGTGTGGCCATATCTGAAACATTTGCTGAGAGATGCTGTGAT 1193
 DB 661 ATCAAGATTTGATGTGTGGCCATATCTGAAACATTTGCTGAGAGATGCTGTGAT 720
 QY 1194 TGCTGCTGAATTAAGAGTACTCCAGCTTCTAATTTGAAATCTCAAGATGAGAAATCT 1253
 DB 721 TGCTGCTGAATTAAGAGTACTCCAGCTTCTAATTTGAAATCTCAAGATGAGAAATCT 780
 QY 1254 TGTCGGGTCATGTCATCTTCAAGATGAGAAATTTCCAGTSCAAATGCTCATGCTCT 1313
 DB 781 TGTCGGGTCATGTCATCTTCAAGATGAGAAATTTCCAGTSCAAATGCTCATGCTCT 840
 QY 1314 GGAAGAGCTAAGTATCCAGATTCAGACATATTTTGGAGAAATTTGATGAGAAATGCA 1373
 DB 841 GGAAGAGCTAAGTATCCAGATTCAGACATATTTTGGAGAAATTTGATGAGAAATGCA 900
 QY 1374 TTTCTCTGCGAGTCACTGCTGATATTAATTTCTATGAAATGCTGATTTTATCATC 1433
 DB 901 TTTCTCTGCGAGTCACTGCTGATATTAATTTCTATGAAATGCTGATTTTATCATC 960
 QY 1434 CAGGACATACCAAGAAATGCTGGAAGCAAAATCTGTTGACAGATGAGAGTATAC 1493
 DB 961 CAGGACATACCAAGAAATGCTGGAAGCAAAATCTGTTGACAGATGAGAGTATAC 1020
 QY 1494 TGCCCTTACTCTGCTGTGTCTGTACGAGTGTGCTGAGGATGATGATGCTGATCCAAA 1553
 DB 1321 TGCCCTTACTCTGCTGTGTCTGTACGAGTGTGCTGAGGATGATGATGCTGATCCAAA 1080
 QY 1554 GTTCAATATATGCTCTCTGAGAGTCAATGCTCATATCTTCCACATACGAGAGGC 1613
 DB 1381 GTTCAATATATGCTCTCTGAGAGTCAATGCTCATATCTTCCACATACGAGAGGC 1140
 QY 1614 CAGGAGACTCACTCTCTCATAGGTCATGCAAAATTTGATTTAGACCCGAGAGCAAA 1673
 DB 1141 CAGGAGACTCACTCTCTCATAGGTCATGCAAAATTTGATTTAGACCCGAGAGCAAA 1200
 QY 1674 CGATGACATATGAGCATCTGATGACCGGTCAAAGCCCATCTCTTCTCATGAGCAAG 1733
 DB 1231 CGATGACATATGAGCATCTGATGACCGGTCAAAGCCCATCTCTTCTCATGAGCAAG 1260
 QY 1734 ACTCGACAGGGTGAAAGACATTAACAGGGGCTGTGCAAGCTTTGCTAAGTGGCTAAGCT 1793
 DB 1261 ACTCGACAGGGTGAAAGACATTAACAGGGGCTGTGCAAGCTTTGCTAAGTGGCTAAGCT 1320

QY 1794 GAGGAGCTGTGTAACCTTGTGTGTGTGCGGGTACATATGATGATCAACAGTCCAAAGCA 1853
 DB 1321 GAGGAGCTGTGTAACCTTGTGTGTGTGCGGGTACATATGATGATGATCAACAGTCCAAAGCA 1380
 QY 1854 CAGGAGAGATGCTGCGAGATGAGAGATGATGATGATGATGATGATGATGATGATGAT 1913
 DB 1381 CAGGAGAGATGCTGCGAGATGAGAGATGATGATGATGATGATGATGATGATGATGAT 1440
 QY 1914 CCGGAGTGTGCGAGATGCTGCGAGAGCAAAAGGGCCCTTAAAGGAGGAGCTATGAG 1973
 DB 1441 CCGGAGTGTGCGAGATGCTGCGAGAGCAAAAGGGCCCTTAAAGGAGGAGCTATGAG 1500
 QY 1974 CTACATGCTGTATACCAATGAGTGTGCTGTGATGAGGCGCTTGTATGAAAGGTTGAGTCT 2033
 DB 1501 CTACATGCTGTATACCAATGAGTGTGCTGTGATGAGGCGCTTGTATGAAAGGTTGAGTCT 1560
 QY 2034 CACCGTGTGAGGCGCATGACCTGTGAGGCTTCTACTTTTGGAGCGCTCAATGAGAGTCC 2093
 DB 1561 CACCGTGTGAGGCGCATGACCTGTGAGGCTTCTACTTTTGGAGCGCTCAATGAGAGTCC 1620
 QY 2094 AGCTGAGATCATGAGCATGAGGCTGTGCGGCTTCCACATTTAGACCCGATCAACCCGAGCA 2153
 DB 1621 AGCTGAGATCATGAGCATGAGGCTGTGCGGCTTCCACATTTAGACCCGATCAACCCGAGCA 1680
 QY 2154 GGCTGTATCTGATGAGCGGCTTCTGTGCAACCGTGTGCAAGCAAGCCAGATCACTGGGT 2213
 DB 1681 GGCTGTATCTGATGAGCGGCTTCTGTGCAACCGTGTGCAAGCAAGCCAGATCACTGGGT 1740
 QY 2214 GAAATATCTGAGAGAGGCTGTGCAAGCAATATGAGAGATGATGATGATGATGATGATGAT 2273
 DB 1741 GAAATATCTGAGAGAGGCTGTGCAAGCAATATGAGAGATGATGATGATGATGATGATGAT 1800
 QY 2274 AGAGAGTGTGATGACACTGCGGCGGCTTACCGGTTTCTGGAAGTACGTTGAGAGCTGCA 2333
 DB 1801 AGAGAGTGTGATGACACTGCGGCGGCTTACCGGTTTCTGGAAGTACGTTGAGAGCTGCA 1860
 QY 2334 GAGGCTGTGAGAGAGGCGGCTTCTGTGAGATGTTCTAATACTGAGATGTTCCGAGAGCTGGC 2393
 DB 1861 GAGGCTGTGAGAGAGGCGGCTTCTGTGAGATGTTCTAATACTGAGATGTTCCGAGAGCTGGC 1920
 QY 2394 GAGAGCGGCTGCTTGTGCAATTTGACCAACCGAGATGCTGGCACTGGCTAG 2453
 DB 1921 GAGAGCGGCTGCTTGTGCAATTTGACCAACCGAGATGCTGGCACTGGCTAG 1980
 QY 2454 CACTGTGTGAGAGCTGAAACCTGAAAGACCTTCAATTTTAAAGGCGGCAAGCGTAG 2513
 DB 1981 CACTGTGTGAGAGCTGAAACCTGAAAGACCTTCAATTTTAAAGGCGGCAAGCGTAG 2040
 QY 2514 CCAATTAATGTCGCGGAGCTGAACCTGTTTTTATATGATGATGATGATGATGATGATGAT 2573
 DB 2041 CCAATTAATGTCGCGGAGCTGAACCTGTTTTTATATGATGATGATGATGATGATGATGAT 2098
 QY 2574 AAATTAATGAGAGAGGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 2633
 DB 2099 AAATTAATGAGAGAGGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGAT 2158
 QY 2634 AAGCTGTGCGTCAATTTCTTGTGCAAGGCGGAGGACCTGTGAGAGTGTGATGATGAT 2693
 DB 2159 AAGCTGTGCGTCAATTTCTTGTGCAAGGCGGAGGACCTGTGAGAGTGTGATGATGAT 2218
 QY 2694 TACATCATATTTCTGTGACCTGTGAAAAA 2723
 DB 2219 TACATCATATTTCTGTGACCTGTGAAAAA 2248

RESULT 4
 US-10-425-114-6561
 ; Sequence 6561, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 6561
LENGTH: 1874
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700571529_F11
US-10-425-114-6561

Query Match 66.6%; Score 1837.4; DB 13; Length 1874;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1858; Conservative 0; Mismatches 16; Indels 1; Gaps 1;

QY 843 GGTATCCCTCATGATGATCTTGGTCAAGCTAATGATGATTTAGGCTTGCAGACAGAGAG 902
DB 1 GGTATCCCTCATGATGATCTTGGTCAAGCTAATGATGATTTAGGCTTGCAGACAGAGAG 60
QY 903 ACAGATGCTATATATCTGACCAAGTCCGTCACATGAAATGAAATGATGTTCTCCGTT 962
DB 61 ACAGATGCTATATATCTGACCAAGTCCGTCACATGAAATGAAATGATGTTCTCCGTT 120
QY 963 AAAAAGAACAGAGGCTTGAATGTTTCCCAAGATTTCTATTTACTGCGGTGATGCCAGA 1022
DB 121 AAAAAGAACAGAGGCTTGAATGTTTCCCAAGATTTCTATTTACTGCGGTGATGCCAGA 180
QY 1023 TGCAGAAAGAACATATGATGATGATGACGCGCTGAGAGATTTGAGAAACAGACATCTTA 1082
DB 181 TGCAGAAAGAACATATGATGATGATGACGCGCTGAGAGATTTGAGAAACAGACATCTTA 240
QY 1083 CATATTAAGAGTTCCTCTCAGAAATGAAATGAGATGATGATGATGATGATGATGATGAT 1142
DB 241 CATATTAAGAGTTCCTCTCAGAAATGAAATGAGATGATGATGATGATGATGATGATGAT 300
QY 1143 TGATGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
DB 301 TGATGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 1203 ATTAAGAGTTCCTCTCAGAAATGAAATGAGATGATGATGATGATGATGATGATGATGAT 1262
DB 361 ATTAAGAGTTCCTCTCAGAAATGAAATGAGATGATGATGATGATGATGATGATGATGAT 420
QY 1263 ATTGCTATCTTACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1322
DB 421 ATTGCTATCTTACAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 480
QY 1323 TAAATATTCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1382
DB 481 TAAATATTCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 540
QY 1383 CCAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
DB 541 CCAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 1443 CCAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1502
DB 601 CCAAGTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 1503 TCTG 1562
DB 661 TCTG 720
QY 1563 AGTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
DB 721 AGTCTCTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780

QY 1623 CACCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
DB 781 CACCTCTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 1683 CATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
DB 841 CATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 1743 GGTGAAGAACATTAAGAGGCTGCTGAGAGCTTTTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 1802
DB 901 GGTGAAGAACATTAAGAGGCTGCTGAGAGCTTTTGTAGTGAAGTGAAGTGAAGTGAAGTGAAG 960
QY 1803 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1862
DB 961 GGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1863 GATCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
DB 1021 GATCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1923 CCGCTGATCTCTGCGCAGACAAAGAGGCGCTGTAACCGGAGCTCTATCGCTACATGCG 1982
DB 1081 CCGCTGATCTCTGCGCAGACAAAGAGGCGCTGTAACCGGAGCTCTATCGCTACATGCG 1140
QY 1983 TGATTAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
DB 1141 TGATTAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 2043 TGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
DB 1201 TGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 2103 CATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
DB 1261 CATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 2163 TCTGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
DB 1321 TCTGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 2223 TGAAGCGGCGCTGAGCGCATATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2282
DB 1381 TGAAGCGGCGCTGAGCGCATATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 2283 GATGACATGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2342
DB 1441 GATGACATGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 2343 GACGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2402
DB 1501 GACGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 2403 GCCGCTTCAATTAAGCAAGCGAGTATGCTGCGCACTGCGATGCGATGCTGCTGAT 2462
DB 1561 GCCGCTTCAATTAAGCAAGCGAGTATGCTGCGCACTGCGATGCGATGCTGCTGAT 1620
QY 2463 CAAGAATGAAACCTGAAGAGCTTCAATTAATTAAGGCGCGAGCGATGCGATGCGATGCGAT 2522
DB 1621 CAAGAATGAAACCTGAAGAGCTTCAATTAATTAAGGCGCGAGCGATGCGATGCGATGCGAT 1680
QY 2523 TGTGCGGAGCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2582
DB 1681 TGTGCGGAGCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740
QY 2583 AAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2642
DB 1740 AAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1799
QY 2643 GCTGCAATTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2702
DB 1800 GCTGCAATTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1859
QY 2703 TTCTGTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2717

Db 1860 TTCTGTGACCTGTG 1874

RESULT 5

US-10-425-114-15113

Sequence 15113, Application US/10425114
Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(531)3
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 15113
LENGTH: 2832
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: LIB305-038-E10_FLI
US-10-425-114-15113

Query Match 49.1%; Score 1352.4; DB 13; Length 2832;
Best Local Similarity 72.6%; Pred. No. 0;
Matches 165; Conservative 0; Mismatches 661; Indels 6; Gaps 1;

QY 10 CGGAGCTGAAACCGCAGCCGAGCATCCGCGACCGGTGAGAGACCTCCACGCGCAC 69
DB 112 CCAAGCTGTGTGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 171
QY 70 CGCAGAGCTGTGTGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGAT 129
DB 172 CGTAAAGACTATTTCT 231
QY 130 CGCAGACCATCT 183
DB 222 CCCCAATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 291
QY 184 CTGCGCAGAGGACCT 243
DB 292 CTTAAATAATGTCCT 351
QY 244 CGGTCGTGCGCATCGCGGTGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 303
DB 352 CCGTTTGTGCGCATCGCGGTGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 411
QY 304 GTTCAGAGCTGACGCTGCGAGCTGACAGTCTGCGAGTACTCTCCGCTTCAAGAGAG 363
DB 412 GTCTGAGCTGACGCTGCGAGCTGACAGTCTGCGAGTACTCTCCGCTTCAAGAGAG 471
QY 364 CTGTGAGAGCGCAGACATGATCCCTGAGTCTGAGAGTCTGAGAGTCTGAGAGTCT 423
DB 472 CTTGAG 531
QY 424 GTCTGAGTCCGAGCGCAATGCTGATCATCTATTTGAGAGAGAGAGAGAGAGAGAG 483
DB 532 GCGACATTTCTGTGCGCATCGCGGTGCGCCCGCGCGCGCGCGCGCGCGCGCGCG 591
QY 484 CGACACTGTCTGATCATGATGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 543
DB 592 CCGACATTTCTGTGCGCATCGCGGTGCGCCCGCGCGCGCGCGCGCGCGCGCGCG 651
QY 544 CTCGCGGCGCAGCGAG 603
DB 652 CTCGCGGCTCAAAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 711

QY 604 GGGAGGCTTCACTGTGTGTCAGCAAGAGTGAAGAGCATCTGTCAAGCTCCCTGTCAG 663
DB 712 TCAGAACTTCACTGTGTGTCAGCAAGAGTGAAGAGCATCTGTCAAGCTCCCTGTCAG 771
QY 664 ACAACATCTACAAATTTGCTTATTAATTTCAAGAGTGGGGCTGAGAGAGAGTGGGG 723
DB 772 ACACTCTATTCAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 831
QY 724 GATACAGAGAGACAGTTTGTGAGAAATGATCCATCTCTCTCTCTCTCTCTCTCTCT 783
DB 832 GATACGCTGAAAGGATTTGAGAAATGATCCATCTCTCTCTCTCTCTCTCTCTCTCT 891
QY 784 GACCATCTACCCCTGAGAGAAATCTCTGAGAGAGATCCCATGATTTTAAAGTGTG 843
DB 892 GATCTCTACAGTGAAGCTTTCTGTGAGAGATCCATGATTTCAATGTGCTATA 951
QY 844 GTATCCCTCATGATTTCTTGTGAGAGTATGATTTAGGCTTGCAGACAGAGAGA 903
DB 952 TTATCTCTCATGAGCTTGTGAGAGAGATGCTGTGGGTTGCTGACACTGTGGG 1011
QY 904 GAGATGCTATATCTGAGACCAAGTCCGTCAGTGAAGATGAGATGCTCCCTTTA 963
DB 1012 CAGGTTGTTATATCTAGATCAAGTGTGCTGCTGAAATGATGCTCTTGGATC 1071
QY 964 AAGAAACAGGCTGATGATTTCCCAAGATTTCTATTTTATCTGCTGATACAGAT 1023
DB 1072 AAGAAACAGGCTGATGATTTCCCAAGATTTCTATTTTATCTGCTGATACAGAT 1131
QY 1024 GCAAAAGAAACATCTGATGATCAGCGCTTGAAGAGATTTAGTGAACAGAGATCTAC 1083
DB 1132 GCAAAAGGAGCAATGACAGCAAGCGCTGAGAAAGTGTGATGACATCTATCTAT 1191
QY 1084 ATATACAGATCCCTTCAAGAAATGAGATCTTAAAGATGATGATCAAGATT 1143
DB 1192 ATTTGCGATTCATTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1251
QY 1144 GATGTGCGCATCTGAGAAACATTTGCTGAGATGCTGCTGATGATTTGCTGAA 1203
DB 1252 GATGTGCGCATCTATCTAGAGACTTATGCAAGAGATTTGCGAGTAAATGCTGAG 1311
QY 1204 TTACAGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1263
DB 1312 TTACAGAGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1371
QY 1264 TTGCTATCTTACAGATGAGAAATTTACAGATGAGATCTGATCTGATCTGATCT 1323
DB 1372 TTATGCTTATTAATGAGATTTACAGATGAGATCTGATCTGATCTGATCTGATCT 1431
QY 1324 AAGTATCGATTCAGACATATTTTGAAGATTTGATGAGAGATGATCTCTCTGC 1383
DB 1432 AATATTCAGATTCAGATTTATTTGAGAGAAATTTGAGATTAATTCACCTTTCA 1491
QY 1384 CAGTTCAGATCTGATTTATTTGATGAGAAATTTGATGAGAGATTTTATCATCACAG 1443
DB 1492 CAATTTACGCTTACCTAATAGCAGATGATTAATGATTTTATCATCACAGATTC 1551
QY 1444 CAGAAATTTGCTGAGAGCAAAATTTCTGTTGACAGATGAGATCTGATCTGATCT 1503
DB 1552 CAGAGATTTGAGAGAGCAAAATTTCTGTTGACAGATGAGATCTGATCTGATCT 1611
QY 1504 CTGCTGCTGTGACAGAGTGTGATGAGATGATGATGATGATGATGATGATGATGAT 1563
DB 1612 CTGCTGCTGTGACAGAGTGTGATGAGATGATGATGATGATGATGATGATGATGAT 1671
QY 1564 GTCTCTCTGAGAGTCAATGCTCATTTCTTCAATTCAGAGAGAGAGAGAGAGAG 1623
DB 1672 GTCTCTCTGAGAGTCAATGCTCATTTCTTCAATTCAGAGAGAGAGAGAGAGAG 1731
QY 1624 ACCCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
DB 1732 ACAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1791
QY 1684 ATTGGGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743

1792 ATGGTTATGTAAGCAATGCAAGCCCAATATTTCTCCATGCGCAAGGCTGACAGA 1851
1744 GTGAAGAACTAAGAGGCGCTGTAAGCTTTGCTAAGTCCGCTAAGCTGAGGAGCTG 1803
1852 GTAAAAAACAATGCTGATGTTGTAAGAAAGCTTTGTAAGAACAGCAATTAAGGGAAC 1911
1804 GTAAACCTTGTCTGCTGCTCCGAGTACAAATGATGTCACAAAGTCCAAAGACAGGAAAG 1863
1912 GTCAACCTTGTCAAGTATGCTGCTGTTATATGATGTAAGAAAGTCCAGTACAGAGAA 1971
1864 ATGCGGAGATAGAGAGATGCAATGCAATCAATCAAGACCAACACTGTTCCGCGAGTTC 1923
1972 ATTCAGAAATTTGAAAGATGCAATGAGCTCAATGAAAGATTAACCTTATGTTGATTTT 2031
1924 CGCTGATCTCTGCTCCAGACAAACAGGCGCGTAAACGCGAGCTCTATGCTATAGTCT 1983
2032 CGTTGATGCTGCTCCAAACAAATGAGGACGTAATGAGGAGCTGATGCTGACATAGCA 2091
1984 GATACCATGCTGCTTCTGTAACAGCCGCTTGTATGAGAGCTTCCGCTCCACCGCTCT 2043
2092 GACACAGAAAGTGTCTTCTGCTGCTGCTGCTTCTATGAGAGCTTTGAGCTTACAGT 2151
2044 GAGGCGATGACCTGTGCTCTCTTCTTCTGAGAGCTCTCAAGAGTCCAGCTGAGATC 2103
2152 GAGGCGATGATGAGAGCTCCCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGAGATC 2211
2104 ATAGAGATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2163
2212 ATGAGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2271
2164 CTGATGCGCGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2223
2272 CTATAGTGAATTTTCTCAAAAGAGCAAGGAGGAGCCCAAGCTTGAAGAAATATCT 2331
2224 GAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2283
2332 GATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2391
2284 ATGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2343
2392 ATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2451
2344 ACGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2403
2452 ACTGACAGATATCTGAGATGTTCTATATCTCAAGTCCGATTTGCAAAATCTGTT 2511
2404 CGCTTGCATTTGACCAACCGCATGCTTCTC 2435
2512 CGCTAGCTAAGATGATGCAAGTTACTAGC 2543

RESULT 6

US-10-424-599-98889

Sequence 98889, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 98889

LENGTH: 3191

TYPE: DNA

ORGANISM: glycine max

FEATURE:

NAME/KEY: unsure

LOCATION: (1)-(3191)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_6030C.1
US-10-424-599-98889

Query Match 48.14; Score 1325.6; DB 13; Length 3191;
Best Local Similarity 72.44; Pred. No. 0;
Matches 1762; Conservative 0; Mismatches 664; Indels 8; Gaps 3;

10 CGAAGCTGAAACCGCAACGAGATCCGAGACCGCGCGAGACACCTCCAGCGCAC 69
204 CCAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 263
70 CGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 129
264 CTTAAGCACTATTTCT 323
130 CGGACCAATCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 183
324 CCCCATAATTTGATGATGAACTTGACAAATCCCTGCGATGATCAAGCAATAGTAT 383
184 CTCGCGGAGAGACCTTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 243
384 CTTAAATATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
244 CGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
444 CTTTGTGAGCAATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 503
304 GTTACAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 363
504 GTCTGTGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAG 563
364 CTGTGCAAGCGGACGAC-AATGATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
564 CTTGTGATGAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 623
423 TGTCTGAGTCCGAGCGCAATGCTGATGATGATGATGATGATGATGATGATGATG 481
624 TGCCACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683
482 ACCGACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
684 ATCTCACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
542 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
744 TCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
602 TGGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
804 TTTCAAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 863
662 ACAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
864 ATGACCTCTATCAAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 923
722 GTGATACAGAGAGATGTTGAAATGATGATGATGATGATGATGATGATGATGATG 781
924 GTGATACAGAGAGATGTTGAAATGATGATGATGATGATGATGATGATGATGATG 983
782 CAGACCATCTACCTGAGAAATTTGAGAGAGATCCCATGATTTTAACTGTTG 841
984 CTGATCTCTTCACTAGAGACTTTTCTGAGAGAGTCAATGATGATGATGATGATG 1043
842 TGTATCCCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 901
1044 TATATCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1103
902 GACAGATGCTATATATGAGCAAGTCCGCTGCACTGAGAAATGATGATGATGATG 961
1104 GCGAGGTGTTATATATGATGATGATGATGATGATGATGATGATGATGATGATG 1163

QY 962 TAAAGAAACAGGAGCTTAAAGTTTCCCAAGATTCATGTTACTGCTGCTGATACAG 1021
DB 1164 TCAAGAAACAGGAGCTTAAAGTTTCCCAAGATTCATGTTACTGCTGCTGATACAG 1223
QY 1332 ATGCAAAAGGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1081
DB 1224 ATGCAAAAGGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1283
QY 1382 AATATTTGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141
DB 1284 AATATTTGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1343
QY 1142 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1201
DB 1344 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1403
QY 1202 AATTAACAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1261
DB 1404 AATTAACAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
QY 1262 CATTCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1321
DB 1464 CATTCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1523
QY 1322 CTAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1381
DB 1524 CTAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1583
QY 1382 GCCAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441
DB 1584 GCCAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1643
QY 1442 ACCAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1501
DB 1544 ACCAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1703
QY 1502 CTTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1561
DB 1704 CTTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1763
QY 1562 TAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1621
DB 1764 TAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1823
QY 1622 TCACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1681
DB 1824 TCACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1883
QY 1582 ACATTTGGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1741
DB 1884 ACATTTGGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1943
QY 1742 GGGTGAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1801
DB 1944 GGGTGAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2003
QY 1802 TGGTAAACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1861
DB 2004 TGGTAAACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2063
QY 1862 AGATTTGGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1921
DB 2064 AGATTTGGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2123
QY 1922 TCCGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1981
DB 2124 TCCGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2183
QY 1982 CTGATTAACCAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2041
DB 2184 CTGATTAACCAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2243

QY 2042 TTGAGGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2101
DB 2244 TTGAGGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2303
QY 2102 TCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2161
DB 2304 TCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2363
QY 2162 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2221
DB 2364 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2423
QY 2222 TTGAGGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2281
DB 2424 TTGAGGCAATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2483
QY 2282 TCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2341
DB 2484 TCAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2543
QY 2342 AGAGGAGGAGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2401
DB 2544 AGAGGAGGAGGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2603
QY 2402 TCCGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2435
DB 2604 TCCGCTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2637

RESULT 7
US-10-425-114-5285
; Sequence 5285, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yinda
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5285
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454567_FLI
US-10-425-114-5285

Query Match 47.5%; Score 1309.8; DB 13; Length 1340;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1328; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
QY 1377 CTTCTGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1436
DB 1 CTTCTGCAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
QY 1437 CACATACCAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1496
DB 61 CACATACCAAGAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 1497 CTTTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1556
DB 121 CTTTACTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 1557 CAATATAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1616
DB 181 CAATATAGTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 1617 GCGACTACCTCTCTTCATGAGTTCATGCAAAATTTGATTATGACCCGGAGCAAAACGA 1676
Db 241 GCGACTACCTCTCTTCATGAGTTCATGCAAAATTTGATTATGACCCGGAGCAAAACGA 300
QY 1677 TGAACATTTGGGATCTGATGACCGGTCAAAAGCCATCTCTTCTTCATGAGCAAGCT 1736
Db 301 TGAACATTTGGGATCTGATGACCGGTCAAAAGCCATCTCTTCTTCATGAGCAAGCT 360
QY 1737 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 1796
Db 361 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 420
QY 1797 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 1856
Db 421 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 480
QY 1857 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 1916
Db 481 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 540
QY 1917 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 1976
Db 541 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 600
QY 1977 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2036
Db 601 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2096
QY 2037 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2096
Db 661 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2156
QY 2097 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2156
Db 721 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2216
QY 2157 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2216
Db 781 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2276
QY 2217 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2276
Db 841 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2336
QY 2277 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2336
Db 901 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2396
QY 2337 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2396
Db 961 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2456
QY 2397 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2456
Db 1021 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2516
QY 2457 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2516
Db 1081 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2576
QY 2517 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2576
Db 1141 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2636
QY 2577 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2636
Db 1200 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2696
QY 2637 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2696
Db 1260 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2756
QY 1260 GGAAGAGGCTGAAGAACATTAACAGGGCTGGTGAAGCTTTTGCTAAGTGGCTTAAGCTGAG 2756

QY 2697 ATCATATTCTGTTGACCTGTG 2717
Db 1320 ATCATATTCTGTTGACCTGTG 1340

RESULT 8
US-09-938-842A-2415
; Sequence 2415, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Zhang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2415
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2415

Query Match 45.3%; Score 1249.8; DB 9; Length 2430;
Best Local Similarity 70.2%; Pred. No. 0;
Matches 1693; Conservative 0; Mismatches 712; Indels 6; Gaps 1;
QY 1 ATGTCTCCCGGACCTGACCGCAACGAGCATTCGGGACCGCTCGAGGACACCTTC 60
Db 1 ATGTCTCCCGGACCTGACCGCAACGAGCATTCGGGACCGCTCGAGGACACCTTC 60
QY 61 CAAGGACCGGACGAGCTGTGCGCTCTCTCCAACTGATGTAAGGAGGAGGAGG 120
Db 61 TCCGCTACCGGACGAGCTGTGCGCTCTCTCTCCAACTGATGTAAGGAGGAGGAGG 120
QY 121 ATCTGACGCGGACCAACATCTCTGACGCGCTGACGAGGCTCCCGGCTCCG 180
Db 121 ATCTGACGCGGACCAACATCTCTGACGCGCTGACGAGGCTCCCGGCTCCG 180
QY 181 GCG-----CTGCGGAGGAGCCCTTCTCGAGCTCCGCTCCGCGGAGGAGGATC 234
Db 181 GCG-----CTGCGGAGGAGCCCTTCTCGAGCTCCGCTCCGCGGAGGAGGATC 234
QY 235 GTGCGCGCGCTGCGTGTGCGCAATCGCGCTGCGCGCGCGCGCGGAGTTGGAGTAC 294
Db 235 GTGCGCGCGCTGCGTGTGCGCAATCGCGCTGCGCGCGCGCGCGGAGTTGGAGTAC 294
QY 241 GTTGTACCACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 241 GTTGTACCACTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 295 CGCGTCAAGCTTCAAGAGCTCAAGCTGAGCACTCAAGCTCGAGTCTCCGCTTC 354
Db 295 CGCGTCAAGCTTCAAGAGCTCAAGCTGAGCACTCAAGCTCGAGTCTCCGCTTC 354
QY 301 CGGTGTAAGTCTTGAAGCTTAAGTGAACATTAACAGTCTCTGAGTATCTTCTTC 360
Db 301 CGGTGTAAGTCTTGAAGCTTAAGTGAACATTAACAGTCTCTGAGTATCTTCTTC 360
QY 355 AAGAGGAGCTGTGACGCGGACCAACATGATCCCTAGCTGTGAGCTTGACTTCGAG 414
Db 355 AAGAGGAGCTGTGACGCGGACCAACATGATCCCTAGCTGTGAGCTTGACTTCGAG 414
QY 361 AAGAGGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
Db 361 AAGAGGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 420
QY 415 CCGTCAATGTCTCAAGTCCCAAGCCCAATTCGCTATCTATTTGAAACGGTGTGAG 474
Db 415 CCGTCAATGTCTCAAGTCCCAAGCCCAATTCGCTATCTATTTGAAACGGTGTGAG 474
QY 421 CCGTCAATGTCTCAAGTCCCAAGCCCAATTCGCTATCTATTTGAAACGGTGTGAG 480
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QY 475 TTCTCAACCGACCTTGTCTCAATGATGTTTCCGAAACGAGGATTCCTTGAGCCCTG 534
Db 475 TTCTCAACCGACCTTGTCTCAATGATGTTTCCGAAACGAGGATTCCTTGAGCCCTG 534
QY 481 TTCTCAACCGACCTTGTCTCAATGATGTTTCCGAAACGAGGATTCCTTGAGCCCTG 540
Db 481 TTCTCAACCGACCTTGTCTCAATGATGTTTCCGAAACGAGGATTCCTTGAGCCCTG 540
QY 535 TTGATTCCTCGGTGCGGACCGGACCAAGGGGATGTTATGATGATGATGATGAT 594

Db 541 CTGATGTTCCCTTGAAGTCTATAGTACAAAGTCTATCGGTGATGTTGAATGATGANT 600
Qy 595 CAAAGCTTGGGAGAGCTTCACTCTGTCTGACCAAGCTGAGAGCACTTGTCAAGCTC 654
Db 601 CAAAGCATATCTAGGCTTCAATCCAGCTTAGTAAAGCAAGATCATCTCTAAGCTT 660
Qy 655 CCTGTGTACACACCTTACTCACAATTTGCTTATAAATTTCAAGATGAGGGCTGAGAAA 714
Db 661 TCACAAAGAACTCCGCTTCTCGGAATTCGAATAGCGGTGCAAGAGATGGGTTTGA 720
Qy 715 GATTGGGCTGATAGAGAGAGATGTTTGAATATGATCATCTCTCTAGACATCAT 774
Db 721 GATGGGAGATACCGCAGAGAGATTTCTGAAATGATGATCTTCTCTGATATTTCTT 780
Qy 775 CAGGCGCAGACCCATCTACCTAGAGAAATTTCTTGGGAGAGATCCCATGATTTTAA 834
Db 781 CAAGTCTCTGATCTTCTGCTTGAAGAAATTTCTTGGGATGATGATGATGATTTTAA 840
Qy 835 GTTGTGTGTGATCCCTCTCATGATGATCTTGTCAAGCTAATGATATGAGCTTGCAC 894
Db 841 GTTGTGATCTTATCTCCACATGATGATTTTGGGCAAGCAATGTTTAAAGCTTACCT 900
Qy 895 ACAGAGAGACAGATGCTCTATATCTGACCAAGTCCGTGACCTAGAAATGAGATGAT 954
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Qy 955 CTGCTTTAAAGAAACAAAGGCTTATGTTTCCCAAGATTTCTATTTTACTGCTG 1014
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Db 1021 ATACCAATGCAAAAGAAATCATGATGACGCGCTTGAAGAGATGACGCGAAACAG 1080
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Db 1081 CATACTCATATATTCCTCGGCTTCTTTAGTCTGAAAGAAATCTCTCGTAAATGAT 1140
Qy 1135 TCAAGATTTGATGTGTGCTATCTGAAACATTTGCTGAGATGCTGCTGTGAAT 1194
Db 1141 TCAAGATTTGATGTGTGCTATCTGAAACATTTGCTGAGATGCTGCTGTGAAT 1200
Qy 1195 GCTGTGATTTCAAGATGCTGACATCTTAATTTGAAATCACTAGATGAGAAATCT 1254
Db 1201 GTGCTGATTTCAAGAGGCTGACGCTTATATCTGATCTATGATGAGAAATCT 1260
Qy 1255 GTGCTGATTTCAAGATGCTGACATCTTAATTTGAAATCACTAGATGAGAAATCT 1314
Db 1261 GTTGTGATTTCAAGATGCTGACATCTTAATTTGAAATCACTAGATGAGAAATCT 1320
Qy 1315 GAAAGACTAAGTATCAGATTCAGATATTTTGAAGAAATTTGATGAGAAATCT 1374
Db 1321 GAAAGAACTAAGTATCAGATTCAGATATTTTGAAGAAATTTGATGAGAAATCT 1380
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Db 1381 TTCTCTGCTGACGCTGCTGATATTAATTTGATGAGAAATTTGATGAGAAATCT 1440
Qy 1435 ACACATATACCAAGAAATTTCTGAGAGCAAAATATCTTGTGACATGATGAGATCACT 1494
Db 1441 ACACATATACCAAGAAATTTCTGAGAGCAAAATATCTTGTGACATGATGAGATCACT 1500
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Db 1501 GCTTTATCTGCTGCTGCTGATGACAGATTTGCTGAGATGATGATGATGATGATG 1560
Qy 1555 TTCAATATGCTGCTGCTGAGATGACATGATGATGATGATGATGATGATGATGATG 1614
Db 1561 TTCAATATGCTGCTGCTGAGATGACATGATGATGATGATGATGATGATGATGATG 1620
Qy 1615 AAGGCACTACCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674

Db 1621 AGGAGCTTACAGCTTTATCATGATTCATATAGAGAAATGCTCTATAGCCTTACAGACT 1680
Qy 1675 GATGAGACATTTGGGATCTGATGACCGCTCAAGGCCATCTCTCTCCATGAGCA 1734
Db 1681 GATGAGACATTTGGGATCTGATGACCGCTCAAGGCCATCTCTCTCCATGAGCA 1740
Qy 1735 CTGACAGAGTGAAGACATTAACAGGCTGCTGAGAGCTTTGCTTAAAGTCCGTAAGCTG 1794
Db 1741 CTGACAGAGTGAAGACATTAACAGGCTGCTGAGAGCTTTGCTTAAAGTCCGTAAGCTG 1800
Qy 1795 AGGAGCTTGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1854
Db 1801 AGGAGCTTGAAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Qy 1855 AGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1914
Db 1861 AGGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy 1915 GGGCAGTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1974
Db 1921 GGGCAGTTCCGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Qy 1975 TACATGCTGATTAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2034
Db 1981 TACATGCTGATTAACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Qy 2035 ACCGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2094
Db 2041 ACCGTGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 2095 GCTGAGATCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2154
Db 2101 GCTGAGATCATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
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Db 2161 GCTGTTATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2215 AATATATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2274
Db 2221 AATATATCTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2275 GAGAGTGTATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2334
Db 2281 GAGAGTGTATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Qy 2335 AGCTGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2394
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Qy 2395 AAGACCTGCTC 2405
Db 2401 AAGACCTGCTC 2411

RESULT 9
US-09-938-842A-2415
; Sequence 2415, Application US/09938842A
; Publication No. US2004009476A3
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCD1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111
 PRIOR FILING DATE: 2001-06-22
 NUMBER OF SEQ ID NOS: 5379
 SEQ ID NO 2415
 LENGTH: 2430
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 US-09-935-842A-2415

Query Match 45.3%; Score 1249.8; DB 11; Length 2430;
 Best Local Similarity 70.2%; Pred. No. 0;
 Matches 1693; Conservative 0; Mismatches 712; Indels 6; Gaps 1;

1 ATGTCGCCCCGAAAGCTGAACCGCAAGCGGATCCGGACCGGTGAGAGACACCTTC 60
 1 ATGGCAACCCCTAAGCTCATAAGGTTCTAAGCAACAAAGATCGGTCAAGACACGCTT 60
 61 CAGGCGACCGGCAACGAGCTGTGGCCCTCTCTCAAGTACGTGAACAAGAGGAGG 120
 61 TCCTGCTACCGCAAGGACCTGTGTCTCTCTCTCAAGTACGTGAACAAGAGGAGG 120
 121 ATCTCGACCGGCAACGAGCTGTGGCCCTCTCTCAAGTACGTGAACAAGAGGAGG 180
 121 ATCTCGACCGGCAACGAGCTGTGGCCCTCTCTCAAGTACGTGAACAAGAGGAGG 180
 181 GCG-----CTGCGGAGGAGGAGCTCTCTCTCAAGTACGTGAACAAGAGGAGG 234
 181 AAGAGAGCTCTCTGATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 235 GTGCGCGCGGCTGT 294
 241 GTTGTACCACTTTTGT 300
 295 CGCGTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 354
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 355 AAGAGAGCTTGT 414
 361 AAGAGAGCTTGT 420
 415 CGGTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 474
 421 CGGTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 480
 475 TTCTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 534
 481 TTCTCAAGCTTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAGAGCTCAAG 540
 535 TTGAGTTTCT 594
 541 CTGTGATTTCT 600
 595 CAAGCTTGT 654
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 655 CCTGTGACCAACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 714
 661 TCACAGAGAACTCGTCT 720
 715 GTTGT 774
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 775 CAAGCTTGT 834
 781 CAAGCTTGT 840
 835 GTTGT 894
 841 GTTGT 900

895 ACAGAGGACAGATGCTATATATCTGACCCAGTCCGTGACATAGAAATGAGTGTCT 954
 901 ACTGTGACAGAGTGTCTATATCTTGTGACCAAGTCGTGCTTGTGACATGAAATGCTG 960
 955 CTCGTGTTAAAGAAACAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1014
 961 TTGAGAAATTAAGAGACAGGAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
 1015 ATACAGATGCAAAAGAAACATGCAATGAGGCTTGTGAGAAATGAGAAATGAGAAACAG 1074
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 1201 GTGTGTGATTTGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260
 1255 GTGTGTGATTTGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1314
 1261 GTGTGTGATTTGAGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1320
 1315 GAAAGACTTAAGTATCCAGATTTCAAGATTTTGTGAGAAATGAGAAATGAGAAATGAG 1374
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 1375 TTCTCTGCGAGTCACTGT 1434
 1381 TTCTCTGCGAGTCACTGT 1440
 1435 AGCAGATTCAGAAATTTGTGAGAAATTTGTGAGAAATTTGTGAGAAATTTGTGAGAA 1494
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 1495 GCTTTTACCTGT 1554
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 1621 AAGGACTCACT 1680
 1675 GATGACATATGT 1734
 1681 GATGACATATGT 1740
 1735 CTGCAAGGCTGAAAGAACTTAAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1794
 1741 CTGCAAGGCTGAAAGAACTTAAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1800
 1795 AAGGACTGTAACCTTGT 1854
 1801 AAGGACTGTAACCTTGT 1860
 1855 AAGGAGAGATGCGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 1914
 1861 AAGGAGAGATGCGGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 1920
 1915 GAGGAGT 1974
 1921 GAGGAGT 1980
 1975 TACATGCTGATACCAATGT 2034

Db 1981 TACATCGCGATACAGAGGTCCTTTGCTCAGCTCGGCTCTACAGAGCTTTTGACTT 2040
Qy ACCGCTGTTAAGCCATGACCTGTTGGCTTCTACTTTTGGCAAGCTCCATGAGAGTCCA 2094
Db 2035 ACGCTGTTAAGCCATGACCTGTTGGCTTCTACTTTTGGCAAGCTCCATGAGAGTCCA 2094
Qy 2041 ACGCTGTTAAGCCATGACCTGTTGGCTTCTACTTTTGGCAAGCTCCATGAGAGTCCA 2100
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Qy 2101 GCGAGATCATAGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2160
Db 2155 GCTGTAACTGATGAGCCGACTTCTTGACCGGTGCAAGCAAGACCCAGATCATGGGTG 2214
Qy 2161 GCGGTAACTGATGAGCCGACTTCTTGACCGGTGCAAGCAAGACCCAGATCATGGGTG 2220
Db 2215 AATATATCTGAGAGAGGCTTGACGCGCATATACAGAGATCATGAGATGATATCTCA 2274
Qy 2221 AAGGATCATAGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2280
Db 2275 GAGAGGTTGAGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2334
Qy 2281 GAGAGATGATGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2340
Db 2335 AAGCTGAGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2394
Qy 2341 GCTGTGAGAGCATGGGCTCTCGGGCTTCCCATGATGACCCCTACCAAGCCGAGAG 2400
Db 2395 AAGAGCTGCTC 2405
Qy 2401 AAGAGCTGCTC 2411

RESULT 10
US-10-217-939-29
/ Sequence 29, Application US/10217939
/ Publication No. US200301545-2A1
/ GENERAL INFORMATION:
/ APPLICANT: MITTENDORF, VOLKER
/ APPLICANT: HARBET, HEIKO A.
/ APPLICANT: CIRPOS, PETRA
/ TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS III
/ FILE REFERENCE: 16313-0157
/ CURRENT APPLICATION NUMBER: US/10/217,939
/ PRIOR FILING DATE: 2002-08-12
/ PRIOR APPLICATION NUMBER: 60/311,414
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 29
/ LENGTH: 2394
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
US-10-217-939-29

Query Match 42.84; Score 1181.2; DB 15; Length 2394;
Best Local Similarity 70.54; Pred. No. 0;
Matches 1575; Conservative 0; Mismatches 659; Indels 0; Gaps 0;

Qy 184 CTGCGCGAGGAGCCCTTCTGACGCTCCGCTCCGCGAGAGAGCGATCGTGGCGG 243
Db 151 CTTAACAAAGTCATCATGAAAGTTCTGAGCTGACAGAGAGGCAATGTTTGCCT 210
Qy 244 CCGTGTGCGCATTCGGGCGCGCGCGCGCGAGATTGGAGATGATCGCGGTCAC 303
Db 211 CCAATTTGCTTGTGCTTATACGTTCCAGACCTGGGTATAGGGAATATGTCGGTGAAT 270
Qy 304 GTTCAAGAGCTCAGCGTGAAGCACTCAAGCTCTGAGATACCTCGCTTCAAGAGAG 363
Db 271 GTGTATAGAGTGAAGCGATGATTAATTAAGCTTTCTGATATATCTTGGTTAAGAGAG 330
Qy 364 CTGTGACGCGGCAAGCAATGATCCCTAGCTTCTGAGCTTGAATCTTGAGCCCTTCAAT 423
Db 331 CTGTATATGCGCATGCAATGAGATTAATCTCTTGAACCTTGAACCTTCAAT 390

Qy 424 GTTCAAGTCCACAGCCCAATGCGATCATCATCTATTGAAACGCTGTGCAATTCCTCAAC 483
Db 391 GCAACATTTGCTCGCCCAACTGTTCAATCATCATGAGGAAATGAGGTTGATCCCTCAAT 450
Qy 484 CGACACTTGTCTCAATCATGTTTCCGCAACAGGATTTGTTGAGAGCCCTTGTGATTC 543
Db 451 GGTCACTCTCTCAATTAATGTTCCGTAAACAAAGAAAGATGAGCTTGTGCTTGAAT 510
Qy 544 CTGCGGCGCACCGGCAACAGGAGCATGTTATGATGATGATGATGATGATGATGATGATGAT 603
Db 511 CTGCGCACTCAACAAACATGATGAGCGCTCTTATGATGATGATGATGATGATGATGATGATGAT 570
Qy 604 GGAAGGCTTCACTGTGTGCTGACCAAGCTGAGAGCACTTGTCAAGCTCCCTGCTGAC 663
Db 571 CCAATACTTCAAGGAGCTTTGCAAGAGAGAGAGAGTCTTCTTAACCTCCCTGCGCA 630
Qy 664 AGACCACTTCAATTTGCTTATTAATTTCAAGAGTGGGCTTGAGAGAAAGTGGGCT 723
Db 631 ACACCACTTCAATTTGCAATTTGAACTACAGAGGATGGATTTGAAAGGAGATGGGCT 690
Qy 724 GATAGAGCAAGCATGTTTGGAAATGATCCATCTCTTCAACATCATTCAGAGCGCCA 783
Db 691 GACACGACACAGAGGTTTCAAGAAATGTCATCTTCTTGAACATCTCAGAGCACT 750
Qy 784 GACCATCTACCTAGAGAAATCTTGGAGAGATCCCAATGATTTTAAAGTTTGTG 843
Db 751 GATCTTCTGTCTTGAAGAGTTTCAAGAGAGATCTTCAATGTTGATGAT 810
Qy 844 GATCTCTCTCATGATATCTTGTCAAGCTAAATGATGATGATGATGATGATGATGATGATGAT 870
Db 811 TTGCTCTCGATGATGATCTTGTGCAAGCAAGCTTGTGCTGCTGATGATGATGATGATGATGAT 870
Qy 904 CAGATGCTATATATCTGACCAAGTCCGTGCACTAGAAATGATGATGATGATGATGATGATGATGAT 963
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Db 931 CAGAGCAAGAGCATGAAAGTTATCCAAAGATTTCTCATTTGATGATGATGATGATGATGATGATGAT 990
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Db 991 GCAAAAGGAAATCATGACATGACCGGCTGAGAGATTTGAGACACAGCATATCTTAC 1050
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Qy 1384 CAGTTCAGTGTGATATATTTGCAATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1443
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Db 1411 CAAGAAATTTGCTGAGAGCAAAATATCTGTTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1470

227 CACCCCAATGAGCTTGTGCGCTTTTACCAAGCTGAAAACTTTGGAAAGGATATGCT 286
126 GCAAGCCGACCAATCTCGAGCGCTGAC---GAGGTCCAAGGCTCCGGGCTCCGGC 182
287 GAAAGCCCAACCAATCATTTGCGAGTACAAACAAATCGAATCCCTGAGGCTGAGCGGAGAA 346
183 GCTGCGCAAGGAGCCCTTCTGAGCTCTCGCTCCGCGCAAGAGGGATGCTGCTCC 242
347 GCTCAAGGATGATGCTTTGAGAGATGCTCTGAGGCACTCAAGAGGCGATTTGATCCC 406
243 GCGGTGTGAGCAATCGAGTGGCGCGCGCGCGGAGTTGGAGAGTACGTCCGCTCA 302
407 CCAATGGGTGACTTGGCAATCGCTTACGCTTGGCTGATGCTGAGAGTATGAGGCTCA 466
303 CGTTCAAGAGCTCAAGCTGAGAGCACTGCTGAGAGTACCTCGCTTCAAGAGAG 362
467 GGTGATGAGTGGCTGTTGAGAGCTGAGAGTCTTGAAGTACCTGCAAGTCAAGAA 526
363 GCTTGTGAGCGCGCAAGCAATGATCCCTACGTTCTTGAAGTCTGATCTGAGCCCTTGA 422
527 GCTTGTGAGAGAGCGCGCAACCAACCTTGTGTTGAGTCTGAGCTTGAAGCTTGA 586
423 TGTCTCAGTCCAGCGCGCAACCTGCTGATCATCTATTGGAAGCGGTGAGCTTCTCA 482
587 TGCTCTCTTCCCGCTCTTCTCTGATGAGTCAATGGCAATGGCGTGAAGTCTCTGA 646
483 CCGACACTTGTCTCAATGATGTTCCGCAAGGATGCTTGAAGCTTGTGAGT 542
647 CAGGACCTGTGATCAAGCTCTTCCATGACAAAGAGAGCATGTACCTCTGCTCAACT 706
543 CCTCGTGGCCACCGGCAACAGGAGCATGTTATGATGCTTATGATGATGATGATGAT 602
707 CTTTGGCGCAACACTACAAAGGAGATGACATGATGTTGAGAGAGATGCGAGTCT 766
603 GGGAGAGCTTCACTGCTGCTGAGCAACCAAGCTGAGAGCACTTGTCAAGAGCTCCCTGCTGA 662
767 CAGTCTCTGCAAGGTGCGCTGAGAGAGCTGAGAGCACTGCTGCAAGCTTCAAGCTGA 826
663 CACACATCTCAACATTTGCTTATTAATTTCAAGATGCGGCGCTGAGAGAGTGGG 722
827 TACCCCAATCTGAAATTTCAACAGGTTCAGAGAACTTGTCTGAGAGAGGTTGGG 886
723 TGAATACAGAGAGCAATTTTGGAAATGATCATCTCTTGAAGATCATTCAGGCGG 782
887 TGAATGCGTAAAGCGGCAAGAGACTTACCTCTCTGAGCTCTTGAAGGCCCC 946
783 AAGCCATCTACCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTTTGT 842
947 AATTCCTGCAACCTTGAAGAGTCTTGGAAAGATCCCATGAGTTCATAGTCTTAT 1006
843 GGTATCCCTCATGATCTTGTGTGAGTAAATGATTAAGCTTGTCCAGAGAGG 902
1007 CCTCTCCCTCATGATCTTGTGTGAGTAAATGATTAAGCTTGTCCAGAGAGG 1066
903 AAGATCTGATTAATCTGAGCAACAGTCCGTGACAGAAATGAGATGTTCCGTT 962
1067 CCAAGTGTCTAATCTTGAATCAAGTGGCTTGAAGAGTCTTGAAGAGTCTTGAAG 1126
963 AAGAAACAGAGGCTTGAATGTTCCCAAGATTTCTATTTACTCGCTGATACAG 1022
1127 CAGAGATGATGCTTGAATCAACAGTCCGTAAGATCTTATTTGCAACAGGTTGCTCTCTGA 1186
1023 TGCAGAGAGCAATCATGCAATAGCGGCTTGAAGATTTAGTGAACACAGATCTTA 1082
1187 TGAATCTGAGCAACCTGATGAGCGGCTTGAAGAGTCTTGAAGAGTCTTGAAG 1246
1083 CATATTCAGATTCCTTCAAGATGAATGGAATGGAATCTTAAGAAATGATATCAAGAT 1142
1247 TATCTTCGATGCTTCAAGAGAGAGAGATGATGATGATGATGATGATGATGAT 1306
1143 TGAATGATGCTTCAATCTGAGAAATTTGCTGAGAGTCTGCTGATGAAATTTGCTGCTGA 1202

1307 TGAAGTGGCGGCTACTGAGAGACTTACATGATGACGTGGCGATGAGATTTGCTGAG 1366
1203 ATTTCAGAGTACTCAGACTTCAATATGAGAACTACAGTATGAGAAATCTTGTGCGCTC 1262
1367 GCTTCAAGCAATCTTGAAGTCTGATGAGAACTTACAGTATGAGAACTTGTGCGCTC 1426
1263 ATTGCTATCTTCAAGATGAGAAATTCAGTGAACATTTGCTCATGCTCTGAGAAAGAC 1322
1427 TTTGCTGCGCAACAGATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1486
1323 TGAATTCAGATTCAGATATTTTGAAGATTTGATGAGAAATTTGATGATGATGATGAT 1382
1487 TAAATGATTAATCTGAGCTTCTTACAGAGAGTGTGAGATTAATGATGATGATGATGAT 1546
1383 CAGTTCAGTCTGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
1547 CAGTTCAGTCTGATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1606
1443 CCAAGAAATTTGCTGAGAGCAAAATTAATGTTGAGAGATGATGAGATGATGATGATGAT 1502
1607 CCAAGAGATTCGCGAGAAACAAAGAGACCGTGGCCAGTACAGTCAATGAGCTTCAAC 1666
1503 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
1667 AATGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1726
1563 AGTCTCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
1727 CAGTCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1786
1623 CACCTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
1787 GACCTCTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1846
1683 CATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1742
1847 CAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1906
1743 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1802
1907 TGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1966
1967 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2023
1803 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
1967 GGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2023
1863 GATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
2024 GAGGCGGAGTTCAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2083
1923 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1982
2084 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2143
1983 TGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
2144 CAGACCAAGAGGCGCTTGTGAGAGCTGCTTCTTCAAGGCTTGTGAGAGCTGAGG 2203
2043 TGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
2204 TGAAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2263
2103 CATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
2264 CATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2323
2163 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
2324 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2383
2223 TGAAGAGAGGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2282
2384 CAGGCGGAGCTCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2443

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 DB 1013 CCTTCCCTCATGATGATTTGTCAGACTATGATAGGCTTGCCAGACAGAGAG 1072
 QY 903 ACAGATCGCTATATATGAGCAAGTCCGTCATGAGAAATGAGATGATTCGGTT 962
 DB 1073 CCGATGCTCATATCTTGATGATGATGAGGCTGATGAGAAATGATTCGGTT 1132
 QY 963 AAGGAAAGAGGCTTGATGATTTCCCAAGATTCATGATGATGATGATGATGAT 1022
 DB 1133 CAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1192
 QY 1023 TCCAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1082
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 DB 1253 TATCTTCCCTCATGATGATTTGAGAAAGAGATGATGATGATGATGATGAT 1312
 QY 1143 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1202
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 QY 1203 ATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1262
 DB 1373 GCTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
 QY 1263 ATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322
 DB 1433 TTTGCTCCCTCATGATGATTTGAGAAAGAGATGATGATGATGATGATGAT 1492
 QY 1323 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1382
 DB 1493 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1552
 QY 1383 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1442
 DB 1553 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1612
 QY 1443 CCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1502
 DB 1613 CCAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1672
 QY 1503 TCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1562
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 QY 1563 AGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1622
 DB 1733 AGTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1792
 QY 1623 CACCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1682
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 DB 1853 CATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1912
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 DB 1913 GGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1972
 QY 1803 GGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1862
 DB 1973 GGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2029
 QY 1863 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
 DB 2030 GATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2089

QY 1923 CCGTGAATCTCTGCTCCAGACAAACAGAGGCGGCTTACGCTATGCTATCTCC 1982
 DB 2090 CCGTGAATCTCTGCTCCAGACAAACAGAGGCGGCTTACGCTATGCTATCTCC 2149
 QY 1983 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2042
 DB 2150 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2209
 QY 2043 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
 DB 2210 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2269
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 DB 2270 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2329
 QY 2163 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
 DB 2330 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2389
 QY 2223 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2282
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 QY 2283 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2342
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 QY 2343 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2402
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 DB 2570 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2592

RESULT 15
 US-10-425-114-17596
 ; Sequence 17596; Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Sreen, Steven E.
 ; APPLICANT: Tabasta, Jack E.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ. ID NOS: 73128
 ; SEQ. ID NO 17596
 ; LENGTH: 3419
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3069-052-F8_FLI
 US-10-425-114-17596

Query Match 42.6%; Score 1173.4; DB 13; Length 3419;
 Best Local Similarity 68.3%; Pred. No. 0;
 Matches 1656; Conservative 0; Mismatches 76; Indels 6; Gaps 2;

QY 6 TGCCTGAAAGCTGAAACGCGAAGCAGATCCGCGCTGAGACACCTTCACAGC 65
 DB 567 TGAACCTGCTGAGCCGCTTCAAGCTGAGGAGGCAATGCGACTATCTTCC 626
 QY 66 GCAACGGAAGAGCTGCGCTCTCTCAAGTACTGAAACAGAGGAGGAGATCT 125
 DB 627 CACCCCAATAGCTTGTGCGCTTCTCAAGCTGAAACAGGAGGAGATCT 686

126 GCAGCCGACACACATCTCTGACGCGCTGAC---GAGGTCCAGGGCTCCGGGTCCGAGC 182
Db GAGGCCACACAGATCATTTGCGAGTACACATGAGATCCTTGAGGCTGAGCGAGAA 746
Qy 183 GCTGCGCAGAGGACCTTCTCTGACGCTCTCGCTCCGCGAGAGGCGCATGCTGTCG 242
Db GCTCAGAGATGCTTTGAGGATGCTCTGAGGGGAGCTCAGAGGCGCATATGATCC 806
Qy 243 GCGCTTCTGCGCATTCGCGTGCGCCGCCGCGGAGAGTTGGAGTACGTCGCTCA 302
Db CCGATGGGTGACATTCGATCCGCTAGGCTGAGCTGCTGCTGAGTATGAGGCTCA 866
Qy 303 GATTACAGAGCTCAGCGTGCAGAGCTCAGCTCCGAGTACCTCCGCTTCAAGAGGA 362
Db GCTCAGATGAGCTCGCTTGGAGAGCTGAGATCTCTGAGTACCTGCACTTGAAGAA 926
Qy 363 GCTTGTGACGCGCAGACATGATCCTACGTTCTGAGCTTGAAGCTTGAAGCTTCA 422
Db GCTTGTGAGAGAGGCCCAACACACACTTGTCTTGAAGCTGAGCTTGAAGCTTCA 986
Qy 423 TGTCTCAGTCCGACGCCCAATCGCTCATCTCATTTGAGAAAGCTGAGCTTCA 482
Db TGCCTCTTCCCGCTCTCTCTGCAAGTCCATTTGCAATGGCGTGAAGTCTTCA 1046
Qy 483 CCGACACTTGTCTCATATGCTCCGACACAGAGATTTGAGAGCTTGAAGCTTGAAGT 542
Db CAGGACCTGTATCAAGCTCTTCCATGACAGAGAGAGATGATCCCTTGTCTCACT 1106
Qy 543 CCTCGTGGCCACCGGACACAGGGGCTATTTATGCTTAAATGATGAAATCAAGCTT 602
Db CCTTGGCGCCCAACTACAGAGAGATGACATGATTTGAACGACGATCCGAGCT 1166
Qy 603 GGGGAGGCTGAGCTGCTGCTGACCAAGAGTGAAGAGCACTTGAAGAGCTCCGCTGA 662
Db CAGTCTCTGCAAGGTGCTGAGAGAGCTGAGAGCACTGCTCACTTCAAGCTCA 1226
Qy 663 CACACATCTCACAATTTGCTTATTAATTTCAAGAGTGGGCTTGAAGAAAGTTGGG 722
Db TACCCATATCTGAAATTTCAACACAGTTCCAGAGACTTGTGAGAAAGGTTGGG 1286
Qy 722 TGAATACAGAGACATGTTTGGAAATGATCCTCTCTTGAACATCATTCAGGCGC 782
Db TGAATGCGTACGCGTACAGAGAGCTATCCACTCTTGAAGCTCTTGAAGCGCC 1346
Qy 783 AAGCCATCTACCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTGT 842
Db AATTCCTGACCCCTGAGAGAGTTCTTGAAGAGATCCCATGATGTTAAATGCTTAT 1406
Qy 843 GGTATCCCTCATGATCTTGTGTCAGCTAATGATTAAGCTTGCAGACACAGAG 902
Db CCTCTCCCTCATGATCTTGTGTCAGCTAATGATCTTGGGTTACCTGACACCGAG 1466
Qy 903 ACGATGCTCTATATCTGACCAAGTCCGTGCACTAGAAATGAGATGTTCTCGTT 962
Db CAGGTTGTCTACATCTTGAATCAAGTGCCTATGAGAAAGCAATCTGCTGAGAT 1526
Qy 963 AAGAGAAAGAGGCTTGAATTTCCCAAGATTTCTATGTTACTCGGCTGATACGA 1022
Db CAGGAGTGTGCTTGAATCAAGCGGAGATCTTATTTGACAGAGTTGCTCTCTGA 1586
Qy 1023 TGCAGAAAGACATCATGCAATCGGCTTGAAGATTAAGTGAACACAGACTTCA 1082
Db TCGAATGCAACCACTGTGGCGAGGCTTGAAGTCTTGGACCGAGCACTGCA 1646
Qy 1083 CATATTACAGATTCCTTCAAGAAATGAATTAAGTAAATGATATCAAGATT 1142
Db TATCTTCCGCTGCAATTCAGAAACAGAAACGGAATCGTTGCAATGATTCGAGT 1706
Qy 1143 TATGTTGGCCATATCTGAGAAATTTGCTGAGATGCTGCTGAGAAATGCTCTGA 1202
Db TGAATGCTGGCTGATCTGAGACCTTACATGATGAGCTGGCGCATGAGATTCCTGAG 1766

Qy 1203 ATTACAGGTACTCCAGACTTATATTAATGGAATCAAGTATGATGAAATCTTGTGGCTC 1262
Db GTTCAAGGCAATCCGACCTGATCATGAGAAATCAAGTGAAGCAAACTTGTGCTG 1826
Qy 1263 ATTGCTATCTTACAGATGAGAAATTAACAGTGCACATTTGCTCATGCTCTGAGAAAG 1322
Db TTTGCTCGCCCAAGATGAGTGTGTTACTCATGTAATGCTCCAGGCTTGAAGAAAC 1886
Qy 1323 TAAATATCCAGATTCAGACATATTTTGAAGAAATTCATGAGAAATACATTTCTCTG 1382
Db TAAATATCCAGATTCAGACATCTTACTGAGAAAGTTTGAAGTCACTACCATCTCTG 1946
Qy 1383 CCAAGTCTACTGCTATATTAATGCTATGAAACATGCTGATTTTATCATGACAGACATA 1442
Db CCAAGTCTACTGCTATATTAATGCTATGAAACATGCTGATTTTATCATGACAGACATA 2006
Qy 1443 CCAAGAAATGCTGAGAGCAAAATTAATGCTGAGAGTATGAGAGTCAATGCTTTC 1502
Db CCAAGAGATGCGCGAGAAACAGAGACCGTGGCCAGTACAGTCAACATGGCGTTCA 2066
Qy 1503 TCGCCTGGTCTGACCGAGTTGTCATGAGGATGATGCTTTCATGATCCAAAGTTCAAT 1562
Db AATGCTGAGCTGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2126
Qy 1563 AATGCTGAGCTGATCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1622
Db CAGTCTGCTGAGCTGATCCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2186
Qy 1623 CACCTCTCTCATGCTTCAATGAGAAATTTGATTAAGACCGGAGCAAAAGATGAGCA 1682
Db GACCTCTCTTACCGGAGATGAGAGCTCTCTGAGACCAACCGAGAACGAGCA 2246
Qy 1683 CATGGGCACTGATGACCGGCTCAAGCCCATCTCTTCCATGAGCAAGCTGACAG 1742
Db CAGGTTGCTTGAAGACAGGACAGGACAGGACAGGACAGGACAGGACAGGACAGG 2306
Qy 1743 GGTGAAGACATTAAGGCTGCTGAGAGCTTTGCTAAGTGGCTTGAAGTGAAGCT 1802
Db TGTGAAGACATTAAGGCTGCTGAGAGCTTTGCTAAGTGGCTTGAAGTGAAGCT 2366
Qy 1803 GGTGAAGACATTAAGGCTGCTGAGAGCTTTGCTAAGTGGCTTGAAGTGAAGCT 1862
Db GGTGAAGACATTAAGGCTGCTGAGAGCTTTGCTAAGTGGCTTGAAGTGAAGCT 2426
Qy 1863 GATCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1922
Db GATCGGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2486
Qy 1923 CCGCTGATCTTCCGACAGCAAGGCGGCTTAAACGCGAGCTCTATGCTTAACTG 1982
Db CCGCTGATCTTCCGACAGCAAGGCGGCTTAAACGCGAGCTCTATGCTTAACTG 2546
Qy 1983 TGAATCCATGAGGCTTGTGACAGCGGCTTGAAGAGCTTGGCTGCTGCTGCTGCT 2042
Db CAGACCAAGGCGCTTGTGACAGCGGCTTGAAGAGCTTGGCTGCTGCTGCTGCT 2606
Qy 2043 TGAAGCATGACCTGTGAGCTTCTACTTTCGAGCGCTTCATGAGAGTCCAGTGAAT 2102
Db TGAAGCATGACCTGTGAGCTTCTACTTTCGAGCGCTTCATGAGAGTCCAGTGAAT 2666
Qy 2103 CATAGAGATGAGGCTTCCGAGCTTCAACTTGAACCGCTACACCCGAGAGGCTTAA 2162
Db CATAGAGATGAGGCTTCCGAGCTTCAACTTGAACCGCTACACCCGAGAGGCTTAA 2726
Qy 2163 TGTGATGCGCACTTCTTGAACCGGCTGAGCAAGCCAGATCACTGAGTGAATATTC 2222
Db CCGCTGCTGAGCTTCTTGAACCGGCTGAGCAAGCCAGATCACTGAGTGAATATTC 2786
Qy 2223 TGAAGCAGGCTGAGCGATATACAGAGATCACTGAGAGATATCACTGAGAGCTT 2282
Db CAGAGCGGCTTCAAGCTATCAAGAGAGATCACTGAGAGCTTCAAGAGCTT 2946
Qy 2283 GATGACATGCGCGGCTTGAAGTGTGAGAGTGTGAGAGCTGAGAGCTGAG 2342

Db	2844	GATGAACCTTCACCGGGGTGTACGGGTTCTGGAAGTACGTGTCCAACTGGAGAGGGCGGA	2903
Qy	2343	GAAGAGGGCTTACTCTTGAATGTTCTACATGAACTTCCGGAGCTGGCGAAGACCGT	2402
Db	2904	GAACCGGCGGTACCTGAGATGCTGTACGCGCTCAAGTACCGCACCATGGCGACACCGT	2963
Qy	2403	GCCGCTTGCATTGACCAACCGC	2425
Db	2964	GCCGCTGGCCGTGAGGGAGAGC	2986

Search completed: May 26, 2004, 02:26:01
 Job time : 794.858 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2004, 14:40:36 ; Search time 694.519 Seconds
(without alignments)

16863.873 Million cell updates/sec

Title: US-10-080-114A-11

Perfect score: 2757

Sequence: 1 atgctgcgccgaagctgaa.....aaaaaaaaagggcgccgcg 2757

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2003cs.*
9: Geneseq2003cs.*
10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2757	100.0	2757	6	AAD45856 Corn Sus3
2	2714	98.4	2737	6	AAD45849 Corn sus3
3	1809.6	65.6	2412	7	ADA69581 Rice gene
4	1249.8	45.3	2430	6	AB214610 Arabidops
5	1181.2	42.8	2394	7	AB276372 A. thalia
6	1179.8	42.7	2563	2	AAQ80005 Sucrose-s
7	1173.4	42.6	2908	6	AAD45852 Corn suc
8	1172	42.5	2418	7	AB276371 A. thalia
9	1162	42.1	2450	7	ADA71337 Rice gene
10	1162	42.1	2451	9	ADC08208 Rice DNA
11	1162	42.1	2451	9	ADC07855 Rice DNA
12	1135.6	41.2	2754	9	ADC68521 S. arundi
13	1134.6	41.2	2829	6	ABK98516 cDNA sequ
14	1133	41.1	2494	3	AAC66090 Rice suc
15	1133	41.1	2714	9	ADC68423 Lolium pe
16	1133	41.1	2716	9	ADC68520 Lolium pe
17	1133	41.1	2746	6	ADA45851 Corn suc
18	1132.6	41.1	2906	3	AA67143 Eucalyptu
19	1132.4	41.0	2957	9	ADC68424 Lolium pe
20	1131	41.0	2913	3	AAA67087 Eucalyptu
21	1131	41.0	3103	3	AAC62807 Sucrose s
22	1131	41.0	3103	6	ABK17072 Eucalyptu
23	1128.2	40.9	2825	9	ADC68523 S. arundi

24	1124.4	40.8	2950	9	ADC68522 Lolium pe
25	1104.6	40.1	2625	6	ABK52880 Cotton su
26	1094.2	39.7	2360	3	AAC66096 PSS3 cDNA
27	1062.6	38.5	2427	6	AB213815 Arabidops
28	1062.6	38.5	2427	7	ADA68333 Arabidops
29	940.2	34.1	2334	7	ADA71106 Rice gene
30	940.2	34.1	2334	9	ADC07857 Rice DNA
31	940.2	34.1	2334	9	ADC08296 Rice DNA
32	899.6	32.6	2210	7	ADA69957 Rice gene
33	830.8	30.1	2397	7	ADA70504 Rice gene
34	830.8	30.1	2397	9	ADC07859 Rice DNA
35	789.6	28.6	2361	9	ADC07861 Rice DNA
36	775	28.1	1209	6	ABK98492 Consensus
37	574.6	20.8	1374	9	ADC08717 Wheat DNA
38	482.8	17.5	2700	2	AA21641 Arabidops
39	482.4	17.5	1546	9	ADC07853 Rice DNA
40	459.2	16.7	2492	6	ADA42841 Maize suc
41	453.4	16.4	697	6	ABK98493 cDNA sequ
42	449.8	16.3	1169	3	AA67120 Pinus rad
43	442.4	16.0	705	6	ABK98494 cDNA sequ
44	430.6	15.6	1145	3	AA67119 Pinus rad
45	397.4	14.4	428	8	ADA58861 Maize suc

ALIGNMENTS

RESULT 1	AAD45856	standard; DNA; 2757 BP.
ID	AAD45856	
XX	AAD45856	
AC	AAD45856	
XX	AAD45856	
DT	29-AUG-2003	(revised)
DT	27-DEC-2002	(first entry)
XX		
DE	Corn Sus3-Sorghum EST chimeric DNA.	
XX		
KW	Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;	
KM	transgenic plant; plant breeding; grain breakage; grain strength; enzyme;	
XX	cellulose; corn; Sus3; chimeric; gene; ds.	
OS	Zea mays.	
OS	Sorghum propinquum.	
OS	Chimeric.	
XX		
Key	Location/Qualifiers	
CDS	1..2430	
FT	/product= "Corn Sus3-Sorghum EST chimeric protein"	
FT	/tag= a	
FT	/tag= b	
FT	/note= "Sorghum propinquum EST DNA"	
FT	40..2757	
FT	/tag= c	
FT	/note= "Corn Sus3 DNA"	
XX		
PN	WO200267662-A1.	
XX		
PD	06-SEP-2002.	
XX		
PP	21-FEB-2002; 2002MO-US005137.	
XX		
PR	22-FEB-2001; 2001US-0270777P.	
XX		
PA	(PION-) PIONEER HI-BRED INT INC.	
XX		
PI	Dhuga KS, Helentjaris TG, Niu X,	
XX		
DR	WPI: 2002-691625/74.	
DR	P-PsDB: AA28502.	
XX		
PT	New polynucleotide and its encoded sucrose synthase, useful for	

modulating the level of sucrose synthase in transgenic plants (e.g. maize or soybean) to improve stalk length, reduce grain breakage, or improving plant or grain strength.

Claim 1: Page 116-119; 125pp; English.

The invention relates to two sucrose synthases, shrunken-1 (Sh1) and constitutive sucrose synthase (Ssu1) and their corresponding nucleic acids. The polynucleotide, or its encoded protein, is useful for modulating the level of sucrose synthase in a transgenic plant, increasing cellulose production in the stalk tissue of a transgenic plant, or increasing the concentration of cellulose in the tissues of a seed of a transgenic plant. This is particularly useful in plants (e.g. maize or soybean) breeding, especially for e.g. improving stalk length in maize, reducing grain breakage during combining, transport or movement into storage, or improving plant or grain strength. The present sequence is Corn Ssu3-809uhum EST chimeric DNA. (Updated on 29-Aug-2003 to standardise OS field)

Sequence 2757 BP; 717 A; 679 C; 700 G; 661 T; 0 U; 0 Other;

Query Match 100.0%; Score 2757; DB 6; Length 2757;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTCGCCCGAAGCTGAACCGCAACGAGCATCCGAGCCGCTGAGAGCAACCTTC 60
DB 1 ATGTCGCCCGAAGCTGAACCGCAACGAGCATCCGAGCCGCTGAGAGCAACCTTC 60
QY 61 CAGCGCAACCGCAACGAGCTGTCGCTCTCTTCGAGTACGTCGAGAGGAGGAGG 120
DB 61 CAGCGCAACCGCAACGAGCTGTCGCTCTCTTCGAGTACGTCGAGAGGAGGAGG 120
QY 121 ATCCGCAACCGCAACGAGCTGTCGCTCTCTTCGAGTACGTCGAGAGGAGGAGG 180
DB 121 ATCCGCAACCGCAACGAGCTGTCGCTCTCTTCGAGTACGTCGAGAGGAGGAGG 180
QY 181 GCGCTCGCGCAAGGAGACCTTCCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 GCGCTCGCGCAAGGAGACCTTCCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCT 240
QY 241 CCGCGCTTCGTCGCGCATGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 CCGCGCTTCGTCGCGCATGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 AACGTCACGAGCTCAGGCTGAGAGAGTCAAGTCTCGAGTACCTTCGCTCAAG 360
DB 301 AACGTCACGAGCTCAGGCTGAGAGAGTCAAGTCTCGAGTACCTTCGCTCAAG 360
QY 361 GAGCTTCGAGCGGCAACGAGTATCCCTACGCTTCGAGCTTGAAGCTTCGAG 420
DB 361 GAGCTTCGAGCGGCAACGAGTATCCCTACGCTTCGAGCTTGAAGCTTCGAG 420
QY 421 AATGTCAGTCCAGCGCCCAATCGGTCATCATCTATTTGAAACGCTGTCAGTCT 480
DB 421 AATGTCAGTCCAGCGCCCAATCGGTCATCATCTATTTGAAACGCTGTCAGTCT 480
QY 481 AACGCACTGTCCTCATCATGTCGCAACGAGGATTCCTGAGGCGCTGTCAGT 540
DB 481 AACGCACTGTCCTCATCATGTCGCAACGAGGATTCCTGAGGCGCTGTCAGT 540
QY 541 TTCTCCGTCGAGCAACGAGCAACGAGGATTTATGATGCTTAAATGATGATCA 600
DB 541 TTCTCCGTCGAGCAACGAGCAACGAGGATTTATGATGCTTAAATGATGATCA 600
QY 601 TTGAGGAGGCTTCGATCTGTCGTCGCAAGAGCTGAGAGCACTTGTCAAGCT 660
DB 601 TTGAGGAGGCTTCGATCTGTCGTCGCAAGAGCTGAGAGCACTTGTCAAGCT 660
QY 661 GACACACATCTACATATTTGCTTATTAATTTCAAGAGTGGGCTGAGAGAGGTT 720
DB 661 GACACACATCTACATATTTGCTTATTAATTTCAAGAGTGGGCTGAGAGAGGTT 720
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QY 721 GATGATACAGAGGACATGTTTGGAAATGATCCATCTCTCTGACATCATTCAGG 780
DB 721 GATGATACAGAGGACATGTTTGGAAATGATCCATCTCTCTGACATCATTCAGG 780
QY 781 CCGAGCCATTCACCTTACAGAAATTTCTGGAGAGATCCCATGATTTTAACTGTT 840
DB 781 CCGAGCCATTCACCTTACAGAAATTTCTGGAGAGATCCCATGATTTTAACTGTT 840
QY 841 GTCGATCCCTCATGATGATCTTGTGCAAGTATGATGATGCTTGCAGACAGGA 900
DB 841 GTCGATCCCTCATGATGATCTTGTGCAAGTATGATGATGCTTGCAGACAGGA 900
QY 901 GAGACAGCTGCTATATCTGAGCAACAGTCCGTCAGTAAAGATGATGCTTCCGT 960
DB 901 GAGACAGCTGCTATATCTGAGCAACAGTCCGTCAGTAAAGATGATGCTTCCGT 960
QY 961 TTAAGAAACAGAGGCTGATGTTTCCCAAGATTCATGTTTACTCGGCTGATACA 1020
DB 961 TTAAGAAACAGAGGCTGATGTTTCCCAAGATTCATGTTTACTCGGCTGATACA 1020
QY 1021 GATGAAAGAGACATCATGCAATCAGGCTTGGAGATGATGAGAACAGCATACT 1080
DB 1021 GATGAAAGAGACATCATGCAATCAGGCTTGGAGATGATGAGAACAGCATACT 1080
QY 1081 TACATATTACAGATTCCTTCAGAAATGAAATGAGATTAAGAAATGATATCAAGA 1140
DB 1081 TACATATTACAGATTCCTTCAGAAATGAAATGAGATTAAGAAATGATATCAAGA 1140
QY 1141 TTTGATGTCGCGCATATCTGAAACATTTGCTGAGATGCTGTCGTAATTCGCT 1200
DB 1141 TTTGATGTCGCGCATATCTGAAACATTTGCTGAGATGCTGTCGTAATTCGCT 1200
QY 1201 GAATTAACAAGGATCCGAGCTCATTAATGAGAACTACAGATGAGAAATCTGAGG 1260
DB 1201 GAATTAACAAGGATCCGAGCTCATTAATGAGAACTACAGATGAGAAATCTGAGG 1260
QY 1261 TCATTCGATCTTCAAGATGGAATTAACAGATGAGAACTACAGATGAGAAATCT 1320
DB 1261 TCATTCGATCTTCAAGATGGAATTAACAGATGAGAACTACAGATGAGAAATCT 1320
QY 1321 ACTAAGTATCCAGATTCAGACATATTTGAGAAATTTGATGAGAGATTCATTC 1380
DB 1321 ACTAAGTATCCAGATTCAGACATATTTGAGAAATTTGATGAGAGATTCATTC 1380
QY 1381 TGCGAGTTCAGTCTGATATATGCTATGAAACATGCTGATTAATCATCACAGCA 1440
DB 1381 TGCGAGTTCAGTCTGATATATGCTATGAAACATGCTGATTAATCATCACAGCA 1440
QY 1441 TACCAAGAAATTCGAGCAACAAATACTGTCAGATGAGATGATATCTGCTT 1500
DB 1441 TACCAAGAAATTCGAGCAACAAATACTGTCAGATGAGATGATATCTGCTT 1500
QY 1501 ACTGCTGCTGATCTGACCGAGTGTGCAATGAGATGATGCTTCAAGAGTTCAAT 1560
DB 1501 ACTGCTGCTGATCTGACCGAGTGTGCAATGAGATGATGCTTCAAGAGTTCAAT 1560
QY 1561 ATAGTCTCTCTGAGAGCTGACATGCTATATCTTCACTTCACTACAGAGGCA 1620
DB 1561 ATAGTCTCTCTGAGAGCTGACATGCTATATCTTCACTTCACTACAGAGGCA 1620
QY 1621 CTGACCTCTCTTCAATGCTTCAATGAAATTTGATTTATGACCGGAGCAAAAGAT 1680
DB 1621 CTGACCTCTCTTCAATGCTTCAATGAAATTTGATTTATGACCGGAGCAAAAGAT 1680
QY 1681 CAGATTCGAGCATTCGATGACCGGTCAGAGGCTTCTCTCTGATGAGAGCTGAC 1740
DB 1681 CAGATTCGAGCATTCGATGACCGGTCAGAGGCTTCTCTCTGATGAGAGCTGAC 1740
QY 1741 AGGATGAAGAACTAACAAGGCTGATGAGAGCTTTGCTAAGTCTGAGAGGAG 1800
DB 1741 AGGATGAAGAACTAACAAGGCTGATGAGAGCTTTGCTAAGTCTGAGAGGAG 1800
QY 1801 CTGATTAACCTTGTCTGTCGTCGAGTACAGATGATGCAACAGTCCAGAGGAGA 1860
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[illegible]

RESULT 2	
AAD45849	
ID	AAD45849 standard; cDNA; 2737 BP.

AC	AA045849;	
XX		
DT	27-DEC-2002	(first entry)
XX		
DE	Corn sucrose synthase (Sus3)	cDNA

XX	Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Ssu1;
KX	transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
KM	cellulose; corn; Sus3; gene; ss.
XX	
OS	Zea mays.
XX	
FH	Key
FT	Location/Qualifiers
FT	2..2410
CDS	/*tag= a
	/product= "Corn Sus3 protein"
PV	
XX	MO20267662-A1.
PD	
ED	06-SEP-2002.
XX	
PF	21-FEB-2002; 2002WO-US005137.
XX	
PR	22-FEB-2001; 2001US-0270777P.
XX	
PA	(PTON-) PIONEER HI-BRED INT INC.
XX	
PI	Dhuga KS, Helentjaris TG, Niu X;
DR	WPI: 2002-691625/74.
XX	P-PsDB; AME28493.
PT	New polynucleotide and its encoded sucrose synthase, useful for
PT	modulating the level of sucrose synthase in transgenic plants (e.g. maize
PT	or soybean) to improve stalk length, reduce grain breakage, or improving
PS	plant or grain strength.
XX	
Claim 1;	Page 102-103; 125pp; English.
XX	
CC	The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
CC	constitutive sucrose synthase (Ssu1) and their corresponding nucleic
CC	acids. The polynucleotide, or its encoded protein, is useful for
CC	modulating the level of sucrose synthase in a transgenic plant,
CC	increasing cellulose production in the stalk tissue of a transgenic
CC	plant, or increasing the concentration of cellulose in the tissues of a
CC	seed of a transgenic plant. This is particularly useful in plant (e.g.
CC	maize or soybean) breeding, especially for e.g. improving stalk length in
CC	maize, reducing grain breakage during combining, transport or movement
CC	into storage, or improving plant or grain strength. The present sequence
CC	is corn Sus3 cDNA
XX	
Sequence	2737 BP; 711 A; 672 C; 697 G; 657 T; 0 U; 0 Other;
Query Match	98.4%; Score 2714; DB 6; Length 2737;
Best Local Similarity	99.8% Pred. No. 0;
Matches 2717; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	CCGGGACCGGCTCGAGGACAACCTTCACAGCGCACCGCAAGAGGTCTGCCTCCTC
Db	16 CGGGACCGGCTCGAGGACAACCTTCACAGCGCACCGCAAGAGGTCTGCCTCCTC
QY	CAAATACGTGAACAAGGGAAGGGAATCTTGACACCAGCAACTCTGACAGCGCTCGA
Db	76 CAATACGTGAACAAGGGAAGGGAATCTTGACACCAGCAACTCTGACAGCGCTCGA
QY	156 CGAGTTCAGGAGCTCCGGGCTCCGGCGCTGCCGAGGAGACCTTCTCCAGAGTCTCCG
Db	136 CGAGTTCAGGAGCTCCGGGCTCCGGCGCTGCCGAGGAGACCTTCTCCAGAGTCTCCG
QY	216 CTCGCGCAGAGAAGCGCATCGNCTGCGCGCGCTTCGTGAGCCATCGCGGTGCGCCGCGCC
Db	196 CTCGCGCAGAGAAGCGCATCGNCTGCGCGCGCTTCGTGAGCCATCGCGGTGCGCCGCGCC
QY	276 GGGAGTTGGAGATCACTCCGCGCTCAACGTTTCAAGACTCAGCGTCAAGCACTCAAGT
Db	256 GGGAGTTGGAGATCACTCCGCGCTCAACGTTTCAAGACTCAGCGTCAAGCACTCAAGT
QY	336 CTGGAGTACTCTCGCTTCAAGAGAGAGCTTGTTCAGCGCCAGCAAGTAATCCCTAGCT
Db	315 CTGGAGTACTCTCGCTTCAAGAGAGAGCTTGTTCAGCGCCAGCAAGTAATCCCTAGCT

Db 316 CTGGAGTACCTCCGCTTCAAGAGGAGAGCTGTGACGGCCAGACACATGATCCCTACGT 375
Qy 396 TCTGACCTTGAACCTTCCAGCCGCTCAATGCTCAGTCCCAAGCCCAATGCTATATC 455
Db 376 TCTGACCTTGAACCTTCCAGCCGCTCAATGCTCAGTCCCAAGCCCAATGCTATATC 435
Qy 456 TATGAGAAAGCTGTGAGATCTCAACCGACATTGCTCATCATGTTCCGCAACAG 515
Db 436 TATGAGAAAGCTGTGAGATCTCAACCGACATTGCTCATCATGTTCCGCAACAG 495
Qy 516 GGAATGCTTGAAGCCCTGTGATTTCTCCGTGGCCACCGGACAAAGGGGCAATGTTAT 575
Db 496 GGAATGCTTGAAGCCCTGTGATTTCTCCGTGGCCACCGGACAAAGGGGCAATGTTAT 555
Qy 576 GATGCTTAAGATGATPACAAAGCTGGGAGGCTCAGCTGCTGACCAAGCTGA 635
Db 556 GATGCTTAAGATGATPACAAAGCTGGGAGGCTCAGCTGCTGACCAAGCTGA 615
Qy 636 GAGACACTTGTCAAGAGCTCCCTGCTGACACACATACTACAAATTGCTTAATTTCA 695
Db 616 GAGACACTTGTCAAGAGCTCCCTGCTGACACACATACTACAAATTGCTTAATTTCA 675
Qy 696 AGAGTGGGGCTGAGAAAGGTTGGGTGATACAGACAGACATGTTTGGAAATGATCCA 755
Db 676 AGAGTGGGGCTGAGAAAGGTTGGGTGATACAGACAGACATGTTTGGAAATGATCCA 735
Qy 756 TCTGCTTCTGACATCATTCAGGGCCGACACCATCTACCTTGAAGAAATCTTGGGGAG 815
Db 736 TCTGCTTCTGACATCATTCAGGGCCGACACCATCTACCTTGAAGAAATCTTGGGGAG 795
Qy 816 GATCCCATGATTTTAAAGTTGTGAGTATCCCTCATGAGATCTTGGTCAAGCTTA 875
Db 796 GATCCCATGATTTTAAAGTTGTGAGTATCCCTCATGAGATCTTGGTCAAGCTTA 855
Qy 876 TGTATAGGCTTCCAGACACAGAGACAGATGCTATATCTGACCAAGTCCGTGC 935
Db 856 TGTATAGGCTTCCAGACACAGAGAGCAGATGCTATATCTGACCAAGTCCGTGC 915
Qy 936 ACTGAAATAGATGATGCTCCGTTTAAAGAAACAAAGGCTGATGTTCCCAAAAT 995
Db 916 ACTGAAATAGATGATGCTCCGTTTAAAGAAACAAAGGCTGATGTTCCCAAAAT 975
Qy 996 TCTATGTTTACCTGGCTGATACAGATGCAAAAGGACATCATGACATGACGGCTTGA 1055
Db 976 TCTATGTTTACCTGGCTGATACAGATGCAAAAGGACATCATGACATGACGGCTTGA 1035
Qy 1056 GAGAAATAGAGACACAGCATCTTACATATACAGATGCTCCCTTCAAGAAATGAAATG 1115
Db 1036 GAGAAATAGAGACACAGCATCTTACATATACAGATGCTCCCTTCAAGAAATGAAATG 1095
Qy 1116 GATGCTTAAGAAATGATACAGATGATGAGTGGGCATATCTGAAACATTTGCTGA 1175
Db 1096 GATGCTTAAGAAATGATACAGATGATGAGTGGGCATATCTGAAACATTTGCTGA 1155
Qy 1176 GGATGCTGTGGTGAATTTGCTGAATTAACAAGTACTCCAGACTTATTAATTTGAAA 1235
Db 1156 GGATGCTGTGGTGAATTTGCTGAATTAACAAGTACTCCAGACTTATTAATTTGAAA 1215
Qy 1236 CTACAGATGAGAAATCTTGGCGCTCAATGCTATCTTACAAAGTGGGAATTAACCAAG 1295
Db 1216 CTACAGATGAGAAATCTTGGCGCTCAATGCTATCTTACAAAGTGGGAATTAACCAAG 1275
Qy 1296 CAACATGCTCATGCTGAGAAAGACTAAGTATCCAGATCAGACATATTTTGGAGAA 1355
Db 1276 CAACATGCTCATGCTGAGAAAGACTAAGTATCCAGATCAGACATATTTTGGAGAA 1335
Qy 1356 TTTGATGAGAGATGACATTTTCTCCGTCCAGTTCACTGCTGATATATTTGATGAA 1415
Db 1336 TTTGATGAGAGATGACATTTTCTCCGTCCAGTTCACTGCTGATATATTTGATGAA 1395
Qy 1416 TGTGATTTTATCATCACCAGACATACCAAGAAATGCTGGAACCAAAATACCTTTG 1475

Db 1396 TGTGATTTTATCATCAACAGCATATCAAGAAATTTGCGAAGCAAAAATCTGTTGG 1455
Qy 1476 ACAGATAGAGATCATCTGCTTACCTTGCCTGCTGATCTGACCGAGTTGTCATGGAGAT 1535
Db 1456 ACAGATAGAGATCATCTGCTTACCTTGCCTGCTGATCTGACCGAGTTGTCATGGAGAT 1515
Qy 1536 CGATGCTTGCATCAAAAGTTCAATATATGCTCTCTGAGACTGACATGTCATATCTT 1595
Db 1516 CGATGCTTGCATCAAAAGTTCAATATATGCTCTCTGAGACTGACATGTCATATCTT 1575
Qy 1596 TCCACATACCGAGAGAGCCCAAGGCTCACTCTCTCTCATATGTTCAATGCAAAATTTGAT 1655
Db 1576 TCCACATACCGAGAGAGCCCAAGGCTCACTCTCTCTCATATGTTCAATGCAAAATTTGAT 1635
Qy 1656 TTATGACCCCGAGCAAAACATGAAACAATTGGGCAATCTGATGACCCGTCAAAGCCCAT 1715
Db 1636 TTATGACCCCGAGCAAAACATGAAACAATTGGGCAATCTGATGACCCGTCAAAGCCCAT 1695
Qy 1716 CCTCTTCTCCATGCGCAAGACTCGACAGGCTGAGAAACATTAACGGGCTGTGAAAGCTTT 1775
Db 1696 CCTCTTCTCCATGCGCAAGACTCGACAGGCTGAGAAACATTAACGGGCTGTGAAAGCTTT 1755
Qy 1776 TGTATAGTGGCTTAAAGCTGAGAGGAGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCT 1835
Db 1756 TGTATAGTGGCTTAAAGCTGAGAGGAGCTGTAAACCTTGTGCTGCTGCTGCTGCTGCTGCT 1815
Qy 1836 TGTCAACAAGTCCAAAGACAGAGAAAGATGCGGAGATAGAGAAATGATGATGATCTAT 1895
Db 1816 TGTCAACAAGTCCAAAGACAGAGAAAGATGCGGAGATAGAGAAATGATGATGATCTAT 1875
Qy 1896 CAAGACCAACAATTGTTGGGGAGTCCGCTGATCTCTGCTCCAGACAAACAGGGCCCG 1955
Db 1876 CAAGACCAACAATTGTTGGGGAGTCCGCTGATCTCTGCTCCAGACAAACAGGGCCCG 1935
Qy 1956 TAAAGGAGGCTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 2015
Db 1936 TAAAGGAGGCTTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCT 1995
Qy 2016 GTATGAAAGCTTGGCTCTCAACCTGCTGTAAGGCAATGACCTGTGGGCTTCTACTTTGCG 2075
Db 1996 GTATGAAAGCTTGGCTCTCAACCTGCTGTAAGGCAATGACCTGTGGGCTTCTACTTTGCG 2055
Qy 2076 GACGCTCATGAGAGTCAAGCTGATGATATAGAGATGAGATGAGATGAGATGAGATGAGATGAG 2135
Db 2056 GACGCTCATGAGAGTCAAGCTGATGATATAGAGATGAGATGAGATGAGATGAGATGAGATGAG 2115
Qy 2136 CCGGTACACCCCGAAGAGGGGCTTAAATCTGATGCGCACTTCTTCAACGGTGAAGCA 2195
Db 2116 CCGGTACACCCCGAAGAGGGGCTTAAATCTGATGCGCACTTCTTCAACGGTGAAGCA 2175
Qy 2196 AGACCAATCATCTGGTGAATATATCTGAGCAAGGCTGCAAGCCATATACAGAAATGTA 2255
Db 2176 AGACCAATCATCTGGTGAATATATCTGAGCAAGGCTGCAAGCCATATACAGAAATGTA 2235
Qy 2256 CACATGAGAAATATCTCAAGAGGTTGATATGACATCTGCGGGGCTTACCGTTTCTGAAA 2315
Db 2236 CACATGAGAAATATCTCAAGAGGTTGATATGACATCTGCGGGGCTTACCGTTTCTGAAA 2295
Qy 2316 GTAGTGTGAGAGCTGAGAGGCTGAGAGCAAGGCGCTACCTTGAATGTTTACATACT 2375
Db 2296 GTAGTGTGAGAGCTGAGAGGCTGAGAGCAAGGCGCTACCTTGAATGTTTACATACT 2355
Qy 2376 GAAATGTCGCGAGCTGGCGAAGACCTGTGCGGCTTGCATTTGACCAACCGCAGTACCTTGC 2435
Db 2356 GAAATGTCGCGAGCTGGCGAAGACCTGTGCGGCTTGCATTTGACCAACCGCAGTACCTTGC 2415
Qy 2436 GAACTGTGAGCTGAGTGAACCTTGTGTAACAAGCTGAAACCTGAAGCACTTGAATTT 2495
Db 2416 GAACTGTGAGCTGAGTGAACCTTGTGTAACAAGCTGAAACCTGAAGCACTTGAATTT 2475
Qy 2496 AGGCGCGGAGACGCTAGGCAATTAATGCTGCGGAGCTGAACCTGTTTATTAATGTA 2555
Db 2476 AGGCGCGGAGACGCTAGGCAATTAATGCTGCGGAGCTGAACCTGTTTATTAATGTA 2535

QY		2556	AATTAAGGCGCATATAACAAATTCTAGAAGCAGGTGGTGTGGCACTGTGTGGTTCCGTAC	26175
Dd		2536	C P A T A G C A T A B C A A A T T A C T A G C A G T G G T G C A T G T G T G T T A C	25939
QY		2616	TGTTTACTGTATTTATGTTCACAGCTTCGGCTGCACAATTTCTTGTCGACGAAGCGACGAC	26757
Dd		2596	TGTTTACTGTATTTATGTTCACAGCTTCGGCTGCACAATTTCTTGTCGACGAAGCGACGAC	26555
QY		2676	TGTTGAAGTGTGTAATAAATACATCATATTCTGTGACCTGTGAAAAA	27358
Dd		2656	TGGTGAAGTGTGTAATAAATACATCATATTCTGTGACCTGTGAAAAA	27155
QY		2736	AAAAAAAAAAGGCGCGCGCGC	2757
Dd		2716	AAAAAAAAAAGGCGCGCGCGC	2737

RESULT 3
ADA69581 ID ADA69581 standard; DNA; 2412 BP.
ADA69581 AC ADA69581;
AD A69581; AC
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 2904.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.
XX
OS Oryza sativa.
XX
PN MO2003000898-AI.
XX
XX 03-JAN-2003.
PD
PF 22-JUN-2001; 2001WO-IB001105.
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

Claim 6; SEQ ID NO 2904; 899bp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to CC expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

SEQ Sequence 2412 BP; 633 A; 573 C; 593 G; 600 T; 0 U; 7 Other;

Query March 65.6%; Score 1809.6; DB 7; Length 2412;
Near Local Similarity 84.9%; Pred. Mo. 3;
Matches 2062; Conservative 6; Mismatches 340; Indels 22; Gaps 3;

1 ATGTCGCCCGCGAAGCTGMAACCGAACGCGACATCCGGACCGCGTCCAGACACCCTC 60

Db	1	ATGTGGGGCCCGAAGCTTGAACCGGACCCCGAGCATCCGGACCGCGCTCGAGGACACCTTC	60
Qy	61	CACGCGACCGCAACGAGCTCGTGCGCCCTCTCTCCAAATGACGTGAACAAAGGGAAAGGCG	120
Db	61	CAGCCCGACCGCAACGAGCTCGTGCGCCCTCTCTCCAAATGACGTGAACCAAGGGAAAGGCG	120
Qy	121	ATCTGCAAGCTCGACCAATCTTGACGCGCTCGAGAGGTCCAGGGCTCCGGGCTCCG	180
Db	121	ATCTGCAAGCTCGACCAATCTTGAGAGGCTCGACAGAGGTCCAGAGCTCCGGCGGCGCG	180
Qy	181	GCGCTGCGCGAGGAGACCTTCTCTGAGAGTCTCCGCTCCGCGCGAGAGGAGATGCTGCTG	240
Db	181	GCGCTGCTCGAGAGGCGCCCTTCTCTGAGAGTCTCCGAGTCCGCGTCCGCGAGAGGCGATGCTG	240
Qy	241	CCGCGCTTCGGGCGCATCGCGAGTCCGCGCGCGCCGAGAGTTCGAGAGTACGTCGCGCTC	300
Db	241	CCGCGCTTCTGAGGAGATCGCGAGTCCGCGCGCGCGGAGAGGAGTTCGAGAGTACGTCGCG	300
Qy	301	AACGTTACAGAGCTCAAGCTTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAG	360
Db	301	AACGTGACAGAGCTCAAGCTTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAG	360
Qy	361	GAGTTGTGCAAGCGCCGACCAATGATATCCCTAGTTCCTGAGCTTGAATTCGACCGCTTC	420
Db	361	GAGCTGTGCAAGCGCCAGTCAACAGATCCGTATACCTTGAGCTTGAATTTGAGCCATTC	420
Qy	421	AATGTTCAGTCCGACCGCCAAATCCGATCATCTATTGGAAGAGGTGTCAGATTCCTC	480
Db	421	AATGCTGTGTCAGCGCCAAATCCGATCATCATTAATGGAAGATGGGTCAGATTCCTC	480
Qy	481	AACCGACACTTGTCTCAATCATGTTTCGCAAGCGGATTCCTGAGAGCCCTGTGGAT	540
Db	481	AACGAGCACTTGTCTTGCATCATGTTTCGGAACAAAGATTCGCTGAGAGCCCTCTTGAT	540
Qy	541	TTCCTCCGTGGCCACCGGCAAAAGGGCATGTTATGATGCTTAATGATTAACAAAGC	600
Db	541	TTCCTGTGTGGGCAATCGGCAATAGGATCATG-----ATACAGGT	580
Qy	601	TGGGAGAGGCTTC-AGTCTGAGC-TGACAAAGCTGAGAGCACTTGCAAGCTCCCTG	658
Db	581	CTGGAAAGACTTCAAGTCTGTGCTTGACAAAGCTGAGAGCACTTGTGCAAACTCCCGAG	640
Qy	659	CTGACACACCACTCAACAAATTTGCTTAAATTTCAAGAGTGGGCGCTGAGAAAGGT	718
Db	641	CTGACACCACTACTCAAGTTCGATATPAAATTTCAAGATGGGGAATGGAGAAGGCT	700
Qy	719	GGGGTGATACAGACGAGCATGTTTGGAAATGATCCATCTCCTTCTAGACATCATTCAGG	778
Db	701	GGGGCGACACAGCTGAGTATGCTTGGAGATGATACATCTCCTTCTGATGTGCTTCAAG	760
Qy	779	CGCAGAGCCCATTAACCTAGAGAAATTTCTTGGGAGAGATCCCGATGATTTTAAAGT	838
Db	761	CGCTGATCCATCTACTCTTGAGACGTTCTTGGAAAGATCCCATGATCTTTATATGCG	820
Qy	839	TTGTGTATCCCTCATAGATACCTTGGTCAAGCTAATGATTAAGGCTTCGACAGCAG	898
Db	821	TCTGATGTCTCTCATAGATATTTTGGCCAAAGCAATGTTTGGGCTTACCAATACTG	880
Qy	899	GAGAGCAGATGCTATATTACTGACCAAGTCCGTGCACTGAAATGAGATGATGTTCTCC	958
Db	881	GAGGCGAGATTTGCTATATTACTGACCAAGTCCGTGCACTGAAATGAGATGATGTTCTTA	940
Qy	959	GTTTAAAGAAACAAGGCTGATGTTTCCCAAGATTTCTCATGTGTTCTCGGCTGATAC	1018
Db	941	GCTTAAAGAAACAAGGCTTGAATTTTACCCCTTAAATTTCTTATGTTTACTGGCTGATAC	1000
Qy	1019	CAGATGCAAAAGAAATCATGCAATCAAGCGCTTGAGAGATTAAGTGAACAACAGATA	1078
Db	1001	CAGAGCAAAAGGAAATCATGCAATCAGCGCTTGAGAGATTAAGTGGACACAACATA	1060
Qy	1079	CTTACATATTCAGAGTCCCTTCGAATGAAATGGATCTTAAGAAATGATATTCAA	1138

QY 1 ATGCTGCCCCGAGCTGAACCGCAACGCGAGCATCCGAGCCGCTCGAGGACACCTTC 60
DB 1 ATGCGAAACCTTAGCTCACTAGGGTTCTAAGCAAGGATGCGCTGCAAGACAGCTT 60
QY 61 CACGCGACCGCAACGAGCTGCTGCGCTTCCTTCGAAGTACGTGAACAAAGGAAAGGC 120
DB 61 TCGGTCAACCGCAACGAGCTGCTGCTTCCTTCGAAGTACGTGAACAAAGGAAAGGC 120
QY 121 ATCTGAGCGGACCACTCTCGAGCGGCTCGACGAGTCCAGGGCTCCGAGGCTCCG 180
DB 121 ATCTGAGCGGACCACTCTCGAGCGGCTCGACGAGTCCAGGGCTCCGAGGCTCCG 180
QY 181 GCG-----CTGCGCGAGGAGACCTTCCTGACGTCCTCGCTCCGCGGAGGAGGAGC 224
DB 181 AAGAAAGTCTCTCTGAGTCTCTTTGAGAGAGTCTTAAATCAGCAATGGAAGCTATA 240
QY 235 GTCCTGCGGCTGCTGCGCATCGCGTGCAGCGCGCGCGCGCGAGTTTGGAGTACGTC 294
DB 241 GTGTACACCTTTGTGTGCGTTAGCGGTAGACCAAGACCTGGTGTGGAATATGTT 300
QY 295 CGCGTCAAGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 354
DB 301 CGGTAAAGTCTTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 360
QY 355 AAGGAGAGCTTTCAGCGCGCAACATGATCCCTACGTTCTCGAGCTTGACTTCGAG 414
DB 361 AAGAAAGTCTCTGAGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 420
QY 415 CGGTAAAGTCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 474
DB 421 CCTTTAAGCAACGTCAGCTCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCT 480
QY 475 TTTCTCAACCGAAGCTGCTCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 534
DB 481 TTTCTCAACCGAAGCTGCTCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 540
QY 535 TTTGATTTCTCTGCTGCGCAACGCGCAACGCGCAACGCGCAACGCGCAACGCGCAAC 594
DB 541 CTGATTTCTCTGAGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 600
QY 595 CAAGCTTGGAGAGCTTCAAGCTCTGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 654
DB 601 CAAGCTTGGAGAGCTTCAAGCTCTGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 660
QY 655 CTGCTCAACCACTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 714
DB 661 TCAACAAAGCTCTGCTCTGAGTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG 720
QY 715 GATTGCGGCTGATCAAGCAAGCATGTTTGGAAATGATCCATCTCTCAAGCATCAT 774
DB 721 GATGCGGAGATCAAGCAAGCATGTTTGGAAATGATCCATCTCTCAAGCATCAT 780
QY 775 CAGCGCGCAAGCTTACCTTACAGAAATCTTGGAGAGATCCCATGATTTTAAAC 834
DB 781 CAGCGCTCTGATCTGCTCTTGAAGAGTCTTGGAGATGATCAAGATGTTTAAAC 840
QY 835 GTTGTGTGATCTCTCTCAAGTACTTGTGAGTAACTGATGATGATGATGATGATGAT 894
DB 841 GTTGTGTGATCTCTCTCAAGTACTTGTGAGTAACTGATGATGATGATGATGATGAT 900
QY 895 AAGAGAGAGATCTCTATATCTGAGCAAGCTCTGAGCAAGATGAGATGATGAT 954
DB 901 AAGAGAGAGATCTCTATATCTGAGCAAGCTCTGAGCAAGATGAGATGATGATGAT 960
QY 955 CTCTGTTTAAAGAAAGAGGCTGATGTTTCCCAAGATGATGATGATGATGATGATGAT 1014
DB 961 TTTGAGATTAAGAGAGAGGCTGATGTTTCCCAAGATGATGATGATGATGATGATGAT 1020
QY 1015 ATACCAATGCAAGAGAAATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAG 1074
DB 1021 ATACCAATGCAAGAGAAATCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAG 1080
QY 1075 CATACTTACATATTACAGATGCTCTCTCAAGAAATGAGAAATGAGAAATGAGATA 1134

DB 1081 CATACTTACATATTACAGATGCTCTCTCAAGAAATGAGAAATGAGAAATGAGAAAT 1140
QY 1135 TCAAGATTTGATGTTGCGCATATCTGAAAGAAATTTGCTGAGATGCTGCTGAGAAAT 1194
DB 1141 TCAAGATTTGATGTTGCGCATATCTGAAAGAAATTTGCTGAGATGCTGCTGAGAAAT 1200
QY 1195 GCTGTGAATTAAGAGTATCCAGACTTCATATTGGAATCTCAAGTATGGAATCTT 1254
DB 1201 GCTGTGAATTAAGAGTATCCAGACTTCATATTGGAATCTCAAGTATGGAATCTT 1260
QY 1255 GTGCGCTGATGCTATCTTCAAGATGGAATTAACCAAGTCAACATGCTCATCTG 1314
DB 1261 GTTGCATCTGTTATGAGCAATGATGAGTGTATACCAAGTATCTTATGCAATGCTTTG 1320
QY 1315 GAAAGACTTAAGTATCCAGATTCAGATATTTTGAAGAAATTTGATGAGAAATCCAT 1374
DB 1321 GAGAAAGCAAGATCCAGATTCAGATATTTTGAAGAAATTTGATGAGAAATCCAT 1380
QY 1375 TTTCTGCGAGTCACTGCTGATATATTTGCTATGAAAGATGCTGATTTATCATCACC 1434
DB 1381 TTTCTGCTCAATTCAGCTGATCTTATGCAATGAAACAGAGATTTCAATCATCA 1440
QY 1435 AGCAATACCAAGAAATTTGCTGAAAGCAAAATTACTGTTGAGCAATGAGATCATACT 1494
DB 1441 AGCAATACCAAGAAATTTGCTGAAAGCAAAATTACTGTTGAGCAATGAGATCATACT 1500
QY 1495 GCTTTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1554
DB 1501 GCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
QY 1555 TTTCAATTAAGTCTCTCTGAGCTGATGATGCTATATCTTCAACATACCGAGAGGCC 1614
DB 1561 TTTCAATTAAGTCTCTCTGAGCTGATGATGCTATATCTTCAACATACCGAGAGGCC 1620
QY 1615 AAGGACTCACTCTCTTCAATGTTCAATGCAAAATTTGATTTAGACCGGACCAAAAC 1674
DB 1621 AAGGACTCACTCTCTTCAATGTTCAATGCAAAATTTGATTTAGACCGGACCAAAAC 1680
QY 1675 GATGAACATTTGGGCACTTGAATGACCGGTCAAGGCCATCTCTTCCATGAGCAAG 1734
DB 1681 GATGAACATTTGGGCACTTGAATGACCGGTCAAGGCCATCTCTTCCATGAGCAAG 1740
QY 1735 CTGACAGGCTGAGAAATTAAGAGGCTGCTGCAAGCTTGTGATGAGCTCAAGCTG 1794
DB 1741 CTGACAGGCTGAGAAATTAAGAGGCTGCTGCAAGCTTGTGATGAGCTCAAGCTG 1800
QY 1795 AAGGAGCTGTTAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1854
DB 1801 AAGGAGCTGTTAACTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
QY 1855 AAGGAGAGATCGCGGATTAAGAAATGATGATGATGATGATGATGATGATGATGAT 1914
DB 1861 AAGGAGAGATCGCGGATTAAGAAATGATGATGATGATGATGATGATGATGATGAT 1920
QY 1915 GAGGAGTCTGCTGATCTGCTGCAAGAAAGAGGCTGCTGCAAGGCTGCTGATGCT 1974
DB 1921 GAGGAGTCTGCTGATCTGCTGCAAGAAAGAGGCTGCTGCAAGGCTGCTGATGCT 1980
QY 1975 TACATGCTGATATCCATGCTGCTTCTGATACCGGCTGATGAAAGCTTGGCTTC 2034
DB 1981 TACATGCTGATATCCATGCTGCTTCTGATACCGGCTGATGAAAGCTTGGCTTC 2040
QY 2035 ACGCTGTTGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2094
DB 2041 ACGCTGTTGAGGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
QY 2095 GCTGAGATCATGAGCATGCGTCTGCGGCTTCCACATGACCCGATACCCCGAAGC 2154
DB 2101 GCGAGATCATGAGCATGCGGCTCTCGGCTTCCACATGAGCCGATACCCCGAAGC 2160
QY 2155 GCTGTTATCTGATGCGGCTCTTCTGACCGGCTGCAAGCAAGCCGATCATCTGCGG 2214

QY 1204 TTACAAAGTACTCCAGACTTTCATTAATGGAACTACAGATGATGAAATCTTGCGCTCA 1263
 DB 1171 TTGCAAGGATGTAACCAATCTCATCTATGCGACTACAGATGATGAAATCTTGCTTCT 1230
 QY 1264 TTGCTATCTTACAGATGGGAATTAACCGATGCAAAATGCTCATCTCGGAAAGACT 1323
 DB 1231 TTGTTAGCTAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1290
 QY 1324 AAGTATCCAGATTCAGACATTAATTTGGAAATTTGGATGAGAAATCAATTTCTCTGC 1383
 DB 1291 AAGTATCCAGATTCAGACATTAATTTGGAAATTTGGATGAGAAATCAATTTCTCTGC 1350
 QY 1384 CAGTTCATCTGATTAATTAATTTGGATGAGAAATCAATTTCTCTGC 1443
 DB 1351 CAGTTCATCTGATTAATTAATTTGGATGAGAAATCAATTTCTCTGC 1410
 QY 1444 CAGAAATTTGCTGAGAGCAAAATCTGTTGACAGATGAGATGATCTACTCTTACT 1503
 DB 1411 CAGAAATTTGCTGAGAGCAAAATCTGTTGACAGATGAGATGATCTACTCTTACT 1470
 QY 1504 CTGCGCTGATCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
 DB 1471 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1530
 QY 1564 GTCTCTCTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
 DB 1531 GTCTCTCTGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
 QY 1624 ACCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 DB 1591 ACCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1650
 QY 1684 ATGCGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
 DB 1651 ATGCGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1710
 QY 1744 GTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
 DB 1711 GTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1770
 QY 1804 GTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
 DB 1771 GTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1830
 QY 1864 ATGCGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
 DB 1831 ATGCGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1890
 QY 1924 CGCTGATCTCTGCGGAGCAAAACAGAGCCGTTACCGGAGCTTATGCTCATGCTGCT 1983
 DB 1891 AGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1950
 QY 1984 GATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
 DB 1951 GATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2010
 QY 2044 GAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
 DB 2011 GAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2070
 QY 2104 ATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
 DB 2071 ATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2130
 QY 2164 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
 DB 2131 ACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2190
 QY 2224 GAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
 DB 2191 GAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2250
 QY 2284 ATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2343

DB 2251 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2310
 QY 2344 ACAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2403
 DB 2311 ACAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2370
 QY 2404 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2417
 DB 2371 CCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2384
 RESULT 6
 AA080005
 ID AA080005 standard; cDNA; 2563 BP.
 XX
 AC AA080005;
 XX
 XX 25-MAR-2003 (revised)
 DT 05-AUG-1995 (first entry)
 XX
 DE Sucrose-synthase.
 XX
 KM Sucrose-synthase; sugarbeet; sucrose; crop improvement; ss.
 XX
 XX Beta vulgaris.
 OS
 XX
 FH Key location/Qualifiers
 FT CDS 3..2303
 FT /*tag= a
 XX
 XX DE4317596-A1.
 PN
 XX
 XX 01-DEC-1994.
 PD
 XX
 PF 24-MAY-1993; 93DE-04317596.
 XX
 XX 24-MAY-1993; 93DE-04317596.
 PR
 XX
 PA (SCHD) SCHERING AG.
 XX
 PI Heese H, Mueller-Roeber B;
 XX
 XX WPI; 1995-007485/02.
 DR P-PSDB; AAR66222.
 XX
 PT New DNA sequences encoding sucrose regulating enzymes of sugar beet - for
 PT regulating sucrose concn. specifically ADP glucose pyrophosphorylase,
 PT sucrose phosphate synthase and sucrose synthase.
 PS Claim 4; Page 72-78; 78pp; German.
 XX
 CC cDNA encoding sugarbeet sucrose-synthase was isolated from a cDNA library
 CC in phage lambda Zap. Alterations to the coding sequence may be designed
 CC to by-pass the plant's regulatory mechanisms, allowing manipulation of
 CC the sucrose content of sugarbeet. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 SQ Sequence 2563 BP; 736 A; 480 C; 602 G; 745 T; 0 U; 0 Other;
 Query Match 42.7%; Score 1177.8; DB 2; Length 2563;
 Best Local Similarity 70.9%; Pred. No. 7e-256;
 Matches 1592; Conservative 0; Mismatches 647; Indels 6; Gaps 2;
 QY 184 CTGCGGAGGAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 243
 DB 21 CTGCGGAGGAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 80
 QY 244 CCGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 303
 DB 81 CCGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 140
 QY 304 GTTACAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 363

141 GTCTCCGAATGATGAGAGAGCTAAGTGTGTAGATATCTCCATTTCAAGAGAA 200
QY 364 CTGTGAGAGGCGAGCAATGATCCCTAGCTTTCAGAGCTTGTGAGCCCTTCAAT 423
Db 201 CTGTGATGGAAGGCTGATGACCACTATGTGCTGAGCTTGTGAGCCCTTTAAT 260
QY 424 GTCTCAATCCAGGCGCAATCGGTCAATGCTTATGAGAAAGGCTGTGAGCTTCAAC 483
Db 261 GAATCAATTCAGCTCCAGCTCCCTTTCATTAATGATGATGATGATGATGATGATGAT 320
QY 484 CGACACTTGTCTCAATCATGTTCCGCAAGAGATGCTTGAAGCCCTGTGATTTTC 543
Db 321 CGGAGCTGTGATGAGAGATGTTCTGCAAGAAATGCTTGAAGCCGTGATTTTAT 380
QY 544 CTCCGTGCGCAAGGCGCAAGAGGCTGTTATGATGCTTATGATGATGATGATGATGAT 603
Db 381 CTGAGAGGCAAAACATTAAGAGATGCTCATGATGATGATGATGATGATGATGATGAT 440
QY 604 GGGAGGCTTCACTGTGCTGAGCAAGAGCTGAGAGCACTGTCAAGCTCCGTGAC 663
Db 441 CAGGCTTCAAGCTGATGATGCTAAGCTGAGATTTCTTATCAAACTTCCAGCAAT 500
QY 664 ACACCACTCACAATTTGCTTATTAATTTCAAGAGTGGGCTGAGAGAGGTTGGGCT 723
Db 501 AACTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 560
QY 724 GATACAGAGAGCAATGTTTGAATGATGATGATGATGATGATGATGATGATGATGAT 783
Db 561 GATCTGCTGAAGGCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
QY 784 GACCATCTACCTGAGAAATCTTGGGAGAGATCCCATGATTTTAAAGCTTGTG 843
Db 621 GATCGCTTCAATGAGCAATTTCTGAGAACTTCCCATGATGATGATGATGATGATGAT 680
QY 844 GTATCCCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
Db 681 TGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
QY 904 CAGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
Db 741 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
QY 964 AAGAAAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
Db 801 AAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
QY 1024 GCAAAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
Db 861 GCTAAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 920
QY 1084 ATATTAAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1143
Db 921 ATCTGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 980
QY 1144 GATGATGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1203
Db 981 GATGATGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
QY 1204 TTAAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1263
Db 1041 TTGAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1100
QY 1264 TTGAGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
Db 1101 TTATGATGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1160
QY 1324 AAGTATGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
Db 1161 AAGTATGAGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1220
QY 1384 CAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1443

1221 CAATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1280
QY 1444 CAAGAAATGCTGAG 1503
Db 1281 CAAGAGATGATGAG 1340
QY 1504 CTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
Db 1341 TTTCGGGAG 1400
QY 1564 GTCTCTGATGAG 1620
Db 1401 GTCTGAG 1460
QY 1621 CTCACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1521 CACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1580
QY 1741 AGGAG 1800
Db 1581 CAGATGAG 1640
QY 1801 CTGATGAG 1860
Db 1641 CTGAG 1700
QY 1861 GAGATGAG 1920
Db 1701 GAATGAG 1760
QY 1921 TTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1761 TTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
QY 1981 GCTGATGAG 2040
Db 1821 TGTGAG 1880
QY 2041 GTTGAAG 1940
Db 1881 GTTGAAG 2000
QY 2101 ATCATGAG 2160
Db 1941 ATTAAG 2000
QY 2161 AATGATGAG 2220
Db 2001 AATGATGAG 2057
QY 2221 TCTGAG 2280
Db 2058 TCTGAG 2117
QY 2281 TTGATGAG 2340
Db 2118 TTATGAG 2177
QY 2341 GAG 2400
Db 2178 GAG 2237
QY 2401 GTGAG 2425
Db 2238 GTTCCGAG 2262

RESULT 7
AADA5852

ID AAD45852 standard; cDNA; 2908 BP.
 XX AC AAD45852;
 XX DT 27-DEC-2002 (first entry)
 XX DE Corn sucrose synthase (Sus1) cDNA.
 XX XX Sucrose synthase; shrunken-1; Sh1; constitutive sucrose synthase; Sus1;
 XX KW transgenic plant; plant breeding; grain breakage; grain strength; enzyme;
 XX OS cellulose; corn; chromosome 9; gene; ss.
 XX XX Zea mays.
 XX XX Key Location/Qualifiers
 XX FH 28.2478
 XX FT CDS /*tag= a
 XX PT /product= "Corn Sus1 protein"
 XX XX WO200267662-A1.
 XX PN 06-SEP-2002.
 XX PD 21-FEB-2002; 2002WO-US005137.
 XX PF 22-FEB-2001; 2001US-0270777P.
 XX PR (PION-) PIONEER HI-BRED INT INC.
 XX XX Drugga KS, Helentjaris TG, Niu X;
 XX XX WPI; 2002-691625/74.
 XX DR P-PSDB; AAE28501.
 XX XX New polynucleotide and its encoded sucrose synthase, useful for
 XX PT modulating the level of sucrose synthase in transgenic plants (e.g. maize
 XX PT or soybean) to improve stalk length, reduce grain breakage, or improving
 XX FT plant or grain strength.
 XX XX Example 10; Page 110-114; 125pp; English.
 XX CC The invention relates to two sucrose synthases, shrunken-1 (Sh1) and
 XX CC constitutive sucrose synthase (Sus1) and their corresponding nucleic
 XX CC acids. The polynucleotide, or its encoded protein, is useful for
 XX CC modulating the level of sucrose synthase in a transgenic plant,
 XX CC increasing cellulose production in the stalk tissue of a transgenic
 XX CC plant, or increasing the concentration of cellulose in the tissues of a
 XX CC seed of a transgenic plant. This is particularly useful in plant (e.g.
 XX CC maize or soybean) breeding, especially for e.g. improving stalk length in
 XX CC maize, reducing grain breakage during combining, transport or movement
 XX CC into storage, or improving plant or grain strength. The present sequence
 XX CC is corn Sus1 cDNA. Corn Sus1 gene is located at chromosome 9
 XX SQ Sequence 2908 BP; 623 A; 815 C; 808 G; 662 T; 0 U; 0 Other;
 XX
 Query Match 42.6%; Score 1173.4; DB 6; Length 2908;
 Best Local Similarity 68.3%; Pred. No. 7.2e-255;
 Matches 1656; Conservative 0; Mismatches 761; Indels 6; Gaps 2;
 6 TCCTCCGAGCTGACCGCAACGCGAGCATCCGGACCGCTCGAGACACACCTCCACGC 65
 45 TGACCTGTCTGAGCGGCTCCACAGGTGACGGAGCGCATGCGGACTCATCTCTGC 104
 66 GCACCGCAACGAGCTCGTCCCTCTCTCCAGTACGTGAACAAAGGGAGGGATCCCT 125
 135 CCACCCCAATGAGCTTGTGCGGCTCTTCCAGGCTGMAAAACCTTGGAAAGGGTATGCT 164
 126 GCAGCGGACCAATCTCTGACGCGCTCGAC---GAGTCCAGGCTCCGGGTCCGGC 182
 165 GCAGCGGACCAATGATCATTTGCCAGGTACAAATGCGATCCCTGAGGCTGAGCGCGAGAA 224
 183 GCTCGCGAGGGACCTTCTCTGACGCTCCCTCCGCTCCGCGCAGGAGCGGATCGTCTGCC 242

Db 225 GCTCAAGGATGGTGTCTTTTGGAGATGTCTCTGAGGCGAGCTCAGAGGCGGATGTCTATCCC 284
 Qy 243 GCCGTTGCTGGCCATCGCGGTGCGCGCGCGCGCGGAGTTTGGGAGTAGTCTCGCGCTCAA 302
 Db 285 CCCATGGGTGCACTTGGCCATCCGGCCCTAGGGCTGTGTCTGGGAGTATGTGAGGGTCAA 344
 Qy 303 CGTTCACGAGCTCAGCGTCCGAGCAGCTCAGCTCTCGAGTAGTACCTCCGCTTCAAGGAGGA 362
 Db 345 CGTCACTGAGCTCGCTGTGTGAGGAGCTGAGAGTCTCTGAGTAGTCTCAGTTCAGGAACA 404
 Qy 363 GCTTGTGCAAGCGCCAGCAATGATCCCTACGTTCTCGAGCTTGAGTCTGAGCGCTTCAA 422
 Db 405 GCTTGTGGAAGAGGCGCCCAACAACACTTGTCTTCTGAGCTGAGTCTTGTGAGCCATTCAA 464
 Qy 423 TGTCTCAGTCCCAAGCGCCCAATCGGTTCATCATCTATTGGAAAGGTTGTCAGTTCCTCAA 482
 Db 465 TGCCTCTCTCCCGCGCTCTCTCTGTCAAAGTCCATTTGGCAATGGCGTGCAGTTCCTCAA 524
 Qy 483 CCGACACTTGTCTCAATCATGTTCGCAACAGGGATTCCTTGGAGCCCTGTGTGATTT 542
 Db 525 CAGGACACTGTCTCATCAAGCTCTTCCATGCAAGGAGAGCATGTACCCCTTGTCTCACTT 584
 Qy 543 CTTCCGTGGCCACCGCCACAGGGGCAATGTTATGATGCTTTATGATGATAGATATCAAGCTT 602
 Db 585 CTTTCGCGCCCAACAATAAGGGATGACCATGATGTTGAACGACAGAAATCCGAGTCT 644
 Qy 603 GGGGAGGCTTCAGTCTGTCTGACCAAGCTGAGGAGCACTTGTCAAAGCTCCCTCTGCTGA 662
 Db 645 CAGTGTCTGCAAGGTGCGCTGAGGAAGCTGAGGAGCACCTGTCCACCTCAAGCTGA 704
 Qy 663 CACACCACTACTCAAAATTTGCTTATAAATTTCAAGAGTGGGGCTGGAGAAAGTTGGGG 722
 Db 705 TACCCCACTCTGAAATTTCAACACAGGTTCCAGGAATTTGGTCTGGAGAAAGTTGGGG 764
 Qy 723 TGATACAGCAGCAGATGTTTTTGAATGATCTCTCTCTCTAGACATCATTCAGGCGCC 782
 Db 765 TGATGCGCTAAGCGTGCACAGGAGACTTCCACCTCTCTCTGAGCTCTCTGAGGCGCCC 824
 Qy 783 AGACCACTACTCCCTAGAGAAATTTCTGGGAGGATCCCATGATTTTAAAGTTGTGT 842
 Db 825 AGATCGCTCACCTCGAGAGATTCCTTGAACGATCCCGCTGTTCAATGTCTGAT 884
 Qy 843 GGTATCCCTCATGGATATCTTGGTCAAGCTAATGATTTAGGCTTGCACACACAGAGG 902
 Db 885 CCTCTCCCTCATGGTTACTTCTGCTCAAGTATGCTTGGGTTACCTGACACCGGAGG 944
 Qy 903 ACAGTCTCTATATATCTGGAACCAAGTCTGCTGACATAGAAATGAGATGTTTCCGTTT 962
 Db 945 CCAGGTTGTCTATCATCTTGGATCAAGTGGCGCTATGGAGAACGAAATGCTGCTGAGAT 1004
 Qy 963 AAAGAAACAGGCTTGTGATGTTTCCCAAGATTTCTCATGTTTACTCGGCTGATACCGA 1022
 Db 1005 CAAAGCAGTGTGTCTTGAACATACGCGCGAAGATTCCTTATGTCACAGGTTGTCCTCTGA 1064
 Qy 1023 TGCAAAAGGAACATCATGCAATCAGCGGCTTGAGAGATTTAGTGAACACACAGCANACTTA 1082
 Db 1065 TGCACTGCGCACCACTGTGGCCAGCGCTTGAGAGGTCCTTGGCACCGCAGCACTGCCA 1124
 Qy 1083 CATATTACGAGTTCCCTTCAGAAATGAATGGGATCTTAAAGAAATGGATATCAAGATT 1142
 Db 1125 TATCTCTCGGTGCCATTCAGAAACGGAATCGTTTCGCAAGTGGATCTCGCGATT 1184
 Qy 1143 TGATGTGCGCCATATCTGMAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGCTGA 1202
 Db 1185 TGAAGTCTGCGCTACTGAGACTTACATGATGAGCTGCGCGCATGAGATTTCTTGAGA 1244
 Qy 1203 ATTACAGGTACTTCCAGACTTCTAATTTGAAACTACAGTATGATGGAATTTGTGGGCTC 1262
 Db 1245 GCTTCAGGCCAATCTCTGACCTGATCATCGGAACCTACAGTACGAGAAACCTTGTGGGTG 1304
 Qy 1263 ATTGCTATCTTCAAGATGGGAATTCCTCAGTGGCAATTTGCTCATCTCTGGAAGAC 1322
 Db 1305 TTTGCTCGCCCAAGATGGGTGTACTCTACTGTACCATTTGCCATTCGCTTGAAGAAC 1364

1323	QY	TAAGTATCCAGATTCAGACATA	TTTTGGAGAATTTGGATGGAAGTACCAATTTCTCTG	1381
1365	DB	TAAGTATCCCTAACTCCGACCT	CTACTGGAAGAAGTTGAGGATCACTTACCACCTTCTCGTG	1424
1383	QY	CCAGTTTCACTGCTGATATAAT	TGCTATGACAAATGCTGATTTTATCATCACACGACACATA	1442
1425	DB	CCAGTTTCAACCATGACTTGAT	TGCAATGAAACATGCGGACTTCTATCATCACCAGTACCTT	1484
1443	QY	CCAAGAAATTTGTCGAAGCAAAA	TAATCTGTTGGACAGTATGAGAGTCAATCTCCCTTTTAC	1502
1485	DB	CCAAGAGATCGCCGGAAACAAG	GACACCGTCGGCAGTACAGTCCACATGCGGTTCCAC	1544
1503	QY	TCGTCCCTGGCTCTGACCGAGT	CTGCCATGCGATGATGCTTCGATGCCAAGTTCAATAT	1562
1545	DB	AATGCTTGGCCTGTACCGCGT	TGTCCACGGCATTTGATGTTTCTGACCCCAAGTTCAACAT	1604
1563	QY	AGTCTCTCCTGGAGCTGCATG	TCCATATATCTTTCCACATACCGGAGAAGCCCAAGCGACT	1622
1605	DB	CGTGTCTCTCGCGCGGACCTG	TCCATCTACTTTCCCGTACACCGAGTTCGCACAAAGGCT	1664
1623	QY	CACCTCTCTTCACTGGTTCAAT	CGAAAATTTGATTTATGACCCGAGCGAAACGATGAACA	1682
1665	DB	GACCTCCCTTCCACCCCGAGAT	TGAGAGCTCTGTATCAGCCAAACCGAGAAACCGGAGCA	1724
1683	QY	CATTGGGCATCTGGATGACCGG	TCAAGCCCATCTCTTCTCCATGCGAAGACTCCACAG	1742
1725	DB	CAAGTTCTGTTGAACGACAGG	AAACATCATCTTCTCCATGGCTGCTCTGACCG	1784
1743	QY	GGTGAAGACATTAACAGGCTG	GTGCGAAGCTTTTGTAACTGCGTAAAGCTGAGGAGCT	1802
1785	DB	TGTGAAGAACTTGACTTGGG	TGTGGAGCTGTACGGCCGGAAACAAGCGGCTGCAGGAGCT	1844
1803	QY	GGTAAACCTCTGTGCTCGTTG	CCGGGTACATGATGTCAACAAGTCCAAAGCAAGCAAGA	1862
1845	DB	GGTGAACCTCTGTGGTCTGTG	CCGGCACCA---TGGCAACCTTCCAAAGACCAAGGAGGA	1901
1863	QY	GATCGCGGAGATAGAGAAGAT	GCATGAACCTCATCAAGACCCCAACCTTGTTCGGGCGAGTT	1922
1902	DB	GCAGGCCGAGTTCAAGAAGAT	TTTGACCTCATCGAGCAGTACAACTGAACCGGCACAT	1961
1923	QY	CCGCTGGATCTCTGCTCGAC	AAACAGGCGCGTAAACGGGAGCTCTATCGCTACATCGC	1982
1962	DB	CCGCTGGATCTCCGCCACAG	ATGAACCCGCTCCGCAACGGCGAGCTGTACCGCTACATCTG	2021
1983	QY	TGATACCCATGCTGTGCTTTG	CTACAGCCGGCTCTGATGAAGCGTTCGCTCACCCGTCG	2042
2022	DB	CGACACCAAGGGCGCTTCTG	TGCAGCGCTGTTTCTACGAGGCTTTCGGGCTGACGGTGT	2081
2043	QY	TGAGGCCATGACCTGTGGCTT	CCCTACTTTTCGGGACGCTCCATGAGAGTTCGACTGAGAT	2102
2082	DB	TGAGGCCATGACCTGGGCTG	CCGCTCCGCTACCATCGACCTTACCGGGGCAAGGCGTCCGC	2141
2103	QY	CATAGAGCATGGCGTCTCGG	CGTTTCCACATGTGACCCGCTACCAACCCGCAACAGGCTGTGTA	2162
2142	DB	CATCGTGACCGGCTGTCTG	CTCTGCTACCATCGACCTTACCGGGGCAAGGCGTCCGC	2201
2163	QY	TTTGATGGCGGACTTCTTCG	ACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATC	2222
2202	DB	CCTGCTCGTGGACTTCTTCG	ACAAGTCCAGGCGGAGCCGAGCCATGTGAGCAAGATCTC	2261
2223	QY	TGGACGAGGCTTCAGGGCAT	ATACGAGAGTACATGGAAGATATACTTCAGAGAGTT	2282
2262	DB	CCAGGGCGGCTCCAGGAT	TCGAGGAGATGACCTGGAAGCTGTACTTCGAGAGGCT	2321
2283	QY	GATGACACTGGCCGGGCTCT	ATCGGTTTCTGGAAGTACGTTCTCGAAGCTCCAGAGGCTGGA	2342
2322	DB	GATGACCTTCAACCGGCGT	GTATCGGGTCTTGAAGTACGTTCCCACTCGAGAGGCGCGA	2381
2343	QY	GACGAGCGCTACTGTGAGAT	GTGTTCTATCATATGAAATTCGCGAGCTGGCGAAGACCGT	2402
2382	DB	GACCCCGGCTACTCGAGAT	GTGTTATCGGCTCAAGTACCGCACCATGCGCAGACCGT	2441

QY	2403	GC	CGCTTGC	AATG	CAAC	ACCG	2425
Db	2442	GC	CGCTG	CGCGT	GGAGG	GAGC	2464
RESULT 8							
ABZ76371	ABZ76371 standard; cDNA; 2418 BP.						
XX	AC	ABZ76371;					
XX	DT	12-JUN-2003 (first entry)					
XX	DE	A. thaliana LMP encoding cDNA-clone ID Pk118.					
XX	KW	Lipid metabolism protein; LMP; seed storage; plan					
XX	OS	Arabidopsis thaliana.					
XX	FH	Key	Location/Qualifiers				
XX	FT	CDS	1..2418				
XX	FT		/*tag= a				
XX	FT		/product= "LMP"				
XX	FT		/note= "lipid metabolism protein"				
XX	PN	WO2003014376-A2.					
XX	XX						
XX	PD	20-FEB-2003.					
XX	XX	12-AUG-2002; 2002WO-US025586.					
XX	PR	10-AUG-2001; 2001US-0311414P.					
XX	PA	(BADI) BASF PLANT SCI GMBH.					
XX	PI	Mittendorf V, Haertel H, Cirpus P;					
XX	DR	WPI; 2003-256595/25.					
XX	DR	P-FSDB; ABR39585.					
XX	PT	New nucleic acid molecule encoding lipid metaboli					
XX	PT	producing transgenic plants, for modulating seed					
XX	PT	lipid or fatty acid, in plants, and for evolution					
XX	PT	structural studies.					
XX	XX	Claim 1; Fig 12A; 108pp; English.					
XX	CC	The invention relates to isolated lipid metabolis					
XX	CC	polynucleotides. The LMP functions as a modulator					
XX	CC	compound in a plant. The LMP nucleic acid and pro					
XX	CC	producing transgenic plants and in modulating the					
XX	CC	compounds. These are used to modify or increase l					
XX	CC	cofactors, and enzymes in microorganisms and plan					
XX	CC	LMP nucleic acid and protein may be used in ident					
XX	CC	being Arabidopsis thaliana, as markers for specif					
XX	CC	genome, and in evolutionary and protein structura					
XX	CC	ABZ76358-373 represent A. thaliana LMP encoding c					
XX	SQ	Sequence 2418 BP; 676 A; 491 C; 562 G; 689 T; 0 U					
Query Match 42.5%; Score 1172; DB 7;							
Best Local Similarity 70.9%; Pred No. 1.4e-254;							
Matches 1556; Conservative 0; Mismatches 640;							
QY	222	GC	AGG	GC	AT	CGT	CTCGTCCCGCTCGTGCCCATCGCG
Db	213	GC	AGG	A	GC	AT	TTTGCTCCATTGTTCTTTGGCT
QY	282	TT	GGG	AGT	AC	GT	TCACAGAGCTCAGCGTC
Db	273	T	AGG	AA	T	AT	GTATGATGATGAGCTGAGCTA
QY	342	GT	ACC	T	CCG	CTT	CAAGGAGAGCGCTGTGACGCGCCAGCAC

Db 333 ATATCTTCGGTTTAAGAGAGAGCTCGTTAATGGCCATGCCAATGAGATTAATCTCCCTTGA 392
QY 402 GCTTGACTTCGAGCCGTTTCAATGTCTCAGTCCCAAGCCCAATGGTGCATCATCTATTGG 461
Db 393 ACTTGATTTTGAACCTTTCAATGCAACATTTGCTTCCGCGCCAACTGCTTCATCATCCATTGG 452
QY 462 AAGCGGTGSCAGTTCCTCAACGACACTTGTCTCAATCATGTGTTCCGCAACAGGATGG 521
Db 453 GAATGGGGTTTCAGTTCCTCAATCTGCTCACTCTCTCAATTATGTGTTCCGTAAACAAGAAAG 512
QY 522 CTTGGAGCCCTGTTGCAATCTCCCTCGGCGCCACCGGCACAAAGGCGCATGTTATGATGCT 581
Db 513 CATGGAGCCCTTGTGTGATTTCTCCGACCTCAACAACATGATGCGCTCTCTATGATGCT 572
QY 582 TAATGATAGATAAAGCTTGGGAGGCTTCAGTCTGTGTGTCGACCAAGCTGAGGAGCA 641
Db 573 GAATGATCGAATACAGAAATATCCCATACTTCAGGGAGCTTTGGCAAGCAGAGGAGTT 632
QY 642 CTTGTCAAGCTCCCTGTCACACACCATACTCACAAATTTGCTTATRAATTTCAAGAGTG 701
Db 633 CTTTCTTAACCTTCTCTGCGCAACACCATACTCTGCAATTCGAATTCGAATTTCAAGGGAT 692
QY 702 GGGCTTCGAGAAAGTTGCGGTGATACAGCAGGACATGTTTGGAAATGATCCCATCTCCT 761
Db 693 GGGATTTGAAAGGGGATGGGTGACACAGCAGCAGAGGTTTCAGAAATGGTGCATCTCT 752
QY 762 TCTAGACATCATTCAGGGCCAGACCCATCTACCTTAGAGAAAATTTCTGGGAGGATCCC 821
Db 753 TCTGGACATACTCAGGACACCTGATCTCTCTGTCTTGAGAGCGTTTCTAGGAAGGATTC 812
QY 822 CATGATTTTAACTGTTGTGGTATCCCTCATGGATACTTTGTCAAGCTAATGATTT 881
Db 813 TAGTGCTTCAAGTTGATGTTTGTCTCCGATGGTTACTTTGGCCAAAGCCAAATGCTT 872
QY 882 AGGCTTCGACACAGGAGGACAGATCGTCTATATCTGACCAAGTCCGTCACATAGA 941
Db 873 GGGTCTCCCTGATACTGGTGACAGGTTGCTCATCTTGTGATCAAGTACGTGCATTTGA 932
QY 942 AATGAGATGGTCTCCGTTTAAAGAAACAGGGCTTGATGTTTCCCAAGATTCAT 1001
Db 933 AATGAGATGCTCCTTAGGATACAGAAAGCAGGACTGGAAGTTATTCMAAGATTCAT 992
QY 1002 TGTACTCGGCTGATACAGATGCAAGGACATCATGCAATCAGGGCTTGAGAGAT 1061
Db 993 GTTAAACAGACTGCTCCGAAAGCAAGGAAACAGTGCACACAGAGTTAGAAAGAGT 1052
QY 1062 TAGTGAACACAGCATACTTACATATTACGAGTTCCCTTCAGAAATGAAATGGGATACT 1121
Db 1053 TAGTGGTACAGAACACGCACACATTTCTGCGAATACCAATTTAGGACTGAAAGGGAATCT 1112
QY 1122 TAAGAAATGATATCAGATTTGATGTGTGCGCATATCTGGAACATTTGCTGAGGATGC 1181
Db 1113 TCGCAAGTGAATCTCAAGGTTTGTATGTCTGCGCATACCTGAGACTTTTGACAGGATGC 1172
QY 1182 TGCTGGTGAATGCTGCTGCAATTACAGGTTACTTCCAGACTTCATAATTTGAAACTACAG 1241
Db 1173 ATCAATGAAATTTCTGCGAGTTGAGGGGTGACCAATCTCATATTTGCAACTACAG 1232
QY 1242 TGATGAAATCTTTGTGCGCTCATTTGCTATCTTCAAGATGGGAATTTACCCAGTGCACAT 1301
Db 1233 TGATGAAATCTCGTTGCTCTTTGTTAGCTAGTAAGCTAGTGTGTGATACAGTGTATAT 1292
QY 1302 TGCTCATGCTCTGGAAGAGCTAAGTATCCAGATTCAGACATATTTTGGAGAAATTTGGA 1361
Db 1293 TGCTCATGCTTTAGAGAAACCAAGTACCCCGAGTCTGACATTTTACTTGGAGAAACCATGA 1352
QY 1362 TGAGAGTACCATTTCTCCGAGTTCATGCTGATATTAATTTGCTATGACATGCTGA 1421
Db 1353 AGATAGTATACATTTTCAAGTCAAGTTCATGCGAGATCTAATTTGCCATGAATAATCCGA 1412
QY 1422 TTTTATCATCAGCAGCATACCAAGAAATTTGCTGGAAAGCAAAATACTGTTGACAGTA 1481

Db 1413 TTTTATCATCAGCAGCATACCAAGAGATTTGCGGGAAGCAGAAACAATGTTGGGCAATA 1472
QY 1482 TGAGAGTCATACTGCTTTTACTCTGCTCGTGTCTGTACCGAGTTGTCCATGGGATCGATGT 1541
Db 1473 CGAGAGCCACACAGCTTTTCACTATGCTGCTTTTACCAGGTGTTTCATGGAATGATGT 1532
QY 1542 CTTTGAATCAAGATTCATATAGTCTCTCTGGAGCTGACATGCTCCATATACITTTCCACA 1601
Db 1533 CTTTGAATCCTAAGTTTAAATATAGTCTCTCCAGGAGCTGATATGACCATATACITTTCCATA 1592
QY 1602 TACCAGAGGCCAAGCGACTCACCTCTCTTCAATGCAATTCGAAATTTTCAATTTATGA 1661
Db 1593 TTCTGACAGGAAGAAGACTCACCTGCTCATGAGTCATATGAGAACTCTCTTTAG 1652
QY 1662 CCGGAGCAAAACGATGAACACATTTGGGCATCTGGATGACCGGTCAAAAGCCCATCTCTT 1721
Db 1653 TCGCGAAACAGAAATGATGAGCATGTGTGTTTACTGAGCGACCAATCGAAGCCCAATCATCTT 1712
QY 1722 CTCCATGSCAAGACTCGACAGGCTGAAAGAACATAACAGGGCTGCTGAGCTTTTCTTAA 1781
Db 1713 CTCTATGGCAAGACTTGAAGGCTGAAAACTTGAAGTGTGATGTAATGCTATGCCAA 1772
QY 1782 GTGCGCTAAGCTGAGGAGCTGTAAACCTTGTGCTGCTGCGCGGTACAAATGATGTCAA 1841
Db 1773 GAATAGCAAGCTTAGAGAGCTTGCATCTTGTATAGTTCGCTGCTACATCGATGAA 1832
QY 1842 CAAGTCCAGGACAGGGAAGAGATCGCGGAGATAGAGAGATGCAAGTAACTCATCAAGAC 1901
Db 1833 TCAGTCCAGGATAGAGAGGAATGGCTGAGATACAAAAGATGCAAGCTCATGTTGAGCA 1892
QY 1902 CCACAACTTGTTCGGGCAAGTTCGCTGATCTCTGCGCAGACAAACAGGCGCCGTAACGG 1961
Db 1893 GTATGATTTACCGTGTAGTGTAGTGTGATAGTCTCTCAAAATGAACCGTGTGCAATGG 1952
QY 1962 CGAGCTTATCGCTACATCGCTGTATCCCATCTGCTGCTTTCGACAGCGGCTTGTATGA 2021
Db 1953 TGAAGCTTACGTTATATCGCAGACACAAAGGTGTTTGTTCAGGCTGCTTTCTATGA 2012
QY 2022 AGGTTGCTCTCACCGTCTGTGAGGCGCATGACCTGTGGGCTTCTTACTTTTCGCAAGCT 2081
Db 2013 AGCATTTGGGCTTACGGTTGTGGAATCAATGACTTGTGCACTTCCCAACGTTTGTACTCG 2072
QY 2082 CCATGGAGCTCCAGCTGAGATCATAGACATGCGCTCTCGGCTTCCCATTTGACCGCTA 2141
Db 2073 TCATGGTGGACCCGACAGATTTATCGAAACCGAGTTTCTGGGTTCCCATTTGACCCATA 2132
QY 2142 CCACCCGAAACAGGCTGTAAATCTGATGGCGGACTTCTTTCGACCGGTGCAAGCAAGACC 2201
Db 2133 TCATCCAGACAGGTTGCAGCTACCTTGGTCAAGCTTCTTTGAGACTGTAAACCAATCC 2192
QY 2202 AGATCACTGGGTGAATATATCTGGAGCAGGCTGAGCGCATATACGAGAGTACACATG 2261
Db 2193 AAATCATTTGGTTTAAATCTCTGAAGGAGGAGCTCAAGCGGAATCTATGAAAGGTACACATG 2252
QY 2262 GAAGATATCTCAGAGGTTGATGACACTGCGCGGCTCTACGTTTCTCGAAGTACT 2321
Db 2253 GAAGAGTATCTCAGAGAGCTGCTTACCTCGCTGGAGTCTATGCAATTTCTGAAACATGT 2312
QY 2322 GTCGAAGCTCGAGAGGCTGGAGAGCGGCTACCTTCAGATGTTTCTACATACATCAAGTT 2381
Db 2313 GTCTAAGCTCGAAAGGAGAGAAACACGAGCTTACCTAGAGATGTTTACTCATTTGAAAT 2372
QY 2382 CCGGAGCTGGCAGAGACCGTGGCGCTTGCATTTGA 2417
Db 2373 TCGTGAATTTGGCCAAATCAATCCGCTGGCAACAGA 2408

RESULT 9
ADA71337
ID ADA71337 standard; DNA; 2450 BP.
XX
AC
XX
ADA71337;

DT 20-NOV-2003 (first entry)
 XX Rice gene, SEQ ID 4660.
 DE Plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.
 XX *Oryza sativa*.
 CS WO200300098-A1.
 XX 03-JAN-2003.
 PD 22-JUN-2001; 2001WO-IB001105.
 XX 22-JUN-2001; 2001WO-IB001105.
 PR (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Quan S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.
 DR Identifying at least one gene involved in plant resistance or response to
 XX pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX Claim 6; SEQ ID NO 4660; 899pp; English.
 XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX Sequence 2450 BP; 556 A; 674 C; 628 G; 592 T; 0 J; 0 Other;
 SQ

Query Match 42.1%; Score 1162; DB 7; Length 2450;
 Best Local Similarity 68.1%; Pred. No. 2.6e-252;
 Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;

16 CTGAACCGCAACGCGAGCATCCGGACCGCGTCGAGGACACCCCTCCACGCGCACCGCAAC 75
 28 CTGAGCCGCTCCACAGCGCTCAGGAGCGCATCGCGACTCCCTCTCCGCCACCCCAAT 87
 76 GAGCTCGTGGCCCTCCTCTCCAGTACGTGAACAAGGGAAGGGGATCTCGAGCGGCAC 135
 88 GAGCTCGTGGCCCTCCTCACCAGGCTGGTTAACTCCGAAAGGGAATGCTTCAGGCCCCAC 147
 136 CACATCTCGAGCGCTCGAGGAGG---TCCAGGCTCGGGGTCCGGCGCTCCCGCAG 192
 148 CAGATCATCTCGAGTACAAACACCAATCTCTGAGGCTGATCGTGAGAGGCTGAAGGAC 207
 193 GGACCTCTCCCGAGCTCCTCCGCTCCCGCAGGAGGCGATCGTCTCGCCCGCTCCGTG 252
 208 GGTGCTTTGAGGATGCTCTGAGGAGTGACAGAGGAGGAGTGTATCTCCCATGGGTT 267
 253 GCATCGCGGTGGCGCGCCCGGAGTTTGGAGTAGCTCCGCGTCAACGTTCAACGAG 312
 268 GCGCTTGGCATCCGCGCGAGGCCCGGTGTCTGGAGTATGTGAGGCTCAATGTGAGCGAG 327
 313 CTCACGTCGAGCAGCTCACAGTCTCGAGTACCTCCGCTTCAAGGAGGAGGCTCTCGAC 372
 328 CTCGCTGTGAGTTGCTGACAGTCCCGAGTACTTGCAGTCTCAAGGACAGCTTGTGAA 387
 373 GGCCAGCAACATGATCCCTACGTTCTCGAGCTTGACTTCGAGCCCGCTTCAATGCTCAGTC 432

Db 388 GAAGGCAACCAACAACTTTGTGCTGAGCTGGATTTGAGCCATTCATGCTCTCTC 447
 QY 433 CCAACGCCCAAAATCGGTCAATCTATTGGAACGGGTGTCAGTTCCTCAACCGCACTTG 492
 Db 448 CCTCGTCTCTCTGTGGAAGTCCATTTGGCAATGGTGTGCAAGTTCCTCAACGGCATCTG 507
 QY 493 TCTCATCATCTTTCCGCAAGGAGTTCCTTGGAGCCCTGTGTGATTTCTCTCCCTGGC 552
 Db 508 TCATCGAAGCTCTTCATGACAGGAGAGCATGTACCCACTGCTCAACTTCTCTCTGTCGA 567
 QY 553 CACCGGCAACAGGGGCACTGTATGATGCTTAATGATAGATACAAAGCTTGGGGAGGCTT 612
 Db 568 CACAACCTACAGGGCATGACCATGATGTTGAATGACAGAAATCGGAGTCTCAGTGTCTC 627
 QY 613 CAGTCTGTGTCACCAAAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACACATAC 672
 Db 628 CAAGGTGCTCTGAGGAAGGCTGAGGAGCATCTTTCTGTGCTTTTCAGCAGACACCCCTTAC 687
 QY 673 TCACATTTGCTTATAAATTTCAAGAGTGGGGCTTGGCAAGAGGTTGGGGTGATACAGCA 732
 Db 688 TCAGAAATTCACACACAGGTTCCAGGAACCTTGTGCTGGAGAAGGGTGGGGTGACTGTGCC 747
 QY 733 GGACATGTTTTCGAAATGATCCATCTCCTTCTAGACATCATTTCAAGCGCCAGACCCATCT 792
 Db 748 AAGCGTCCAGGAGACCATTCACCTCCTTTTGGACCTTCTTGGGCCCTGATCCGTCC 807
 QY 793 ACCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTGTGTGTGTGATCCCT 852
 Db 808 ACCCTCGAGAAGTCTCTTGGAAACAATCCCAATGGTGTTCATATGTCATTTGTCCTCCA 867
 QY 853 CATGATCTTTGGTCAAGCTTAATGATTAATGAGCTTGGCAACACAGGAGGAGATCGTC 912
 Db 868 CACGGTACTTCGCGAAGCCAAATGTCTTGGGTACCTTGACACTGAGGAGGAGGTTGTC 927
 QY 913 TATATACTGGACCAAGTCCGTGCACCTAGAAATAGATGTTCTCCGTTTAAAGAAACAA 972
 Db 928 TACATTTTGGACCAAGTCCGTGCTATGAGATGAGATGCTTCTGAGGATCAAGAGCAA 987
 QY 973 GGGCTGATGTTTCCCAAGATCTCATTTGTTACTTCGGCTGATACACAGATGCAAAAGGA 1032
 Db 988 GGTCTCAATATATACACACGACATCTCTTATTTGTCACAGGTTGCTCCCTGATGCACTGGC 1047
 QY 1033 ACATCATGCAATCAGGGCTTGGAGGATTAATGAGTGGCAACACAGCATCTTACATATTACA 1092
 Db 1048 ACCACTCGGGTCAGCGCTTGGAGAAGGTCCTTGGCACCGAGGACACCCACATCTTACCT 1107
 QY 1093 GTTCCCTTCAGAAATGAAATGCGATCTTAAGAAATGATATCAAGATTTGATGTGTGG 1152
 Db 1108 GTGCTTTCAGAACTGAAATGGAATTTGTCGAAGTGGATCTCAGTTTTGAAGTCTGG 1167
 QY 1153 CCAATATCGGAAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGCTGAATTTAAGGT 1212
 Db 1168 CGGTACTCGGAAACATTCACCTGATGATGTGCGCGCAGAAATTTGCTGAGAGCTCCAGGCC 1227
 QY 1213 ACTCCAGACTTCCATTAATTTGGAACCTACAGTATGAAATCTTTGTGCGCTCATTTGCTATCT 1272
 Db 1228 ATCTGACTTGTATCATCGAAATCTACGTGACGGAACCTTTGTTGCTGCTTGTGCTGCA 1287
 QY 1273 TACAAGATGGGAATTAACCCAGTGCACATTTGCTCATGCTCTGGAAGAAAGCTAAGTATCCA 1332
 Db 1288 CACAAGATGGGTGTATCCCATTTGACCATTTGACCATTTGCCATGCGCTTGAGAAACCAAGTACC 1347
 QY 1333 GATTGACACATATTTTGGAGAAATTTGATGAGAGTACCATTTCTCTGCGGAGTTCAT 1392
 Db 1348 AACTCTGACTCTACTCGAAGAGTGTGAGGATCATCTCACTTCTCATGCGGAGTTCACA 1407
 QY 1393 GCTGATATAATTTGCTATGAACAATGCTGATTTTATCATCACAGCAGACATACCAAGAAAT 1452
 Db 1408 ACTGACTTGTATGCGATGAAACCGCTGACTTCACTCATCACAGTACCTTCCAGAGAT 1467
 QY 1453 GCTGGAAGCAAAATPACTGTTGGACAGTATGAGAGTCACTGCTTACTCTGCTGCTGT 1512

Db 1468 GCCGAAACAGGACACTGTTGGTCAGTATGAGTCTCACATGGCATTACCAATCCCTGGT 1527
 QY 1513 CTGTACCGAGTTGTCATGGATCGATGTTTCGATCCAAAGTTCAATATAGTCTCTCCT 1572
 Db 1528 CTGTACCGAGTTGTCATGGATCGATGTTTCGATCCAAAGTTCAATATAGTCTCTCCT 1587
 QY 1573 GGAGCTGACATGTCATATATCTTTCCATACACCGAGAGGCAAGCGACTCACCTCTCTT 1632
 Db 1588 GGTGCGGACATGTCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
 QY 1633 CATGGTTCAATCGAAATTTGATTTATGACCGGAGCAAAAGATGAACATTTGGGCAT 1692
 Db 1648 CACCCAGAGATTGAGGAGTTGCTCTACAGCGAAGTTGACAAACAGGACACAGTTTATG 1707
 QY 1693 CTGGATGACCGGTCAAGCCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1752
 Db 1708 CTGAAGACAGGAAACAAAGCCCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1767
 QY 1753 ATACAGGGCTGGTCGAAAGCTTTTGTAAGTGCCTAAGCTGAGGAGCTGGTAAACCTT 1812
 Db 1768 TTGCTGCTGTTGTTGAGCTGTATGGTCGAACCTCGCTGCAAGAGCTGGTTAACTT 1827
 QY 1813 GTGCTGTTCCCGGTTCAATATGTTCAACAAAGTCCAAAGACAGGAGAGATGCGGAG 1872
 Db 1828 GTGCTGTTGTTGTTGAGCTGTATGGTCGAACCTCGCTGCAAGAGCTGGTTAACTT 1884
 QY 1873 ATAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1932
 Db 1885 TTCAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1944
 QY 1933 TCTGCCAGACAAACAGGGCCCGTAAAGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCT 1992
 Db 1945 TCCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2004
 QY 1993 GGTGCTTTTGTGAGCGGCTTGTATGAAGCGTTCGCTCTACCCGTCGTTGAGGCGATG 2052
 Db 2005 GGTGCTTTTGTGAGCGGCTTGTATGAAGCGTTCGCTCTACCCGTCGTTGAGGCGATG 2064
 QY 2053 ACTGTGGGCTTCTACTTCTGGGAGCTCTCAATGGAGTCCAGTCCAGTCCAGTCCAGT 2112
 Db 2065 ACTGTGGGCTTCTACTTCTGGGAGCTCTCAATGGAGTCCAGTCCAGTCCAGTCCAGT 2124
 QY 2113 GCGCTCTCGGCTTCCACATGACCGGCTACCAACCGGACAGCTGTTATCTGATGGCC 2172
 Db 2125 SGAGTGTCTGGCTTCCACATGACCGGCTACCAACCGGACAGCTGTTATCTGATGGCC 2184
 QY 2173 GACTTCTTCAACCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2232
 Db 2185 GAGTTCTTTGAGAGTGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2244
 QY 2233 CTGACGCGATATACGAGAGTACATGGAATATATCTCAGAGAGGTTGATGACACTG 2292
 Db 2245 CTGACGCGATATACGAGAGTACATGGAATATATCTCAGAGAGGTTGATGACACTG 2304
 QY 2293 GCGGGGCTTACGGTTTCTGGAAGTACGTTGGAAGCTCGAGAGGCTGAGAGAGGAGGAG 2352
 Db 2305 ACCGGGCTTACGGTTTCTGGAAGTACGTTGGAAGCTCGAGAGGCTGAGAGAGGAGGAG 2364
 QY 2353 TACCTTGAGATGTTTACATATCTGAAGTTCGCGAGCTGGGAGACCGTTCGCGCTTGCA 2412
 Db 2365 TACCTTGAGATGTTTACATATCTGAAGTTCGCGAGCTGGGAGACCGTTCGCGCTTGCA 2424
 QY 2413 ATTGACCAACCGGAGTAG 2430
 Db 2425 GTGAGGGCGAGCCGTCG 2442

RESULT 10
 ADC08208
 ID ADC08208 standard; DNA; 2451 BP.
 XX
 AC
 XX

DT 18-DEC-2003 (first entry)
 XX Rice DNA sequence Seq ID513 related to grain filling.
 DE plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX Oryza sativa.
 OS WO2003000905-A2.
 PN 03-JAN-2003.
 XX 21-JUN-2002; 2002WO-IB002450.
 XX 22-JUN-2001; 2001US-0300112P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 20-DEC-2001; 2001US-0342327P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
 XX WPI; 2003-229341/22.
 DR P-PSDB; ADC08209.
 XX New plant genes encoding polypeptides having an activity involved in or
 associated with the synthesis, metabolism or degradation of carbohydrates
 in the plant grain useful in generating plants having improved
 nutritional properties.
 Claim 35; SEQ ID NO 513; 130pp; English.
 CC This invention, in the area of plant biotechnology, relates to novel
 polynucleotides comprising a nucleotide sequence encoding a protein which
 is involved in or associated with the synthesis, metabolism or
 degradation of carbohydrates in the plant grain and the expression of
 which is up-regulated during grain filling. The plant is selected from
 corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 sugarbeet, wheat, and rice. The invention may be useful for the
 improvement of protein, oil, starch, fibre and moisture content of the
 cereal grains. In addition, carbohydrate levels may be modified to a more
 desirable level using the present invention. The present sequence is a
 DNA sequence encoding a rice protein of the invention. Note: The sequence
 data for this patent did not form part of the printed specification, but
 was obtained in electronic format directly from WIPO at
 ftp.wipo.int/pub/publishedpct_sequences.

Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
 Query Match 42.1%; Score 1162; DB 9; Length 2451;
 Best Local Similarity 68.1%; Pred. No. 2.6e-252;
 Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;
 QY 16 CTGAACCGAAACCGGAGCATCCGGGACCGGCTCGAGGACACCTCCACGCGCCGCAAC 75
 Db 28 CTGAGCGGCTTCCACAGGCTCAGGAGGCGCATCGGAGCTCCCTCTCGGCCACCCCAAT 87
 QY 76 GAGCTCGTCCCTCTCTCTCCAAAGTACGTGAACAAGGAGGAGGATCTTCGAGCCGAC 135
 Db 88 GAGCTCGTCCCTCTCTTCCAGGCTGTTTAACTCTGGAAGGAGGATGCTTCAGGCCAC 147
 QY 136 CACATCTTCGAGCGCTCGAGCGAGG---TCCAGGGCTCCGGGCTCCGCGCTCGCCGAG 192
 Db 148 CAGATCAATGCTGAGTACAAACACGCAATCTCTGAGGCTGATCTGAGAGAGCTGAAGGAC 207
 QY 193 GGACCTTCTCTCGAGCTCTCTCGCTCCGGGACGAGGCGGATCTGTCGCGCGCTTCGTG 252
 Db 208 GGTGCTTTTGAGGATGCTCTGAGGAGTGCACAGAGGAGGATGTTATCTCCCATGGT 267

253 GCCATGCGGTGCGCGCGCGCGGAGCTTTGGGAGTAGTCCGCGTCAAGCTTCAAGAG 312
268 GCGCTTGCCATCCGCGCGCGGCGCGGCTGTCTGGGAGTAGTGGGGTCAATGTGAGCGAG 327
313 CTCAGCGTCGAGCAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTGTCTGAC 372
328 CTCGCTGTGAGTGTCTGACAGTCCCGAGTACTTGCAGTTCAAGGACAGCTGTGGAA 387
373 GGCAGGCAATGATCCCTACGCTCTCGAGCTTGAATCTTGAGCGCTTCAATGTCTCAGTC 432
388 GAAGCAGCAACCAACAACTTTGTGCTTGAGCTGGAATTCGAGCCATCAATGCCCTCTTC 447
433 CCAGCCCAAAATCGGTCACTATTTGGAACGCTGTGCACTTCTCAACCGACACTTG 492
448 CTTGCTCTTCTGTGGAAGTCCATTTGSCRATGGTGTGCACTTCTCAACAGGATCTG 507
493 TCTCAATCATGTTCCGCAACAGGATTTGCTTGGAGCCCTCTTGGATTTCTCTCGTGGC 552
508 TCATCGAAGCTCTTCCATGACAAGGAGAGCATGTACCCACTGCTCAACTTCTCTGTGCA 567
553 CACGGGCAACAGGGGCAATTTATGATGCTTATGATAGTAATCAAAAGCTTGGGGAGGCT 612
568 CACAACCTCAAGGGGATCACCAGTATGTGATGACAGAAATCCGAGTCTCAGTGTCTC 627
613 CAGTCTGTGTGACCAAGCTGAGGAGCACTGTCAAAAGCTCCCTGCTGACACACCATAC 672
628 CAAGGTCTCTGAGGAAGCTGAGAGCACTTCTGCTCTTTCAGCAGACACCCCTTAC 687
673 TCACAAATTTGCTTAAATTTCAAGAGTGGGCTGGAGAAAGTTGGGGTGATACAGCA 732
688 TCAGAAATCCACCACAGGTTCCAGGAATTTGCTGAGAGAGGTTGGGGTCACTGTGCC 747
733 GGACATGTTTGGAAATGATCATCTCTCTAGACATCAATTCAGCGCGCACACCATCT 792
748 AAGCGTCTCCAGGAGACCAATTCACCTCTTTTGGACCTTCTTGGGCGCCCTGATCCGTC 807
793 ACCCTAGAGAAATCTTGGGAGGATCCCATGATTTTAAAGTTTGTGTATCCCT 852
808 ACCCTGAGAGTCTCTTGGACAAATCCATGCTTCTCAATGTTGTCATATGTCCCA 867
853 CATGATATCTTTGGTCAAGCTAATGATATAGCTTTGCCAGACACAGGAGGACAGTCTGC 912
868 CACGTTTACTTCGCGCAAGCCAAATGCTTGGGTTACCTTGACACTGGAGGGCAGGTTGTC 927
913 TATATCTGGACCAAGTCCGTGCACTAGAAATGAGTGGTCTCCGTTTAAAGAAACAA 972
928 TACATTTTGGACCAAGTCCGTGCTATGAGAAATGAGTGTCTTCTGAGGATCAAGCAGCAA 987
973 GGGCTTGATGTTTCCCAAGATTTCTCATTTGTTACTTGGCTGATACCAAGATGCAAAAGGA 1032
988 GGTCTCAATATTACACCAAGCATCTTATTTGTCACCAAGTGTCTCTGATGCACTGGC 1047
1033 ACATCATGCAATCAGCGGCTTGAGAGAAATAGTGGAAACAGACATCTTACATATTAGCA 1092
1048 ACCACTCGCGTCAAGCTCTTGAGAGGTCCTTGGCACCGAGACACACCACTCTACGT 1107
1093 GTTCCCTTCAGAAATGAAATGGGATCTTAGAAATGGATATGATATGATATGATGTCG 1152
1108 GTGCTTTTCAGAAATGAAATGTTTCCCAAGTGAATCTCAGCTTTTGAAGTCTGG 1167
1153 CCATATCTGAAACATTTGCTGAGGATGCTGTGCTGAAATTTGCTGAAATTAACAAGGT 1212
1168 CCGTACCTTGAACATCTCACTGATGTGCGCAGCAATTTGCTGGAGAGCTCCAGGCC 1227
1213 ACTCAGACTTCATTAATTTGAAATCTACAGTATGGAATCTTGTGGGCTCATGTCTATCT 1272
1228 AATCTGACTTGCATCATCGGAAATCTACAGTACGGAACCTTTGTTGCACTTGTCTTGA 1287
1273 TACAGATGGGAATTAACAGTGCAACATTTGCTCATGCTCTGGAAAGACTTAAGTATCCA 1332
1288 CACAAGATGGGTGTACCCATTTGTTACCATTTGCCATTTGCCATGGCTTGAGAAACCAAGTACCCC 1347

1333 GATTTCAGACATATTTTGGAGAAATTCGATGAGAGTACCAATTTCTCTCGCAGTTCACT 1392
1348 AACTCTGACCTCTACTTGGAGAAAGTTTGAGGATCACTACACTTCTCATGCCAGTTACA 1407
1393 GCTGATATAAATTTGCTATGAACAATGCTGATTTTATCATCACCGACACATACCAAGAAAT 1452
1408 ACTGACTGATTTGCGATGAACACCGCTGACTTTCATCATCACCAAGTACCTTCCAAGAGATT 1467
1453 GCTGAAACCAAAATTAATCTGTTGGACAGTATGAGATCACTATGCCCTTTTCTCTGCTCGT 1512
1468 GCGGAAACCAAGGACACTGTTGGTCAGTATGAGTCTCACATGSCATTTCAACATGCTGGT 1527
1513 CTGTACCGAGTTGTCATGCGATCGATGCTTTCGATCCAAAGTTCAAATAGTCTCTCCT 1572
1528 CHTGACCGTGTGTCTCAAGTATGATGTTTTTGACCCGAAAGTTTAAATGTTCTCGCT 1587
1573 GGAGTGCATGCTCCATATATCTTCCATACACGAGAGGCGCAAGCACTCACTCTCTCT 1632
1588 GGTGCGGACATGCTCATCTACTTCCCTTACTCTGAGTCTCTGTAAGAGGCTCACTCCCTC 1647
1633 CATGCTTCAATCGAAATTTGATTTATGACCCGAGCAAAACGATCAACACATTTGGCAT 1692
1648 CACCAGAGATTTGAGAGTGTCTCTACAGCGAAGTTGACAAACGAGCAGCAAGTTTATG 1707
1693 CTGGATGACCGGTCAAAGCCCATCTCTTCCATGGCAAGACTTCGACAGGCTGAAAGAAC 1752
1708 CTGAGGACAGGAAACAGCCCATCATCTTCCATGGCTCTGTTTACCGTGTCAAGAAC 1767
1753 ATAAACAGGCTGTGTCGAAGCTTTTGTAAAGTGGCTTAAGTCTGAGGGAGCTGTGTAACCTT 1812
1768 TTGACTGCTGTGTTGAGCTGTATGTCGCAACCCCTCGCTTCGACAGAGCTGTGTTAACCTT 1827
1813 GTCGCTGTTCCGCGGTACAAATGATGTCAACAAAGTCCAAAGCAGAGGAGAGATCGCGAG 1872
1828 GTGGTGTCTGTGTGAGCC---TGGCAACCCATCTAAGGACAGAGGAGAGCGGTGAG 1884
1873 ATAGAGAGATGCATGAATCATCAAGACCCCAAACTTTTTCGGGCAAGTTCCGCTGGATC 1932
1885 TTCAAGAGATGTTTGACCTTATTGAGCAATACAACTTGAATGGCCACATCCGCTGGATC 1944
1933 TCTGCCAGCAAAACAGGCGCTGTAAGCGGAGCTCTATCGCTACATTCGCTGATACCTAT 1992
1945 TCCGCGCAGATGAACCGTTCGCAACCGTGTAGCTCTACCGTTATCATCTGCGACACCAAG 2004
1993 GGTGCTTCTGTACAGCGCGCTTGTATGAAGGTTGCGTCTCACCGTCTGTGAGGCCATG 2052
2005 GGTGCTTTTGTGACCGCTTTTACGAGGATTCGCTCTCAGTCTCTCAGTCTGTGAGTCCATG 2064
2053 ACCTGTGGCTTCTCTACTTTTCGCGAGCTTCCATGGAGGTCACAGCTGAGATCATAGACAT 2112
2065 ACCTGTGGTCTCCGACATTCGCAACCGCTTATGTGTGTCACAGCTGAGATCATCGTGAAC 2124
2113 GCGTCTCGGCTTCCATGACCGGTACACCCCGGACAGGCTGTGTTAATCTGATGGCC 2172
2125 GAGTGTCTGGCTTCCATATTGACCCATACCAAGGTTGCAAGGCTCTCGGCTGTCTGTT 2184
2173 GACTTCTTCEACCGGTGCAAGCAAGACCCAGATCACTGGTGTAAATATATCTGAGCAGGG 2232
2185 GAGTCTTTGAGAGTGCAGAGAACCCCAAGGCTGAGCAAGATCTCGCAGGCGGT 2244
2233 CTGACGCGCATATACAGAAATGATACATGGAAGATATATCTCAGAGAGGTTGATGACATG 2292
2245 CTTACGCTATCGAGAGAAATACACCTGGAAAGCTTACTCTGAGAGGCTGATGACCTC 2304
2293 GCGGGGTCTAGGTTCTGGAAGTACGTTGCGAAGCTCGAGCTCGAGAGGAGGAGGCG 2352
2305 ACCGCGCTTACGGATCTTGGAGTACGTTCTGAAACCTGAGAGGCGGTGAAACCCGCGC 2364
2353 TACTTGTGATGCTTCTACATATCTGAAGTTTCGCGAGGCTGGGCAAGACCTGCGCTTGA 2412
2365 TACCTTGATGCTGTATGCTCCCTCAAGTACCGACCATGGCTAGCACTGCTCCGTTGGCC 2424
2413 ATTGACCAACCGCAGTAG 2430

Db 2425 GTCAGGGCGAGCGTGC 2442

RESULT 11
ADCC7855
ID ADC07855 standard; DNA; 2451 BP.
XX AC ADC07855;
XX DT 18-DEC-2003 (first entry)
XX DE Rice DNA sequence Seq ID121 related to grain filling.
XX KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.
XX OS Oryza sativa.
XX PN WO200300905-A2.
XX 03-JAN-2003.
XX 21-JUN-2002; 2002WO-IB002450.
XX 22-JUN-2001; 2001US-0300112P.
XX 26-SEP-2001; 2001US-0325277P.
XX 20-DEC-2001; 2001US-0342327P.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX PA Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;
XX WPI; 2003-229341/22.
XX P-PSDB; ADC07856.
XX New plant genes encoding polypeptides having an activity involved in or
XX associated with the synthesis, metabolism or degradation of carbohydrates
XX in the plant grain useful in generating plants having improved
XX nutritional properties.
XX Claim 2; SEQ ID NO 121; 130pp; English.
XX This invention, in the area of plant biotechnology, relates to novel
XX polynucleotides comprising a nucleotide sequence encoding a protein which
XX is involved in or associated with the synthesis, metabolism or
XX degradation of carbohydrates in the plant grain and the expression of
XX which is up-regulated during grain filling. The plant is selected from
XX corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
XX sugarbeet, wheat, and rice. The invention may be useful for the
XX improvement of protein, oil, starch, fibre and moisture content of the
XX cereal grains. In addition, carbohydrate levels may be modified to a more
XX desirable level using the present invention. The present sequence is a
XX DNA sequence encoding a rice protein of the invention. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/publishedpct_sequences.
XX Sequence 2451 BP; 557 A; 674 C; 628 G; 592 T; 0 U; 0 Other;
Query Match 42.1%; Score 1162; DB 9; Length 2451;
Best Local Similarity 68.1%; Pred. No. 2.6e-252;
Matches 1647; Conservative 0; Mismatches 765; Indels 6; Gaps 2;
QY 16 CTGAACCGCAACCGGAGCATCCGGACCGCGTGGAGACACCCCTCCACGGCGACCGCAAC 75
Db 28 CTGAGCCGCTCCACAGCGGTCAAGAGCGCATCGGGGACTCCCTCTCCGCGCCACCCCAAT 87
QY 76 GAGCTCGTGGCCCTCTCTCCAGTAGCTGAACAAGGGGAAGGGCATCCTTGACGGCGCAC 135

Db 88 GAGCTCGTGGCCGCTTCAACGAGCTGGTTAACTCGAAAGGGAATGCTTCAGGCCAC 147
QY 136 CACATCTCGACGCGCTCGACGAGG---TCCAGGGGCTCCGGGGTCCGGCGCTCCGCCGAG 192
Db 148 CAGATCAATGCTGAGTAGACAACAACGCAATCTCTGAGGCTGATCGTGAGAGCTGAAGGAC 207
QY 193 GGACCCCTTCGACGCTCTCCGCTCCGGCGAGGAGGATCGTCTCGCGCGCTTCGTCG 252
Db 208 GGTGCTTTTGAGGATGCTCTGAGGAGTGCAAGAGGGGATGTTATCTCCCATSGGTT 267
QY 253 GCCATCGGGTGGCCGCGCCGCGGAGTTTGGGAGTAGCTCCGCTCAAGCTTCAAGG 312
Db 268 GCCCTTCGCAATCCGCCCGAGGCCCGGTGCTGGGAGTATGTGAGGGTCAATGTGAGCCGAG 327
QY 313 CTGACGCTCGACGAGCTCACAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTTGTGAC 372
Db 328 CTGCTGTGAGTTGCTGACAGTCCCGGAGTACTTGCAGTTTCAAGGAACACGCTTGTGAA 387
QY 373 GGCCAGCACAAATGATCCCTAGTTTCTGAGCTTGACTTCGAGCCGTTCAATGTCTCAGTC 432
Db 388 GAAGGCAACCAACCAACTTTGTGCTTGAGCTGATTCGAGCCATTCATATGCTCTCTTC 447
QY 433 CCAGCGCCAAATCGTCTCATCTATTGGAAACGCTGTGCAAGTTCCTCAACCGACACTTG 492
Db 448 CCTGCTCTCTCTGCGAAGTCCNTGGCAANTGGTGTGCAAGTTCCTCAACGAGCATCTG 507
QY 493 TCCTCAATCATGTTCCGCAACAGGGATTGCTTGAGGCCCTGTGTTGGATTTCTCCGTGGC 552
Db 508 TCATCGAAGCTCTTCCATGACAAGGAGCATGTACCCACTGCTCAACTTCTCTTCGTGCA 567
QY 553 CACCGGCACAAGGGCATGTTATGATGCTTAATGATAGATAACAAGTTGGGAGGCTT 612
Db 568 CACAACCTACAAGGGCATGACCATGATGTTGAATGACAGAAATCCGAGTCTCAGTGTCTC 627
QY 613 CAGTCTGTGTCACCAAGCTGAGGAGCACTTGTCAAAAGCTCCCTGCTGACACACCATAC 672
Db 628 CAAGGTGCTCTGAGGAAGGCTGAGGAGCACTTCTGCTCTTCAGCAGACACCCCTTAC 687
QY 673 TCACAAATTTGCTTATAAAATTCAGAGTGGGGCTGGAGAAAGTTGGGGTGATACAGCA 732
Db 688 TCAGAAATTCACACACAGGTTCCAGAACTTGGTCTGAGAAAGGTTGGGGTGACTGCGC 747
QY 733 GGACATGTTTTGGAATGATCCATCTCTCTAGACATCATTCAGGCCCGACAGCCATCT 792
Db 748 AAGCGTTCACAGGAGACCATTCACCTCTTTGACCTTCTTGAGGCCCTGTATCCGTC 807
QY 793 ACCTTAGAATAATCTTGGGAGGATCCCATGATTTTAACTGTTGTGTGTTATCCCT 852
Db 808 ACCTCGAGAGTTCCTTGGAAACATCCCAATGGTGTTCATGTGTTCATTTATGTCOCA 867
QY 853 CATGGATCTTTGGTCAAGCTAATGATAGGCTTGCCAGACACAGGAGGACAGATGTC 912
Db 868 CAGGTTACTTCGCGCAAGCCAATGTCTGGTGTACCTGCACACTGGAGGCGAGTTGTC 927
QY 913 TATATCTGACCAACTCCGTCACATAGAAATAGATGCTTCCGTTTAAAGAAACAA 972
Db 928 TACATTTTGACCAAGTCCGTTGATGAGAGATGAGATGCTTCTGAGGATCAAGACCAA 987
QY 973 GGGCTGTGATGTTTCCCAAGATTTCTCATGTTTACTTCGGCTGATCCAGATGCAAAAAGGA 1032
Db 988 GGTCTCAATATACACACGATCTTATGTACCAAGGTTGCTCTCTGATGCACTGGC 1047
QY 1033 ACATCATGCAATCAGCGGCTTGAGAAATPAGTGGAAACACAGCATATCTTACATATACGA 1092
Db 1048 ACCACCTGGGTGAGCGTCTTGAGAAAGTCTCTTGGCACCGACACACCCACATCTCTACGT 1107
QY 1093 GTTCCCTTCGAATGAAATGGATGATCTTAAGAAATGGATATCAAGATTTGATGTCGG 1152
Db 1108 GTGCTTTTCAGAACTGAAAATGGAATTTGTTGCAAGTGGATCTCACTGTTTGAAGTCGG 1167
QY 1153 CCATATCTGGAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGTAATTTCAAGGT 1212

Db 1168 CCGTACCTCGAAACATTCACCTGATGATGTCGCGCACGAAATTCCTGGAGAGCTCCAGGCC 1227
QY 1213 ACTCAGACTTCATMAATTCGGAACCTACAGTGTATGGAATCTTGTGGCGTCACTGCTATCT 1272
Db 1228 AATCTCTGACTTGTATCATCTCGAAACCTACAGTGTATGGAATCTTGTGGCGTCACTGCTATCT 1287
QY 1273 TACAAGATGGGAATTCACCGATGCAACATTCCTGATGCTCTGGAAGAGCTAAGTATCCA 1332
Db 1288 CACAAGATGGGTGTACCCATGTACATTCGCCATGCGCTGGAAGAAACCAAGTACCCC 1347
QY 1333 GATTTCAGACATATTTTGGGAAGATTTTCGATGAGAGTACCAATTTCTCTGCCAGTTCACT 1392
Db 1348 AACTCTGACCTCTACTGGAAGAGTTTGGAGATCACTACCACCTTCTCATGCGAGTTTCA 1407
QY 1393 GCTGATATTAATTCGTATGACAACTGCTGATTTATCATCACAGCACATACCAAGAAAT 1452
Db 1408 ACTGACTTCATTCGCGATGAACCAAGCTGCTTATCATCATCACCAGTACCTTCCAAAGAT 1467
QY 1453 GTTGAAGCAGAAATCTCTTGGACAGTATGAGAGTCACTAGCTTCTGCTGCTGCTGCT 1512
Db 1468 GCGGNAACAAGACACACCTGCTGCTGATGAGTCTCATGSCATTCACATGCTGCTGCT 1527
QY 1513 CTGTACCGAGTTGTCTCATGGAATGCGATGCTTCGATCCAAAGTTCAATATAGTCTCTCT 1572
Db 1528 CTGTACCGTGTGTCTCACGATATGATGTTTGTGACCGGAAGTTTAACTGTTCTCGCT 1587
QY 1573 GGAGCTGACATGCTCATATACCTTTCACATACCGAAGAGCCCAAGCACTCCTCTCT 1632
Db 1588 GGTGGGACATGCTCATCTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1647
QY 1633 CATGCTTCAATCGAAATTTGATTTATGATCCCGGAGCAAAACGATGAACACATTTGGGCAT 1692
Db 1648 CACCAGAGATTGAGAGTTGCTTACAGCGAAGTTGACAAACGAGCAAGTTTATG 1707
QY 1693 CTGATGACCGGTCAAGCCCATCTCTCTCTCATGCGCAAGACTCGACAGGGTGAAGAAC 1752
Db 1708 CTGAAGGACAGGAAACAGGCCAATCATCTCTCTCATGCTGCTCTGACCGTGTCAAGAAC 1767
QY 1753 ATAAAGAGGCTGTGCAAGCTTTTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1812
Db 1768 TTGACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1827
QY 1813 GTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1872
Db 1828 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1884
QY 1873 ATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1932
Db 1885 ATCAAGAGATGTTGACCTTATGAGCAATACAACTTGAATGGCCACATCCGCTGGATC 1944
QY 1933 TCTGCCACAGCAAAAGGCGCCGCTAAGCGGAGCTCTATCGCTACATCGCTGATACCCAT 1992
Db 1945 TCGCGCAGATGAACCGTGTGCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2004
QY 1993 GGTCTTTCTGATCAGCGGCTTGTATGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2052
Db 2005 GGTCTTTTGTGAGCGCGCTTCTACAGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2064
QY 2053 ACTGTGGCTTCTACTTTCGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2112
Db 2065 ACTGTGGCTTCTCCGACATTCGCAACCGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 2124
QY 2113 GCGCTTCGCGCTTCTCAGATTCAGCGCTACCCGCAACAGGCTGTTAATCTGATGGCC 2172
Db 2125 GAGTGTCTGGCTTCTCAGATTCAGCGCTACCCGCAACAGGCTGCTGCTGCTGCTGCTGCT 2184
QY 2173 GACTTCTTCGAGCGTTCAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2232
Db 2185 GAGTCTTTGAGAGTGTCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2244
QY 2233 CTGACGCGCATATACAGAGAGTACATGAGAGAGATATCTCAGAGAGGTTGATGACACTG 2292
Db 2245 CTTTACGCTATCGAGGAGAAATACACTGAGAGCTTCTACTCTGAGAGGCTGATGACCTC 2304

QY 2293 GCGGGGCTTACCGTTTCTGGAAGTACGTTCTGAGCTGAGAGGCTGAGAGCGCGC 2352
Db 2305 ACCGGCGTCTACGATTTCTGGAAGTACGTTCTGAGCTGAGAGGCTGGAACCCGCGC 2364
QY 2353 TACCTTGAGATGTTCTACATACCTGGAAGTTCGCGAGCTGSCGAAGACCTGCGCTTGA 2412
Db 2365 TACCTTGAGATGTTCTGATGCTTCAAGTACCGACCATGAGCTAGCACCGTCCGCTGGCC 2424
QY 2413 ATTGACCAACCGCGTAG 2430
Db 2425 GTCGAGGCGGAGCGCTCG 2442

RESULT 12

AD68521
ID ADC68521 standard; cDNA; 2754 BP.
XX
AC ADC68521;
XX
DT 18-DEC-2003 (first entry)
XX
S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:13.
XX
Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;
KW biosynthetic pathway; plant; gene; ss.
XX
Schedonorus arundinaceus.
XX
W02003040306-A2.
XX
15-MAY-2003.
PF 07-NOV-2002; 2002WO-NZ000239.
XX
PR 07-NOV-2001; 2001US-0337703P.
XX
(GENE-) GENESIS RES & DEV CORP LTD.
(WEIG-) WRIGHTSON SEEDS LTD.
PA
Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;
PI Saulsbury KM, Hall C;
XX
WPI: 2003-441544/41.
DR P-PSDB; ADC68365.
XX

PT New polynucleotide encoding polypeptides from Lolium perenne or Festuca
arundinacea, useful for modulating the biosynthesis of lignin, fructan or
tannin in a plant.

PS Claim 1; SEQ ID NO 13; 240pp; English.

XX
The present invention describes isolated polynucleotides (I) encoding
proteins (II) from Lolium perenne and Festuca arundinacea which are
active in lignin, fructan and tannin biosynthetic pathways. Also
described: (1) an isolated oligonucleotide probe or primer comprising at
least 10 contiguous residues complementary to 10 contiguous residues of
(I); (2) a kit comprising the oligonucleotide probe or primer; (3) a
genetic construct comprising (I); (4) a transgenic plant cell comprising
the genetic construct of (3); (5) a plant or its seed, fruit or progeny
comprising the transgenic plant cell of (4); (6) modulating one or more
of the lignin, fructan or tannin compositions of a plant; (7) producing a
plant having one or more of the lignin, fructan or tannin compositions;
and (8) modifying the activity of (II) involved in a lignin, fructan or
tannin biosynthetic pathway in a plant. (I) can be used for modulating
the biosynthesis of lignin, fructan or tannin in a plant. The present
sequence is used in the exemplification of the present invention.

SQ Sequence 2754 BP; 552 A; 685 C; 684 G; 733 T; 0 U; 0 Other;

Query Match 41.2%; Score 1135.6; DB 9; Length 2754;
Best Local Similarity 67.5%; Pred. NO. 2.5e-246;
Matches 1629; Conservative 0; Mismatches 774; Indels 9; Gaps 2;

QY 7 GCGCCGAAGCTGAAACCGCAACGCGAGCATCCCGGACCGCGTCCGAGACACACCTCCACGCG 66
Db 116 GGTGCGCAAGCTGACTGCTCTCCACAGTCTCCGGAGCGCTTGGTGCACCTTCTCCTCC 175
QY 67 CACCGCAAGAGCTGCTGCGCCCTCTCTCCAGTACGTGAACAAAGAGGAGGCGATCCCTG 126
Db 176 CATCCCAAGAGCTCAATGCGCTCTCTTCCAGTATGTTCCAGGCGCAAGAGAAATGCTT 235
QY 127 CAGCGCACCAATCTCCAGCGCTCCGAGAGGTCCAGGGCTCCCGGGTCCCGCGCTC 186
Db 236 CAGCGCACCAAGCTGCTCACTGAGTTCGAAGCATGTTTGGAGTCTG-----ACAAGGAG 289
QY 187 GCGAGGAGACCTTCTCCAGCTCTCCGCTCCGCGCAGAGAGCGATGCTGCTGCGCGCG 246
Db 290 AGTATGCACTTTTCAAGACATCTCCGCTGCTCCGCGCGCAAGCAATGTTGCTTCCGCCA 349
QY 247 TTGCTGCGCCATCCGCTGCGCGCGCGCGCGAGTTCGGAGTACGTCGCGCTCAAGTT 306
Db 350 TGGGTTGCACTTCCCATCAGGCCAGCGCTGCTCTGGACATCATAGGGTGAATGTT 409
QY 307 CAGGAGCTCAGCGTCGAGAGCTCAAGTCTCGAGTACCTCCGCTTCAAGAGGAGCTT 366
Db 410 AGCGATTGCGCGTTGAGGAGCTTACAGTCTCCGAGTACCTAGCATTCAGAGAGAGCTT 469
QY 367 GTCGAGCGCGACACATGATCCCTAGCTTCTCGAGCTTGAATTCGAGCGCTTCAATGTC 426
Db 470 GTTGATGAGCGCGCCAGAGAGTTCGCTGCTGAGCTTGAATTTGAGCGCTTCAATGCC 529
QY 427 TCAGTCCCAAGCGCTTCAATCGCTCATCATCTATGAAAGCGGTGTCAGTTCCTCAACCGA 486
Db 530 TCCCTCCCAAGCTTCCATGTCCTCAAGTCCATGGAATGGGGTGCAGTTCCTTAACCGT 589
QY 487 CACTGTGCTCAATCATGTTCCGCAACAGGANTGCTTGGAGCGCCCTGTTGGAATTCCTC 546
Db 590 CACTGTCTTCAAGCTGTTCCAGGACAAAGAGAGCTCTACCCACTACTGAACTTCCCTG 649
QY 547 CGTGGCCCGGACAGAGGCGATGTTATGCTTCAATGATAGATACAAAGCTTGGGG 606
Db 650 AAGGCCATTAACCAAGGCGCAGCAATGATGCTAAGCAGCAATACGAGCTTCGT 709
QY 607 AGGCTTCAGTGTGCTGACCAAGCTGAGGAGCACTTGTCAAGCTCCCTGCTGACACA 666
Db 710 GGGCTCCATCAGCCCTTAGAAGGCGAGAGAGTATCTAACAGCATCTTGAAGACACC 769
QY 667 CCATACACAAATTTGCTTATAAATTCAGAGTGGGGCTGGAGAAAGTTGGGGTGAAT 726
Db 770 CCGTCTTTGAGTTCAACCAAGCTTCCAAGAGCTTGGGCTTGGAGAAAGGTTGGGGTGAC 829
QY 727 ACAGCAGGACATGTTTGGAAATGATCCATCTCTCTAGACATCTCAGGGCGCAGAC 786
Db 830 ACCGTAGCGGTGACAGGACACATCCACTCTCTCTGCTCTGATCTGCTGAGGCGCCCTGAT 889
QY 787 CCATCTACCTAGAGAAATTTCTTGGGAGGATCCCATGATTTTAAAGCTTGTGTGATA 846
Db 890 CCAGCAGCTTGGAGAAATTTCTTGGAACTATACCGATGATTTCAATGCTGTTATCCTG 949
QY 847 TCCCTCTAGGATCTTGGTCAAGCTAATGATTAAGGCTTGGCTGCGACACAGAGAGCAG 906
Db 950 TCTCCACAGGATATTTGCTCAATCCAAATGTTGGGATACCCCTGATACCGGTGGGCCAG 1009
QY 907 ATCGTCTATATACTGACCAAGTCCGTGACATAGAAATGAGATGCTTCCGTTTAAG 966
Db 1010 GTTGTGATCATTTGGATCAGTCCCGTCTTGGAAATGAGATGCTTCTGAGGATTAAG 1069
QY 967 AAACAGGCGCTGATGTTTCCCAAGATTTCTCATTTGTTACTCGGCTGATACAGATGCA 1026
Db 1070 CAGCAAGGCTTGGACATAACCCCTAGATCTCTCATTTGTCACCAAGTGTGTTGCTGATGCT 1129
QY 1027 AAAGGAACATCATGAAATCAGCGCTTGGAGAGAAATTAGTGGAAACACAGCATACTTACATA 1086
Db 1130 GTTGAACACTACATGTGGCCAGCGGCTGGAGAGGTTATTGGGACTGAGCACACTGACATT 1189

QY 1087 TTACGAGTTCCTTCCAGAAATGAAATGGGATCTTAAAGAAATCGATATCAAGATTTGAT 1146
Db 1190 CTTCTGTTTCCATTCAGAACTGAAAGGGATCTCCGCTAAGTGGATATCTCGTTTIGAT 1249
QY 1147 GTCTGGCCATATCTGGAACATTTGCTGAGGATGCTGCTGGTGAATTTGCTGCTGAATTA 1206
Db 1250 GTCTGGCCATATCTGGAACATTTGCTGAGGATGATACCGGAGATTTGCAAAAGAACTCATGAGAGAAATG 1309
QY 1207 CAAAGTACTCTCAGACTTTCATAATTTGGAATCTACAGTATGGAATCTTGTGGCGCTCATTTG 1266
Db 1310 CAGACCAAGCTGATCTCTATTATTGGCACTACAGTGAOGTAACTTGTGCGCACCTG 1369
QY 1267 CTATCTTACAGATGGAATTTACCCAGTGAACATTTGCTCATGCTCTGGAAGAGCTTAAG 1326
Db 1370 CTCGCGCATTAAGTTGGGAGTTTACCCAGTGAACATTTGCTCCCATGCTTTGGAGAAACCAAA 1429
QY 1327 TATCCAGACTCAGACATATTTTGAAGAAATTTGATGAGAGTACCAATTTCTCTGCTGCCAG 1386
Db 1430 TACCCCACTCAGACATATATTTGGACAAATTTGACAGCCAAATACCAATTTCTCATGCCAG 1489
QY 1387 TTCACTGCTGATATAATTTGCTATGAACAAATGCTGATTTTATCATCACAGCACATACCAA 1446
Db 1490 TTCCTGCTGACCTTATTGCTATGAATCACTGATTTTATCATCACAGCACATTCAG 1549
QY 1447 GAAATGCTGGAAGCAAAATATCTGTTGACAGTATGAGAGTCTACTGCTTTACTCTG 1506
Db 1550 GAAATGCTGGAAGCAAGGACAGCGTGGGCCAGTATGAGTCTTCAATTTGCTTCCGCTC 1609
QY 1507 CTTGCTGCTGACGAGTTGCTGATGGATCGATGCTTTCGATCCAAAGTTCAATATAGTC 1566
Db 1610 CTTGATCTCTACCGTGTGCTCAATGGATGAGGTTGAGTTCGATCCCAAGTTCAATTTGTC 1669
QY 1567 TCTCTGAGCTGACATGCTTCAATATATCTTTTCCATATCCAGAGGCGCAAGGAGCTCAC 1626
Db 1670 TCTCTGAGCAGATATGAGGCTTCTACTTCCCATACACTGAACTGACAGAGGCTTACT 1729
QY 1627 TCTCTTATGCTTCAATCGAAATTTGATTTATGACCCGAGAGCAAGAGTGAACAT 1686
Db 1730 GCTTCCACCTCGAAATTTGAAGAGCTCTTTTACAGCGATGTTGAGAACTCTGACACAAAG 1789
QY 1687 GGGCACTTGTGATGACCGCTCAAGCCCATCTCTTCTCCATGCGCAAGCTCGACAGGCTG 1746
Db 1790 TTTGATTTAGAGCAAGAAACAGCCGATCATTTTCAATGCTGCTGCTTGAACCGTGTG 1849
QY 1747 AAGAACATAACAGGGCTGCTGAGAGCTTTTGTAGTGGCTAAGCTGAGGAGGAGCTGGTA 1806
Db 1850 AAGAACATACAGGCTTGGTTGAGATGTTTGGTAAAGAAATGCTCATCTGAAGGATTTGGCA 1909
QY 1807 AACCTTGTGCTGCTGCGGCTACATGATGTCAAACAGTCCAGGACAGGAGAGATC 1866
Db 1910 AACCTTGTGATTTGCTGCTGCTGAC---ATGGCAAGAGTCCAGGATAGGGAGGAGCAG 1966
QY 1867 GCGAGATAGAGAAATGATGAATCATCAAGACCCACAACTTGTTCGGGCGAGTTCCGC 1926
Db 1967 GCTGAGTTCAAAGAGATGATACAGTCTCATTTAGGAGTACAGCTGAAGGCGCATATCCGG 2026
QY 1927 TGGATCTTCCCGAGCAAAAGGCGCCGTAACGCGAGCTCTATCGCTACATCGCTGAT 1986
Db 2027 TGGATCTCAGCTCAGATGAACCGTGTTCGCAATGCGAGTGTACCGCTACATCTGTGAC 2086
QY 1987 ACCCATGCTGCTTCTGACAGCGGCTTCTATGAAGCGTTCCGCTCTCACCGCTGTGAG 2046
Db 2087 ACCAAGGCGCATTTGCTTCCAGCCCGCTTCTATGAAGCATTTGGCTGACTGTTATCGAG 2146
QY 2047 GCCATGACCTTGGGCTTCTCTACTTTCGCGACCGCTCCATGAGGCTCCAGCTGAGATCATTA 2106
Db 2147 GCCATGACATGCTGTTTCCGACAAATAGCGACATGCTATGCTGGCCAGCTGAAATCATTT 2206
QY 2107 GAGCATGCGGCTCTCGGCTTCCCATGAGCCGCTACCAACCCGAAACAGGCTGTTAATCTG 2166
Db 2207 GTGGATGCTGCTGCTGTTTGCATCGATCTTACCAAGTGAAGGCTGCGAGATATC 2266
QY 2167 ATGGCCGACTTCTTCCAGCGGTGCAAGCAAGCCAGATCACTGGGTGAATATATCTGGA 2226

Db 2267 CTGGTCACTCTTTGAGAAATCCAGCGGATCCAACTCTCGGACAAATGTCGGA 2326
 Qy 2227 GCAGGCTCAGGCATATACAGAAAGTACATGAGAAATATCTCAGAGAGGTTGATG 2286
 Db 2327 GAGGSCCTGAAGAGATTTATGAGAAAGTACACCTGGAAGCTGTACTCAGAGAGGCTGATG 2386
 Qy 2287 ACATGCGCGGCTCTACGCTTTCTGGAAGTACGCTCGAAGCTCGAGAGGCTGAGAGC 2346
 Db 2387 ACCCTGACTGGTATATATGTTCTGGAAGTACGCTGAGCAACCTTGAGAGGCTGAGACT 2446
 Qy 2347 AGCGGCTACCTTGAGATGTTTACATCTACTGAAAGTTCCGCGAGCTGCGAAGACCGTGC 2406
 Db 2447 CGCGGTTACCTTGAGATGTTTACATCTACTGAAAGTACCGAGCTGCGAGCTGAGTTCCA 2506
 Qy 2407 CTTCGAATGAC 2418
 Db 2507 TTGGCTGTCGAC 2518

RESULT 13

ID ABK98516 standard; cDNA; 2829 BP.
 XX AC ABK98516;
 XX DT
 XX DE 21-OCT-2002 (first entry)
 XX DE cDNA sequence encoding perennial ryegrass sucrose synthase.
 XX KW Perennial ryegrass; sucrose phosphate synthase; SPS; invertase; INV;
 KW sucrose synthase; SS; sucrose:sucrose 1-fructosyltransferase; SST;
 KW sucrose transporter; ST; fructan:fructan 1-fructosyltransferase; FFT;
 KW sucrose:fructan 6-fructosyltransferase; soluble carbohydrate transport;
 KW SST; soluble carbohydrate metabolism; plant; gene; ss.
 XX OS
 XX OS Lolium perenne.
 XX PN WO200231130-A1.
 XX PD 18-APR-2002.
 XX PF 10-OCT-2001; 2001WO-AU001275.
 XX PR 10-OCT-2000; 2000AU-00000673.
 XX PR (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
 XX PA (AGRE-) AGRESEARCH LTD.
 XX PI Spangenberg G, Sawbridge TI, Ong EK, Emmerling M;
 XX WPI; 2002-444177/47.
 XX DR P-PSDB; ABG69063.
 XX PT New enzymes and transporter proteins involved in metabolism and/or
 PT transport of soluble carbohydrates, useful as molecular genetic markers,
 PT and in modifying soluble carbohydrate metabolism and/or transport in
 PT plants.
 XX PS Claim 5; Fig 74; 177pp; English.
 XX CC The present invention relates to the isolation of polynucleotide
 CC sequences encoding perennial ryegrass enzymes or transporter proteins
 CC selected from sucrose phosphate synthase (SPS), invertase (INV), sucrose
 CC synthase (SS), sucrose transporter (ST), sucrose:sucrose 1-
 CC fructosyltransferase (SST), fructan:fructan 1-fructosyltransferase (FFT),
 CC and sucrose:fructan 6-fructosyltransferase (SFT). The nucleic acid
 CC sequences of the invention are useful as molecular genetic markers, to
 CC isolate cDNAs and genes encoding homologous proteins from the same or
 CC other plant species, and for the modification of soluble carbohydrate
 CC metabolism and/or transport in plants. The polypeptide sequences may be
 CC used to immunise animals to produce antibodies with specificity for the
 CC proteins, and these antibodies may then be used to screen cDNA expression

CC libraries to isolate full-length cDNA clones of interest. ABK98425-
 CC ABK98516 represent nucleotide sequences encoding perennial ryegrass
 CC enzymes or transporter proteins involved in the metabolism and/or
 CC transport of soluble carbohydrates
 XX SQ Sequence 2829 BP; 697 A; 678 C; 697 G; 757 T; 0 U; 0 Other;
 Query Match 41.2%; Score 1134.6; DB 6; Length 2829;
 Best Local Similarity 67.5%; Pred. No. 4.2e-246;
 Matches 1628; Conservative 0; Mismatches 774; Indels 9; Gaps 2;
 QY 7 GCGCCGAGCTGAACCGCAACGCGAGCATCCGCGAGCGGCTCGAGGACACCTCCACGCG 66
 Db 102 GTGTGCAAGCTGACTGCTCCACACTCTCCGCGAGCGCTTGTGCTGCCACTTCTCTCC 161
 QY 67 CACCGCAACGAGCTGTCGCTCTCTCCAAAGTACGTGAAACAAAGGGAAGGCACTCTG 126
 Db 162 CATCTTAAGAGCTCATTTGCCCTCTTTCAAAGTATGTTTCAACGAGGCAAGAAATGCTT 221
 QY 127 CAGCGCACCATCATCTCGACGCGCTCGACGAGGTCCAGGGCTCCGCGGCTCCGCGCTC 186
 Db 222 CAGCGCACCATCATCTCGACGCGCTCGACGAGGTCCAGGGCTCCGCGGCTCCGCGCTC 275
 QY 187 GCGCGAGGACCTTCTCGACGCTCTCCGCTCCGCGAGGAGCGGATCGTCTGCCGCGCG 246
 Db 276 AGATATGCAACCTTTGAAGACATTAATCCGTCTGCTCAGAGAGCAATTTGCTTGCCTCC 335
 QY 247 TTCGTGCGCATCGCGGTGCGCGCGCGCGGAGTTTGGAGTACCTCCGCGTCAACGCTT 306
 Db 336 TGGGTGCACTGCGCATCAGGCTAGGCGCGGTGCTCGGACTTACATACGCGTGAATGT 395
 QY 307 CAGGAGCTCAGGCTCGAGCAGCTCAAGTCTCGGAGTACCTCCGCTTCAAGGAGGAGCTT 366
 Db 396 AGCAGTTGGCTGTGAGGAGCTGACAGTTCCGAGTACCTAGCAFTCAAGGAACAGCTT 455
 QY 367 GTGAGCGCGCAGCAATGATCCCTACGTTCTCGAGCTTGACTTCGAGCGGTTCAATGTC 426
 Db 456 GTGATGAGCAGCGCAGCAGCAAGTTTGTGCTTGAGCTTGATTTGAGCGCTTCAATGCT 515
 QY 427 TCAGTCCCAAGCCCAATCGGTCACTATATGGAACGGGTGTCAGTTCCTCAACCGA 486
 Db 516 TCGTTCCCGCGCTCTTCCATGTCCAAAGTCCATTTGGAATGGGGTGCAGTTCCTTAAACCGT 575
 QY 487 CACTTGTCTCAATCATGTTCGCAACAGGATGCTTCGAGCGCGCTGTGATTTTCCCTC 546
 Db 576 CACTGTCTTCAAGCTGTTCCAGGACAGGAGAGCTCTACCCACTACTGAACTTCCCTG 635
 QY 547 CGTGGCCACCGGCACAAAGGGGCAATGTTATGATGCTTAAATGATAGATACAAAGCTTGGG 606
 Db 636 AAAGCCCATTAACATACAGGGCACCAATGATGCTAAATGACAGATTCAGAGCGCTTCGT 695
 QY 607 AGGCTTCAGTCTGTGCTGACCAAGCTGAGGAGCACTTGTCAAAGCTCCCTGCTGACACA 666
 Db 696 GGGCTCCAGTCAAGCCCTTAGAAGGCAAGAGATTTTAAACAGCATCCCTCAGGACACC 755
 QY 667 CATACTCACAATTTGCTTATAAATTTCAAGAGTGGGCTCGAGAAAGGTTGGGTGAT 726
 Db 756 CGTCTCTGAGTTCAACCAAGGTTCCAGAGCTTGGCTTGGAGAGAGGTTGGGCGGAC 815
 QY 727 ACAGCAGGACATGTTTTTGGAAATGATCCATCTCTCTTAGACATCATTCAGCGCGCAGAC 786
 Db 816 ACCGCTAAGCGGTACAGGACTCCATCCACTTGTCTTGTACTTCTGAGCGCCCTGAT 875
 QY 787 CCATCTACCTTAGCAAAATTTCTGGGAGGATCCCATGATTTTAAAGTCTGTTGTTGA 846
 Db 876 CAGCGACTTGGAGAGTTCTTGGAACTATACCAATGATTTCAATGTTTCAATGTTTATCTCG 935
 QY 847 TCCCTCATGATATCTTTGGTCAAGCTAATGATTTAGGCTTCCAGAGACACAGGAGACAG 906
 Db 936 TCTCAGCAGGATATTTTGTCTCAATCCATGTTTGGGATACCCCTGATCTAGTGGTGGCAG 995
 QY 907 ATCGCTATATCTGAGCAAGTCCGCTACCTAGAAAATGAGATGTTTCTCGGTTTAAAG 966

996	Db	GTTCGTGACATCTTTGGATCAAGTCCGTGCTTTTGGAGAAATGAGATGCTTCTTGAGATTAAG	1055
967	Qy	AAACAAGGGCTTGATGTTTCCCAAGAAATCTCATTTGTTACTCGGTGATACACAGATGCA	1026
1056	Db		
1056	Db	CAGCAAGGCTTGACATAACCCCTAAGATCCTCATTTGTACACAGGCTTTGCTGTATGCT	1115
1027	Qy	AAAGGAACATCATGCAATCAGGGCTTTGAGAGAAATTAGTGGAAACAACAGCATATTTACATA	1086
1116	Db		
1116	Db	GTTTGGAACTACATGTGGCCAGGGCTCGAGAAAGTTATTGGGACTGAGCACACTGACATT	1175
1087	Qy	TTACGAGTTCCTTTCAGAAATGGAATGCGATCTTTAAGAAATCGATATCAAGATTGAT	1146
1176	Db		
1176	Db	CTCCGTGTTTCATTTTCAGACTGGAAGAGGGATCCTCGTAAGTGGATCTCTCTGTTTGGAT	1235
1147	Qy	GTGTGGCCATCTTGGAATAATTTCTTGAGAGATGCTGCTGGTGAATTTGCTGTGTAATTA	1206
1236	Db		
1236	Db	GTCTGGCCATACCTGGAGACATACACCGAGATGTTTGCAAACGAACTCATGAGAGAAATG	1295
1207	Qy	CAAGGTACTCCAGACTTCATAAATTGGAACATCAGTGAATGGAATCTGTGGGGTCAATG	1266
1296	Db		
1296	Db	CAGACCAAGGCTGATCTCATTTATTTGGCAACTACAGTGAACGTAACCTTTGTGGCCACTCTG	1355
1267	Qy	CTATCTTTACAGATGCGAAATTTACCCAGTGGCAATTTGCTCATGCTCTGGAAAGACTAG	1326
1356	Db		
1356	Db	CTTGGCGATAGTTGGAGTTTACCCAGTGGCACTATGCCCCATGCTTTTGGAGAAACAAAG	1415
1327	Qy	TATCCAGATTTCAGACATATTTTGGAGAAATTTGATGAGAATGACCAATTTCTCTGCGCAG	1386
1416	Db		
1416	Db	TACCAAACTCAGACATATATTTGGACAAATTTGACAGCCAAATACCATTCTCATGCCAG	1475
1387	Qy	TTCTACTGCTGATATAATTTGCTATGAAACAATGCTGATTTATATCATCACGACATACCAA	1446
1476	Db		
1476	Db	TTCACTGTGACCTTATTTGCCATGAAATCACTGATTTTCATCATCACGACCAATTCAG	1535
1447	Qy	GAAATGCTCGAAGCAAAATACTGTTTGGACAGATGAGAGTCACTACTGCTTTACTCTG	1506
1536	Db		
1536	Db	GAAATGCTGGAAGCAAGGACAGGCTGGGGCAGTATGAGTCTCACATGTCTTTCACTCCCTC	1595
1507	Qy	CCTGGTCTGTACCGAGTTGTCATGGGATCGATGCTTTCCGATCCAAAGTTCAATATAGTC	1566
1596	Db		
1596	Db	CTTGATCTTACCGTTTTCATGGGATTTGACGTGTTCCATCCCAAGTTTCACATTTGTC	1655
1567	Qy	TCTCCTGGAGTGCATGTCCATATATCTTTCCACATACCGAAGAGGCCAAGGACTCACCC	1626
1656	Db		
1656	Db	TCTCCTGGAGCAGATATGACTGTCTACTTCCCATACACTGAACTGCAAGAGGCTTACT	1715
1627	Qy	TCTCTTCATGTTCAATCGAABATTTGATTTATGACCCGGGACGAAACGATGACACATT	1686
1716	Db		
1716	Db	GCCTTCACCCCTGAAATGGAAGAGTCCCTTTACAGCGATTTGAGAACTCTGSAACCAAG	1775
1687	Qy	GGGCATCTGGATGACCGGTCAAGGCCCATCCTCTTCTTCATGGCAAGACTCGACAGGTTG	1746
1776	Db		
1776	Db	TTTGATTTGAAGGACAAAGACAGGCTTATCATCTTCTCAATGGCTCGCTTGACCGTGTG	1835
1747	Qy	AAGAACTAACAGGGCTGGTGAAGCTTTTGTCTTAAGTGCCTAAGCTGAGGGAGCTGGTA	1806
1836	Db		
1836	Db	AAGAACTATGACAGGCTTGGTTGAGATTTCCGTAAGAAATGCTCATCTGAAGGATTTGGCA	1895
1807	Qy	ATCCTTGTCTGTTGGCGGGTCAATATGATCTCAAGTGTCCAGGACAGGGAAGATGATC	1866
1896	Db		
1896	Db	AACCTTGTGATTTGTCTGTGTGACCATG---GCAAGAGGTCCAAAGGATAGGGAGGAGCA	1952
1867	Qy	GCGGAGATAGAGATGATGAACTCATCAAGACCCACAACTTTTTCGGGCAAGTTCCCG	1926
1953	Db		
1953	Db	GCTGAGTTCAAGGATGTACGTCTCATTTGAGAGATCAAGTTTGGAGGCCATATCCGG	2012
1527	Qy	TGGATCTCTGCCACAGACAAACAGGGCCCGTTAACGGGAGCTCTATCGCTACATCGCTGAT	1986
2213	Db		
2213	Db	TGGATCTCAGCTCAGATGAACCGTGTTCGCAATGTCAGAGTTGTACCGTACATTTCTGTAC	2072
1387	Qy	ACCATGGTCTTCTGTACAGCGCGCTTCTGTATGAGAGCTTTGGTCTCACCCGCTGTGAG	2046
2073	Db		
2073	Db	ACCAAGGGCGCATTTGTTTCAGCTCGCATTTCTATGAAGCATTTGGCTGTGATGTTGCGAG	2132

Qy	2047	GCCATGACGTGTGGGCTTCTCTACTTTTCGCAACGCTCCATGAGAGGTCCAGCTGAGATCATTA	2106
Db	2133	GCCATGACATGTGTGTTGGCCCAATAGACACATGCGCATGTGTGGCCGACGCTGAAATCAATT	2192
Qy	2107	GAGCATGGCGTCTCGGCTTCCACATTGACCCCTACACCCGAAACAGGCGTGTTAATCTCG	2166
Db	2193	GTGAATGGTGTCTCTGTTTGGACATCGATCTCTTACCAAGTGCACAGGCTCGAGATATC	2252
Qy	2167	ATGCGCGACTTCTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAAATATATCTGGA	2226
Db	2253	CTGGTCAACTTCTTGGAGAAATCCACGGCGGATCCAACTTACTTGGGCAAAATGTCCGAA	2312
Qy	2227	GCAGGCGTCAGCGGCTATACGAGAAGTACACATGGAAGATATACTCAGAGAGGTTGATG	2286
Db	2313	GGTGGCCCTGAAGAGAAATTATGAGAGACTACACTGGAAGCTGTACTCAGAGAGGCTGATG	2372
Qy	2287	ACACTGCCGGGCTCAACGTTTCTGGAAGTACTGTCGAAGCTCCAGAGGCTGGAGACG	2346
Db	2373	ACCTGACTGGTGATATGTTTTCTGGAAGTATGTGAGTAACTTGGAGGGCGTGAGACT	2432
Qy	2347	AGCGCTACCTTCAGATGTTTCTACATACTCAAGTTCGCGAGCTGGCGGAAGACCGTCCCG	2406
Db	2433	CGCGGTACCTTCAGATGTTTCTACGCTCTGAAGTACCGGACGCTGGCTGCTGCAGTTCCA	2492
Qy	2407	CTTGCAATTTGA	2417
Db	2493	TTGGCTGTCGA	2503

RESULT 14	
AAC66090	
ID	AAC66090 standard; cDNA; 2494 BP.
XX	
AC	AAC66090;
XX	
DT	13-FEB-2001 (first entry)
XX	
DE	Rice sucrose synthase cDNA sequence.
XX	
KW	Cold resistance; transgenic plant; sucrose decomposition; rice;
KW	sucrose synthase; ss.
XX	
OS	Oryza sativa.
XX	
FN	JF2000245279-A.
XX	
PD	12-SEP-2000.
XX	
PF	01-MAR-1999; 99JF-00052102.
XX	
PR	01-MAR-1999; 99JF-00052102.
XX	
PA	(MITA) MITSUI CHEM INC.
XX	
DR	WPI; 2000-675173/66.
DR	P-PSDB; AAY85664.
XX	
PT	Novel method for the reinforcement of cold resistance in a plant
PT	comprising introducing a vector encoding an enzyme that decomposes
PT	sucrose into the plant.
XX	
PS	Claim 1; Page 8-11; 22pp; Japanese.
XX	
CC	This invention relates to a method for the reinforcement of cold
CC	resistance in a plant, comprising introducing an expression vector
CC	a DNA encoding an enzyme for decomposing sucrose connected downstr
CC	a promoter expressible in the plant, and expressing the enzyme in
CC	plant body. Included in the invention are an expression vector use
CC	the method; a transformed plant carrying the expression vector; an
CC	transformed rice carrying the above expression vector. The method
CC	for reinforcing cold resistance in a plant. The present sequence
CC	represents cDNA encoding sucrose synthase used in the method

981	Db	CAGCAAGCCCTTGATATCACACCTAAGATCCTCATTTGTATAACGAGGCTGTTTGCCTTGATGCT	104
1027	Qy	AAAGGAACATCATGCAACTCAGCGCGCTTGAAGAAATTAGTGGAAACACAGCATATCTTACATA	1086
1041	Db	GTTGGTACTACATGCGGCCAGCGGTGGAGAAGGTTATTGSACTGAGCACACTGACATT	1100
1087	Qy	TTAGGAGTTCCTTCAGAAATGAATAAGGATTAATTGAAGAAATGGATATCAAGATTTGAT	1146
1101	Db	CTTCGTGTTCCATTCAAGAGTGAAGATGGTATCCTCCGCAAGTGGATCTCCCGTTTGGAT	1160
1147	Qy	GTCTGCGCATATCTGGAAACATTTCTTGAGGATGCTCGTGGTAAATTTGCTGCTGAATTA	1206
1161	Db	GTCTGCGCATTCCTGGAAACATACACTGAGATGTTGCAAAACGAATTTATGAGGGAATG	1220
1207	Qy	CAAGGTACTCCGACACTTCAATAATTGGAACCTACAGTGAATGGAATCTTTGGGGCTCATTTG	1266
1221	Db	CAAGCCAAACCTGATCTCATCAITGCGCAATTAAGTGAAGAAACCTTTGTGCCACTCTG	1280
1267	Qy	CTATCTTACAGATGGGAATTACCCAGTGCACAAATTTGCTCATGCTCTGGAAGAACCTAG	1326
1281	Db	CTGGCTCACAAATTAGGAGTTAGCCAGTGTACCAATTTGCTCATGCTTTGGAGAAAACCCAA	1340
1327	Qy	TATCCAGATTACAGACATATTTTCSAGAAATTTTCGATGAGAAAGTACCAATTTCTCTGCCAG	1386
1341	Db	TACCCCACTCAGACATATATTGGACAGATTTGACGCCAGTACCACTTCTCATGCCAA	1400
1387	Qy	TTCACTGCTGATAAATTTGCTATGSAACAATGCTGATTTTATCATCACCGACACATACCAA	1446
1401	Db	TTCACTGCTGATCTTATCGCCATGAATCACTGATTTTATCATCATCCAGTACATATCCAA	1460
1447	Qy	GAATTTGCTGGAAAGCAAAATATCTGTTGGACAGTATGAGAGTCAATAGTCTTTACTCTG	1506
1461	Db	GAATTTGCTGGAAAGCAAGCACTGTGGGCGAGTATGAATTCACACATTTGCATTCACCCCTT	1520
1507	Qy	CTGTGCTGTACCGAGTGTCCATGGGATCGAGTCTTCGATCCAAAGTTCAATATAGTC	1566
1521	Db	CTGTGGCTTTACCGAGTTTGCATGGATGATAGATTTTGTATCCCAAGTTTCAACATATGTC	1580
1567	Qy	TCCTCTGGAGCTGACATGTCCATATATCTTCCACATACCGAAGAGGCCAAGCACTCACCC	1626
1581	Db	TCCTCTGGAGCTGACATGATGTCCTACTTCCCGTACACCGAGGCTGACAGAGGCTCACT	1640
1627	Qy	TCCTTTCTAGTTTCAATCGAAATTTGATTTATGACCCCGAGCAAAACGATGAACACATT	1686
1641	Db	GCTTTCCACCTTGAATTTAGGAGACTTCTACAGTGAAGTTCGAGAACCATGAACACAAG	1700
1687	Qy	GGGCATCTGAGTACCGGTCGAAGCCCATCTCTTCCCATGCGACAGCTTCGACAGGGTG	1746
1701	Db	TTTGTATTGAAGGACAGAACAGGCCAATCATCTTCTCAATGCTCTGTCTTGACCCGAGTG	1760
1747	Qy	AAGAACATAACAGGGCTGGTCCGAAGCTTTTGTCTAAGTGGCTTAAGCTGAGGGAGCTGATA	1806
1761	Db	AAGAACATGACAGCTGGTTGAGATGTATGTTAAGATGCAATCTCAGGGATTTGGCA	1820
1807	Qy	AACCTTTGTGTGTTGCCGGGTACAATGATGTCAAAGTTCGAAGGACAGGGGAAGATC	1866
1821	Db	AACCTTTGTGATTTGTTGGTGTACC---ACGGCAATCAGTCCCAAGGACAGGGAGGAGCAG	1877
1867	Qy	GCGGATGATGAGAGATGATGATCACTCATCAAGACCCACAACTTGTTCGGGAGTTCGGC	1926
1878	Db	GCTGAGTTCAAGAAGATGTACCGTCTCTCATTTGACCGTCAAGATTTGAAGGGGACATATCCCG	1937
1927	Qy	TGGATCTCTGCCACAGCAAAACAGGGCCGGTAAACGGCGAGCTCTATCGCTACATCGCTGAT	1986
1938	Db	TGGATCTCAGCTCAGATGAACCGTGTGTGTTAATCGGGAGTTGTACCGATACATTTGTGAC	1997
1987	Qy	ACCATGTTGCTTTTCGTACAGCCCGCTTTGTATGAAGCGTTGGGTTCTACCGTGTGTGAG	2046
1998	Db	ACCAAGGGAGTCTTTGTCAGCGCTGCATTTATGAAGCGTTTGGTCTGACTGTCTGCAGAA	2057
2047	Qy	GCCATGACCTGTGGGCTTCTCTTTTCGGGACGCTCCATGGAGGTCAGCTGATGATCATATA	2106
2058	Db	GCCATGACATGTGGTTTGGCAACATTCGCAACATGCTATGGTGGCCCTGCTGAGATTATT	2117

QY	2107	GAGCATGGCGTCTCGGGTCCACATTGACCGGTACCACCCGAAACAGGCTGTAAATCTG	2166
Db	2118	GTTCATGGGGTGCTGTGCGCATTTGATCCCTTACCACAGTGACAGGCTGCTGATATC	2177
QY	2167	ATGCCCACTTCTTCGACCGGTCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGA	2226
Db	2178	TTGGTCAACTCTTTTGAGAAAGTCAACGAGATTACCTTACTGGACATATTTCCACAG	2237
QY	2227	GCAGGGCTGCAGCGCATATACGAGAAGTACACATGGAGAGTTATCTCAGAGAGGTTGATG	2286
Db	2238	GGAGGCTCGCAGAGAGATTACGAGAAGTACACCTGGAAGCTGTACTCTGAGAGGCTGATG	2297
QY	2287	ACACTGCCGGGFTACGGTTCCTGGAAGTACGTGTCGAGCTCCGAGAGGCTGGAGACG	2346
Db	2298	ACCTTGACTGGTGATACGGATTCTGGAAGTACGTAAAGCAACCTTGAGAGCGCGAGACT	2357
QY	2347	AGGCGCTACCTTGAGATGTTCTCATATCTGAAAGTTCCGCGAGCTGGCGAAGACCGGTGCCG	2406
Db	2358	CGCGGTTACATTGAGATGTTCTATGCTCTGAATACCGCAGACCTGSCCAGCGCGGTCCCA	2417
QY	2407	CTTGCAATTGA	2417
Db	2418	TTGGCTGTGCA	2428

RESULT 15

ID ADC68423 standard; cDNA; 2714 BP.

ADC68423;

DT 18-DEC-2003 (first entry)

DE Lolium perenne fructan biosynthesis protein cDNA SEQ ID NO:133.

KW Lolium perenne; Festuca arundinacea; lignin; fructan; tannin;

KW biosynthetic pathway; plant; gene; ss.

OS Lolium perenne.

PN WO2003040306-A2.

15-MAY-2003

07-NOV-2002: 2002WIN-NZ0000239

XX
PR 07-NOV-2001: 2001HS-0337703P

XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (WRIG-) WRIGHTSON SEEDS LTD

PI Demmer J, Forster RL, Gibson JB, Shenk MA, Norriss MG, Glenn M;
 PI Saulsbury KM, Hall C;
 PI

AA
DR
WPI: 2003-441544/41.

DR WPT: ZC03-441544/
DR P-PSDB: ADC68459.

XX New polynucleotide encoding polypeptides from *Lolium perenne* or *Festuca*
 PT arundinacea, useful for modulating the biosynthesis of lignin, fructan or
 PT tannin in a plant.

PS Claim 1: SEO ID NO 133: 240pp- English

The present invention describes isolated polynucleotides (I) encoding proteins (II) from *Iolium perenne* and *Festuca arundinacea* which are active in lignin, fructan and tannin biosynthetic pathways. Also described: (1) an isolated oligonucleotide probe or primer comprising at least 20 contiguous residues complementary to 10 contiguous residues of (I); (2) a kit comprising the oligonucleotide probe or primer; (3) a genetic construct comprising (1); (4) a transgenic plant cell comprising the genetic construct of (3); (5) a plant or its seed, fruit or progeny comprising the transgenic plant cell of (4); (6) modulating one or more

of the lignin, fructan or tannin compositions of a plant; (7) producing a plant having one or more of the lignin, fructan or tannin compositions; and (8) modifying the activity of (II) involved in a lignin, fructan or tannin biosynthetic pathway in a plant. II) can be used for modulating the biosynthesis of lignin, fructan or tannin in a plant. The present sequence is used in the exemplification of the present invention.

Sequence 2714 BP; 656 A; 664 C; 671 G; 723 T; 0 U; 0 Other;

Query Match 41.1%; Score 1133; DB 9; Length 2714;
Best Local Similarity 67.5%; Pred. No. 9.5e-246;
Matches 1627; Conservative 0; Mismatches 775; Indels 9

QY	7	GC	CC	GA	AG	CT	GA	AC	CG	GA	CA	CC	CT	CC	CG	CG	66
Db	48	GC	TC	CA	AG	CT	CG	GA	CG	CG	CG	CT	CT	CT	CG	CG	1.07

QY	67	108
Db	CACCGCAACGAGCTGGTCGCCCTCTCTTCAAGTACGTGAACAAGGGGAAGGCATCCTG	1267
Db	CATCTCTACGAGCTCATTCGCCCTCTTTTCAAGTATGTTCAACGAGGCACAGGAATGCTT	167

QY 127 CAGCCGNCACATCTCTCGACGCGCTCGACAGGTCACAGGCTCCGGGGTCCGGCGCTC 186

DB 168 CAGCGCCACACGCTGCTCACTGAGTTTGAAGCCTT-----GTTTGAGGCTGACCAAGGAG 221

Qy	187	GCAGAGGACCCCTCTCTGACGCTCCGCTCCGCGCAGGAGCGATCGTCTGC	246
		CGCG	
Dp	222	AGATATGACCCCTTTGACGACATCTCCGCTGCTTCAGTAAGCAATTCGCTGC	281
		CGCG	

Qy	247	TTCTGGCCATCGGGGTGCGCCCGCGCTTGGAGTACTCCGCGTCAACGTT	306
Dβ	282	TGCGTTGCACTGGCCATCAGGCTCTGGTCTGGAGCTATATACGCGTCAATCTT	341

Qy	307	CACAGCTCAGCGTCGAGCGCTCACAGTCTCGAGTAGCTCCGGTTCAAGGAGGAGCTT	366
Db	342	AAGGAGTTGGCTGTGAGCGACTCAGTTCCAGTATCTTCCCATTCATTCGATTCGATTC	401

QY
Db

367 GTGAGCGGCCAGCAATGATCCCTACGTCTCGAGCTTGACTTCGAGCGCCTTCAATGC 426
|||||
402 GTTAGTGGCGACCGCCGACGACACTCTCCGTTGCGATTGATTTTATGCGCTTGAATGCG 461
|||||

QY 427 TCAGTCCGACGCCAAATCGGTGCATCATTCATGAAACGGTGTCCAGTTCCTCAACCGA 486

[illegible][illegible]

QY 607 AGCGTTTCAGTGTGTGTCGACCAAGCTGAGGACACTTGTCAAGCTCCCTGCTACACA 666

QY 667 C C T A C C A C A T T T G C T T A T A A A T T T C A A G A G T G G G C C T C G A A A C G T T G G G T G A T 726

QY 727 ACAGCAGGACATGTTTGGAAATGATCCATCTCTTCTTAGACATCATTCAGGCGCCAGAC 786

QY 787 CCATCTACCCCTAGAGAAATCTTGGGGAGGATCCCCATGATTTTAACTTTGTTGGTGA 846

847 TCCCCTCATGTACTTTGGTCAAGCTAATGTATTAGGCTTGCACACACAGGAGACAG 906

Qy	907	ATCGCTATATAC	TGGACCAAGTCCGTGCACTAGAAAAATGAGATGGTTCTCCGTTTAAAG	966
Db	942	GTTCGTGTACATCTTTGGATCAAGTCCGTGCTTTGGAGAAATGAGATGCTTCTGAGGATTAAG	1001	
Qy	967	AAACAAGGGCTTGATGTTTCCC	AAAGATTTCTCATTGTTACTCGCTGGTGATACCAAGATCA	1026
Db	1002	CAGCAAGGCCCTTGACATAAACCCCTAAGATCTCTCATTGTCAACAGGCTGTTTGCCTGATGCT	1061	
Qy	1027	AAAGGAACATCATGCAATCAAGCGCTTGAGAGAAATAGTGGAAACACAGCATACTTACATA	1086	
Db	1062	GTTCGAACATCATGTGCCACGCGCTCGAGAAAGTTATTGGGACTGAGCACATGACATT	1121	
Qy	1087	TTACGAGTTTCCTTCAGAAATGAAAAATGGGATACCTTAAGAAATGGATATCAAGATTTGAT	1146	
Db	1122	CTCCGTGTTCCNTTCAGAACTGAGAGGGGATCTCCCGTAAGTGAATCTCTCGTTTGTGAT	1181	
Qy	1147	GTGTGGCCATACCTGGAACATTTGCTTGAGATGCTCTGGTGAATTTGCTGCTGAATTA	1206	
Db	1182	GTCTGGCCATACCTGGGAGATACACCGAGGATGTTGCNAACGGAACCTCATGAGAGAAATG	1241	
Qy	1207	CAAGGTACTCCAGACTTCATAATTTGGAACCTTACAGTGATCGAAATCTGTGGCGGTCAATG	1266	
Db	1242	CAGACCAAGCCTGATCTCTATTATTGGCACTACAGTSGCGGTAACTTTGTGCGCACTCTG	1301	
Qy	1267	CTATCTTCAAGATGGGAAATTACCCAGTCAACATTTCTCATGCTCTGGAAGAAAGACTTAAG	1326	
Db	1302	CTTGGCGATAAAGTTGGGAGTTACCCAGTGCACCAATTTCCCATGCTTTGGAGAAAACAAAA	1361	
Qy	1327	TATCCAGATTCAGACATATTTTGGAGAAATTCGATGAGAGTACCAATTTCTCTGTCGCAG	1386	
Db	1362	TACCCCAACTCAGACATATATTTGGACAAATTTGACAGCCAAATACCAATTTCTCATGCCAG	1421	
Qy	1387	TTCACTGCTGATATAATTTGGTATGAACAAATGCTGATTTATATCATCAGCAGACATACCAA	1446	
Db	1422	TTCACTGCTGACCTTATTGCACTGAATCACTGTGATTTCACTCATCAGCAGCAATTTCCAG	1481	
Qy	1447	GAATTTGCTGGAAGCAAAAATACTGTTTGGACAGTATGAGAGTCATATGCGCTTTACTCTG	1506	
Db	1482	GAATTTGCTGGAAGCAAGGACAGCGTGGGCCAGTATGAGTCTCACATTTGCTTTCACCCTC	1541	
Qy	1507	CCGTGCTGTACCGAGTTGTCATGGGATCGATGTCTTCGATCCAAAGTTCAATATAGTC	1566	
Db	1542	CCGTGATCTCTACCGTGTGTCCATGGGATTTGAGTGTTCGATCCCAAGTTTCAACATGTC	1601	
Qy	1567	TCTCTGGAGCTGACATGTCCATATATCTTTCCATACCCAGAGGCCAAGCGACTCAAC	1626	
Db	1602	TCTCTGGAGCGATATGATCTGTCTACTTCCCTCATCTGAACTGACAGAGGCTTTACT	1661	
Qy	1627	TCTCTTCATGGTTCAATCGAAAAATTTGATTTATGACCCGGAGCAAAAAGTAAACATTT	1686	
Db	1662	GCCTTCCACCTGAAAATTGAAGAGTCTCTTTACAGTGTATTTGAGAACTCTGAACACAAAG	1721	
Qy	1687	GGGCACTGATGACCGGTCAAAGCCCATCTCTTCTCCATGGCAAGACTCGACAGGGTG	1746	
Db	1722	TTTGTATTGAGGACAAGAAACAAGCCTATCATCTCTCAAATGGCTCGCTGTGACCGGTG	1781	
Qy	1747	AAGAAACATAACAGGCTGTGTGAGCTTTTGTCTAAGTGCCTAAGCTGAGGGAGCTGATA	1806	
Db	1782	AAGAACTGACAGCCTTGGTTGAGATGTTTGGTAAGAAATGCTCATCTGAAGGATTTTGGCA	1841	
Qy	1807	AACTTTGCTGCTGTGTCGGGTCAATGATGTCAAAAGTCCAGGACAGGGAGAGATC	1866	
Db	1842	AACTTTGCTGATTTGCTGTGGTGACATG---GCNAAGGAGTCCAAAGNATAGGAGAGGACAG	1898	
Qy	1867	GGGAGATGAGAAAGATGCAATGAACTCATCAAGACCCCAACAATTGTTTCGGGCAAGTTCCCG	1926	
Db	1899	GCTGAGTTCAAAAGGATGTACAGTCTCATTTGAGAGGTACAAGCTGGAGGGGCCATATCCCG	1958	
Qy	1927	TGATCTCTCCACAGACAAACAGGGCCGTTAAAGGGGAGTCTTATCGCTACATCGCTGAT	1986	
Db	1959	TGGATCTCAGCTCAGATGAACCGGTGTTTCGCAATTCAGAGATTTGACCGCTACATTTCTGAC	2018	
Qy	1987	ACCATGCTGCTTTTCGTACACCGCGGCTCTGTATGAAGCGTTTCGGTCTCACCGCTGTTGAG	2046	

Db	2019	ACCAAGGGCGCATTTGTTGAGCGTCGATCTATGAAGCAATTTGGCGCTGACTGTTGTCGAG	2078
Qy	2047	GCCATGACTGTGGGCTTCTACTTTTCGGACGCTCCATGAGGTCACAGCTGAGATCATTA	2106
Db	2079	GCCATGACATGTGGTTTGCCCAATAGCGACATGCCATGTGGCCGAGCTGAATCAATT	2138
Qy	2107	GAGCATGGCGTCTCGGGCTTCCACATTCAGCCGCTACCACCCGACAGGCTGTTAATCTG	2166
Db	2139	GTGAATGGTGTCTGGTTTGCAATCGATCCTTACACAGTGCAAGGCTCGAGHTATC	2198
Qy	2167	ATGCGCGACTTCTTCGACCGGTGCAAGCAAGACCCAGATCACTGGGTGAATATATCTGGA	2226
Db	2199	CTGCTCAACTTCTTTGAGAAATCCACGGCAGATCCAACTTACTGGGACAAAATGTCGGA	2258
Qy	2227	GCAGGGCTCGAGCGCATATACGAGAAGTACACATGGAAGATATATCTCAGAGAGGTTGATG	2286
Db	2259	GGTGGCTGAAGAGAAATTTATGAGAAGTACACCTGGAAGCTGTACTCAGAGAGGCTGATG	2318
Qy	2287	ACACTGGCCGGGCTCTAOGGTTTCTGGAGTAGTGTCGAGCTCGAGGTCGAGGGCTGGAGCG	2346
Db	2319	ACCTTGACTGGTGTATATGGTTTCTGGAAGTATGTGAGCAACCTTGAGAGGGCTGAGACT	2378
Qy	2347	AGGCGGTACCTTCAGATGTCTACATCACTTGAAGTTCGGCGAGCTGGGCGAAGACCGTGCCG	2406
Db	2379	CGCGGTACCTTCAGATGTCTAOGCTCTGAAGTACCGCAGCTGGCTGCTGCAGTTCCA	2438
Qy	2407	CTTGCAATTGA	2417
Db	2439	TTGGCGGTGCA	2449

Search completed: May 25, 2004, 16:03:57
Job time : 702.519 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 24, 2004, 11:23:39 ; Search time 13.932 Seconds

(without alignments)
2995.894 Million cell updates/sec

Title: US-10-080-114A-2

Perfect score: 4217

Sequence: 1 STHASGRVEDTLHAHNEI.....YILKERELAKTVPLAIDPQ 802

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3397.5	80.6	809	1 SUS2_PEA	Q4301 pisum sativ
2	3158	74.9	766	1 SUSY_BETVU	Q42652 beta vulgar
3	3105.5	73.6	805	1 SUS2_ARATH	Q00917 arabidopsis
4	3005	71.3	820	1 SUS2_TULGE	Q41607 tulipa gesn
5	2993.5	71.0	802	1 SUS1_MAIZE	204712 zea mays (m
6	2965	70.8	816	1 SUS2_MAIZE	P49036 zea mays (m
7	2983.5	70.7	805	1 SUSY_PRAAU	Q01330 phaseolus a
8	2983.5	70.7	805	1 SUSY_SOYBN	P13708 glycine max
9	2983.5	70.7	808	1 SUS1_ORYSA	P30298 oryza sativ
10	2982	70.7	805	1 SUS1_TULGE	Q41608 tulipa gesn
11	2974	70.5	816	1 SUS2_ORYSA	P31924 oryza sativ
12	2948	69.9	816	1 SUS3_ORYSA	Q43009 oryza sativ
13	2944.5	69.8	805	1 SUS1_SOLTU	P10691 solanum tub
14	2944.5	69.8	805	1 SUSY_LYCES	P49037 lycopersico
15	2944.5	69.8	806	1 SUSY_VICFA	P31926 vicia faba
16	2931.5	69.5	805	1 SUSY_MEDSA	O65026 medicago sa
17	2925.5	69.4	805	1 SUS2_SOLTU	P49039 solanum tub
18	2922	69.3	816	1 SUS2_HORVU	P31923 hordeum vul
19	2910.5	69.0	808	1 SUS1_DRAUC	P49035 daucus caro
20	2899	68.7	807	1 SUS1_HORVU	P31922 hordeum vul
21	2861.5	67.9	801	1 SUS2_DAUCA	O49845 daucus caro
22	2855.5	67.7	806	1 SUS1_ARATH	P49040 arabidopsis
23	2844.5	67.5	803	1 SUSY_ALNGL	P49034 alnus glutu
24	587.5	13.9	218	1 SUSY_SACOF	P31925 saccharum o
25	450	10.7	1056	1 SPS_VICOL	P31928 spinacia ol
26	445	10.6	1059	1 SPS_VICFA	Q43876 vicia faba
27	444	10.5	1068	1 SPS_MAIZE	P31927 zea mays (m
28	441.5	10.5	1045	1 SPS_BETVU	P49031 beta vulgar
29	436.5	10.4	1053	1 SPS_SOLTU	Q43845 solanum tub
30	425	10.1	1054	1 SPS_CRAPL	O04912 craterostig
31	414	9.8	1057	1 SPS1_CITUN	O22060 citrus unsh
32	408.5	9.7	1081	1 SPS2_CRAPL	O04933 craterostig
33	351	8.3	1049	1 SPS_ORYSA	Q43802 oryza sativ

34	160.5	3.8	390	1 YG07_METJA	Q59002 methanococ
35	156	3.7	377	1 YPJH_BACSU	P42982 bacillus su
36	147	3.5	480	1 Y486_MYCTU	Q11152 mycobacteri
37	145.5	3.5	381	1 RPAK_SALTY	P26470 salmonella
38	142.5	3.4	428	1 Y486_MYCLE	P54138 mycobacteri
39	141.5	3.4	603	1 UGST_PEA	Q43092 pisum sativ
40	133.5	3.2	5430	1 MACF_HUMAN	Q9upn3 homo sapien
41	133.5	3.2	5938	1 MAC4_HUMAN	Q96pk2 homo sapien
42	127	3.0	477	1 GLGA_STRPN	Q97qs5 streptococ
43	126	3.0	358	1 YC07_KLEPN	Q48453 klebsiella
44	123.5	2.9	503	1 ALG2_YEAST	P43636 saccharomyc
45	123	2.9	484	1 GLGA_VIBCH	Q9krb6 vibrio chol

ALIGNMENTS

RESULT 1					
SUS2_PEA					
ID	SUS2_PEA	STANDARD;	PRT;	809 AA.	
AC	O24301;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2).				
GN	SUS2.				
OS	Pisum sativum (Garden pea).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.				
OX	NCBI_TaxID=3888;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=cv. Frisson; TISSUE=Seed coat;				
RA	Buchner P., Porat M., Rochat C.;				
RT	"Cloning and characterization of a cDNA encoding a second sucrose				
RT	synthase gene in pea (Pisum sativum L.).";				
RL	(In) Plant Gene Register PGR98-105.				
CC	- - FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and				
CC	fructose for various metabolic pathways.				
CC	- - CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.				
CC	- - SIMILARITY: Belongs to the glycosyltransferase family 1. Plant				
CC	sucrose synthase subfamily.				
CC	-----				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AJ001071; CAA04512.1;				
DR	PIR; T06497; T06497.				
DR	InterPro; IPR001296; Glyco trans 1.				
DR	InterPro; IPR000368; Sucrose synth.				
DR	Pfam; PF00534; Glycos_transf_1; 1.				
DR	Pfam; PF00862; Sucrose synth; 1.				
KW	Transferase; Glycosyltransferase; Multigene family.				
SQ	SEQUENCE 809 AA; 92208 MW; 6C5BBF708C37DE75 CRC64;				

Query Match 80.6%; Score 3397.5; DB 1; Length 809;
Best Local Similarity 78.9%; Pred. No. 1.1e-218;
Matches 636; Conservative 80; Mismatches 21; Indels 9; Gaps 2;

Qy	1	STH-----ASGRVEDTLHAHNEIALLSKYVKNKGILQPHILDALDEVGSGGR	53
		: : : : : : : : :	
Db	2	STHPKTRVPSIDRVDQTLTAHNEIALLSKYVKNKGILQPHILDELDNLGSDHA	61
		: : : : : : : :	
Qy	54	A--LAEGPFIDVLRSAQEAIVLPFVAIAVRPPGVWYVVRVNVVHLSVQLTVSEYLR	111
		: : : : : : : :	
Db	62	TLDLKNGPFQIINSAQEAIVLPFVAIAVRPPGVWYVVRVNVVHLSVQLTVSEYLS	121

Db 663 DGA-EKMTFFVKCEDPNTWKISGGLLRKERTWQKYSERLMTAGVGFVKYVSK 721

Qy 770 LERLETRRYLEMYILKRELAKTVPLAIDQ 800
Db 722 LERRETRRYLEMYILKRELAKTVPLAIDQ 752

RESULT 3

SUS2 ARATH STANDARD; PRT; 805 AA.
AC Q00917; Q9FJ2C;
DT 01-APR-1993 (Rel. 25, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase).
GN AT5G4190 OR K21P3.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC YEDLINE=92119221; PubMed=1531031;
RA Chopia S., Del-Favero J., Dolferus R., Jacobs M.;
RT "Sucrose synthase of Arabidopsis: genomic cloning and sequence
RT characterization."
RL Plant Mol. Biol. 18:131-134 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and PAC clones."
RL DNA Res. 5:379-391 (1998).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- INDUCTION: By anaerobic stress.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
CC in positions 9 and 12.

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EMBL; X60987; CAA3303.1; ALT_FRAME.

DR EMBL; AB016872; BAB10337.1; -;
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR000368; Sucrose synth.
DR Pfam; PF00534; Glycosyl_transf_1; 1.
DR Pfam; PF00862; Sucrose synth; 1.
KW Transferase; Glycosyltransferase; Multigene family.
FT CONFLICT 35 35 Q -> H (IN REF. 1).
FT CONFLICT 133 133 D -> H (IN REF. 1).
FT CONFLICT 156 157 FL -> LV (IN REF. 1).
FT CONFLICT 281 282 PH -> RY (IN REF. 1).
FT CONFLICT 286 286 G -> A (IN REF. 1).
FT CONFLICT 298 298 G -> A (IN REF. 1).
FT CONFLICT 648 648 A -> V (IN REF. 1).
FT CONFLICT 718 723 ATLVSF -> GSLAL (IN REF. 1).
SQ SEQUENCE 805 AA; 92007 MW; 448F92326CCA755E CRC64;

Query Match 73.5%; Score 3105.5; DB 1; Length 805;

Best Local Similarity 74.3%; Pred. No. 3.3e-199; Mismatches 98; Indels 5; Gaps 3;
Matches 579; Conservative 97;

Qy 24 LSKYVNVKGIQPHHILDA-LDEVQSGGG-RALAEQFELDLVLSAQEAIVLPPFVAIAV 81
Db 29 LVRYVAQKGILQSHQILDEFLATVKVDGLEDLNKSPFNKVL--QEAIVLPPFVALAI 85

Qy 82 RPRPGWVEYVRVNVHLSVEQLTVSEYLRKEELVDQCHNDPVVLELDFEFNVSVPEN 141
Db 86 RPRPGVREYVRVNVYELSDHLTVSEYLRKEELVNGHANGDVLLELDFEFNATLPRT 145

Qy 142 RSSSIGNGVQFLNRHLSSIMFRNRDCLEPLDLFLGRHRRHGHVMMMLDRIOQLGOSVL 201
Db 146 RSSSIGNGVQFLNRHLSSIMFRNKESPELEFLRTHKHGRPMMLDRIONIFILQAL 205

Qy 202 TKAEHLKSLPADTPYSQFAYKFOENGLKGMGTAGHVLMIHLDDIIOQDPSTLEK 261
Db 206 ARAEEFLSKPLATPYSEPEFELQGMGFERGWDTAQKVSEMVHLLDILQADPSVLET 265

Qy 262 FLGRIPMIENVVVSPHGVEGOANVLGLPDTGGQIVVLDQVRALENEMVYLRKKOGLDV 321
Db 266 FLGRIPMVENVVVSPHGVEGOANVLGLPDTGGQVYVLDQVRALENEMVYLRKKOGLDV 325

Qy 322 SPKILIVTRLIPDAKGTSCNORLERISGTQHTYTLRVEFFERNENGLKWKISRFDPVWPYLE 381
Db 326 IPKILIVTRLIPDAKGTSCNORLERISGTQHTYTLRVEFFERNENGLKWKISRFDPVWPYLE 385

Qy 382 TPAEDAAGEIAEALQGTDPDFIIGNYSDGNLVSALLSYKMGITQCNIAHALEKTKYPSDI 441
Db 386 TPAEDASNEISAEALQGVNLIIGNYSDGNLVSALLSKLGLVIOCNIAHALEKTKYPSDI 445

Qy 442 FWKQPEKHFSCQFTADIIAMNADPIITSTQEIAGSKNTVGOYSHSHTAFTEPGLYRV 501
Db 446 YWRNEEDKHFSCQFTADIIAMNADPIITSTQEIAGSKNNVGOYSHSHTAFTEPGLYRV 505

Qy 502 VHGIDVDFPKFNIVSPGADMSIVFPHTKAKRLTSLHGSIENTLIYDPEQNDHEHGLHDDR 561
Db 506 VHGIDVDFPKFNIVSPGADMTIIFPYSDEKRLTALHSEIEELLFSAEQNDHEHGLHDDR 565

Qy 562 SKPILFEMARLDKRNITGLVEAPAKCAKRELNVLVVAGYNDVNKSKOREEIAETKM 621
Db 566 SKPILFEMARLDKRNITGLVECVAKSKLRELANLVVGVYIDENQSRDREEMAEIQKM 625

Qy 622 HELIKTHNLGQFRWISAOOTFRANGELYRIADTHGAFVQPALYEAAGLTVEAMTGL 681
Db 626 HSLIEQYDLHGEPFRIIAAQMNRANGELYRIADTKGVFVQPAFYEPAGLTVEESMTCL 685

Qy 682 PTATLHGSPAEIIEHGVSGFHDIPYHPQAVNLMADEDFDRCKQDPDHVWNISGAGLQRI 741
Db 686 PTATCHGSPAEIIEHGVSGFHDIPYHPQAVNLVSVFEETCNTNPNHNVKISGGLAKRI 745

Qy 742 YEKYTWKIYSERLMTAGVYGVFWKYVKLERLETRRYLEMYILKRELAKTVPLAIDQ 800
Db 746 YERYTWKYSERLMTAGVYGVFWKVKLERLETRRYLEMYILKRELAKTVPLAIDQ 804

RESULT 4

SUS2 TULGE STANDARD; PRT; 820 AA.

AC Q41607;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2).
OS Tulipa gesneriana (Tulip).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
OC Tulipa.
OX NCBI_TaxID=13306;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-cv. Apeldoorn;
RA Balk P.A., de Boer A.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X96939; CAA65640.1; -;
CC InterPro; IPR001296; Glyco_trans_1.
CC InterPro; IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC Trnstranse; Glycosyltransferase; Multigene family.
CC SEQUENCE 820 AA; 93015 MW; AA75AF88D74A0EED CRC64;
CC -----
CC Query Match 71.3%; Score 3005; DB 1; Length 820;
CC Best Local Similarity 69.7%; Pred. No. 1.7e-192;
CC Matches 556; Conservative 118; Mismatches 122; Indels 2; Gaps 2;
CC -----
CC QY 3 HASGRVEDTLHAHRELVALLSKYVNGKGILOPHHILDALDEVQSGGR-ALAEQPEL 61
CC Db 10 HVSRELTDTLSAHKNELLASRFVQKQGLPHQLITEYEAVIPADREKLDGVFE 69
CC QY 62 DVLRSQAQEAIVLPFFVAIAVRPPGVWYVYVNVVHLSVEQLTVSSYLPKELVPGQEN 121
CC Db 70 DVLKAAQEAIVPFPVVALAIRPPGVWYVYVNVVSELAVEELTVPEYLPQKEELVDGSGQ 129
CC QY 122 DPVLELDEPPNVSPVPRNRSSIGNGVQFLNRHLSIFNRDCLLEPLDLRGRHK 181
CC Db 130 SNFTLELDEPPNVSPVPRNRSSIGNGVQFLNRHLSIFNRDCLLEPLDLRGRHK 189
CC QY 182 GHVWMLNDRIQSLGRQSVLTAEELSLKLPADTPYSQAYKFEWGLKGMGDTAGHVL 241
CC Db 190 GTSWMLNDRIQTLGALQASLRRADEVLSLPLDTPYDFGHRFCGLKGLKGMGDNKRVH 249
CC QY 242 EMHLLDLDI-QAPDPSTLKEFLGRIPMIFNVVWVSPHGYFQANVLGLPDTGCGQIVYILD 301
CC Db 250 ENHLLDLDLEAPDPCTLENFLGTIDPVENVVLSLPHGYFQANVLGYPDTCGQVYILD 309
CC QY 302 QYRALENEMVLRLKKGDLVSPKILIVTRLIIDPAKGTSCNORLERISGTHTVILRVPFR 361
CC Db 310 QYRAEMSEMLRLTKQGLDITPRILIVTRLLPDAVGTTCQRLKVLGTHTHILRVPR 369
CC QY 362 NENGILKKWISRDVWVPLETAEADAAGETAELQGTDPDPIIGNYSDGNLVSALLSYKMG 421
CC Db 370 TENGILKKWISREVPVPLETAEADVAVANAVAGELQATPDLLIGNYSDGNLVSIMAHKLG 429
CC QY 422 ITQCNIAHALEKTKYPDSDIFWKNFDEKHFSQFTADIIAMNNAPIITSTVQETIAGSK 481
CC Db 430 VTQCTIAHALEKTKYPNSDLYMKFKQVHFSCQFTADLIAMNNAPIITSTVQETIAGSK 489
CC QY 482 NTWGVESHTAFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHTEKAKRLTSLGSI 541
CC Db 490 JTWGVESHTGFTPLGLYRVVHGIDVDPKFNIVSPGADMSIYFPHYTEAKRLTALHPEI 549
CC QY 542 ENLIYDPEQNDHEIGHLDKRSKPLFSMARLORVKNITGLVEAFKACAKRELNLVWVA 601
CC Db 550 EELLYSAESTETKFGKDKTKIIFSMARLDKVKMTGLVELYAKNDRLKELNLVWVC 609
CC QY 602 GYNDVNVKSDREBIAETEKQHELIKTHNLFGQFRWISAQNRRNARNGELVYIADTGAFFV 661
CC Db 610 G-DHAKASKDLEBOAELKKWYSLEEKYLDGHTIRWISQAQNNRVNGELVYIADSKGVFV 668

QY 662 QPALYEAFGLTVTEAMTQGLPTFATLHGGAETIIHGVSGFHIDPYHPEQAVNLMADEED 721
Db 669 QPAFTEAFGLTVTESMTQGLPTFATLHGGAETIIHGVSGYHIDPYHGDAAELLVDFFE 728
QY 722 RCKQDPDHWNVISGAGLQRIYKYTKYISERIMTLAGVYGFYKYSKLERLSTRYLEM 781
Db 729 KSKQDQTHDAISNGGLKRIYKYTKYISERIMTLAGVYGFYKYSKLERLSTRYLEM 788
QY 782 FYLKERELAKTVPLAID 799
Db 789 FYALKYRNLAKSVPLAID 806
CC -----
CC RESULT 5
CC SUSI_MAIZE STANDARD; PRT; 802 AA.
CC ID SUSI_MAIZE STANDARD; PRT; 802 AA.
CC AC P04712;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Sucrose synthase 1 (BC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1)
CC DE (Shrunken-1).
CC GN SH-1.
CC OS Zea mays (Maize).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
CC OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
CC OX NCBI_TaxID:4577;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Merr W., Frommer W.-B., Maas C., Starlinger P.;
CC RT "Structure of the sucrose synthase gene on chromosome 9 of Zea mays
CC L";
CC RL EMBO J. 4:1373-1380 (1985).
CC CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways. Most active in the sink
CC tissues where it is responsible for the breakdown of the arriving
CC sucrose.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC -----
CC EMBL; X02400; CAA26247.1; -;
CC EMBL; X02382; CAA26229.1; -;
CC PIR; S07184; YU2MS.
CC MaizeDB; 13861; -;
CC InterPro; IPR001296; Glyco_trans_1.
CC InterPro; IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose synth; 1.
CC Trnstranse; Glycosyltransferase; Multigene family.
CC SEQUENCE 802 AA; 91731 MW; BF1BE860598B680A CRC64;
CC -----
CC Query Match 71.0%; Score 2993.5; DB 1; Length 802;
CC Best Local Similarity 70.0%; Pred. No. 9.5e-192;
CC Matches 559; Conservative 105; Mismatches 131; Indels 3; Gaps 2;
CC -----
CC QY 3 HASGRVEDTLHAHRELVALLSKYVNGKGILOPHHILDALDEVQSGGRALAEQPEL 62
CC Db 9 HSLRERLGLATFFSHPNELIALFSYVHQKGMLOHQLAEFDALFDSKXKA--PFED 66
CC QY 63 VLRSQAQEAIVLPFFVAIAVRPPGVWYVYVNVVHLSVEQLTVSSYLPKELVPGQEN 122
CC Db 67 ILRAAQEAIVLPFFVAIAVRPPGVWYVYVNVVSELAVEELTVPEYLPQKEELVDGSGNS 126

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QY 123 EYVLELDPEFPNVSVPNRSSIGNGVQFLNRHLSIMFNDRDCLPLDPLGRHKG 182
DB 127 NFVLELDPEFPNVSFPNRSKSGIGNGVQFLNRHLSKLPQDKESLYPLNFKAHNYK 186
QY 183 HYVWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKQEWGLKMGWDTAGHVL 242
DB 187 TTWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKQEWGLKMGWDTAGHVL 246
QY 243 MHLHLLDITQAPDPSLTLEKFLGRIPIFNVVVVSPHGYFQANVGLPDTGGQIVILDQ 302
DB 247 TLHLLDLDLEAPDPSLTLEKFLGRIPIFNVVVVSPHGYFQANVGLPDTGGQIVILDQ 306
QY 303 VRALENEMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRVFERN 362
DB 307 VRALENEMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRVFERN 366
QY 363 ENGILKXWISRFDPVWPVYLETFAEDAAGEIAELQGTDPDTIGNYSDGNLVASLLSYKMG 422
DB 367 ENGILKXWISRFDPVWPVYLETFAEDAAGEIAELQGTDPDTIGNYSDGNLVASLLSYKMG 426
QY 423 TQCNIAHALEKTYKYPDSIDFWKFNDEKHYHSCFQADIIAMNADFIITSTYQIAGSKN 482
DB 427 TQCNIAHALEKTYKYPDSIDFWKFNDEKHYHSCFQADIIAMNADFIITSTYQIAGSKN 486
QY 483 TVQYVESHATFTPLGLYRVVGHIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSIE 542
DB 487 TVQYVESHATFTPLGLYRVVGHIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLHGSIE 546
QY 543 NLIYDPEQNDHEHGLDRLSKPILFNSMARLDRVKNITGLVEAFKAKRLNELNVVAVG 602
DB 547 ELIYDVENSEHSEKFLVKDKKKPIFNSMARLDRVKNITGLVEAFKAKRLNELNVVAVG 606
QY 603 YNDVNSKQREELAEKHEMLIKTHNLFCQFNRWISACTNRRANGELYRIADTHGAFVQ 662
DB 607 -DHGKSKQREELAEKHEMLIKTHNLFCQFNRWISACTNRRANGELYRIADTHGAFVQ 665
QY 663 PALYAFGLTVVEMTGLTFTLHGGPAEITLHGVSGPHIDPHYHPEQAVNLMADFPOR 722
DB 666 PALYAFGLTVVEMTGLTFTLHGGPAEITLHGVSGPHIDPHYHPEQAVNLMADFPOR 725
QY 723 CXODPDHWNISGAGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYK 782
DB 726 CXADPSYDWEISQGLQRIYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTYKTY 785
QY 783 YILKFPRELAKTVPLAID 799
DB 786 YALKYRSLASQVPLSPD 802

RESULT 6
SU32_MAIZE
ID SU32_MAIZE STANDARD; PRT; 816 AA.
AC P49036;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2).
GN SUS1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94159796; PubMed=8115551;
RT Huang X.-F., Nguyen-Quoc B., Chourey P.S., Yelle S.;
RT "Complete nucleotide sequence of the maize (Zea mays L.) sucrose
RT synthase 2 cDNA.";
RL Plant Physiol. 104:293-294 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W22;
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RA Nguyen-Quoc B., Huang X.-F., Krivitzky M., Yelle S., Lecharny A.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PHOSPHORYLATION.
RX TISSUE=Leaf;
RC MEDLINE=97037743; PubMed=8883390;
RA Huber S.C., Huber J.L., Liao P.-C., Gage D.A., McMichael R.W. Jr.,
RA Chourey P.S., Hannah L.C., Koch X.;
RT "Phosphorylation of serine-15 of maize leaf sucrose synthase.
RT Occurrence in vivo and possible regulatory significance.";
RL Plant Physiol. 112:793-802 (1996).
CC -1- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC -----
DR EMBL; L22296; AAA33514.1; --
DR EMBL; L33244; AAA33515.1; --
DR MaizeDB; L3861; --
DR InterPro; IPR001296; Glyco trans 1.
DR InterPro; IPR00368; Sucrose synth.
DR Pfam; PF0534; Glycos transf 1; 1.
DR Pfam; PF0862; Sucrose synth 1.
DR Transferase; Glycosyltransferase; Multigene family; Phosphorylation.
KW MOD_RES 15 15 PHOSPHORYLATION.
SQ SEQUENCE 816 AA; 92939 MW; E4DF863BE7AFC4C8 CRC64;

Query Match 70.8%; Score 2985; DB 1; Length 816;
Best Local Similarity 69.8%; Pred. No. 3.6e-191;
Matches 559; Conservative 106; Mismatches 128; Indels 8; Gaps 3;

QY 3 HASGRVEDTLHAHRELVALLSKYVNGKGLQPHHL-----DALDEVQSGGRALAE 58
DB 14 HSVREIGDSLSAHPNELVAVFTRKLNKLGKMLQPHQIIAEYNNAIPEAE---REKLKDG 70

QY 59 PFLDYLSAQEAIVLPFVAIVAPRGWYVYVWVHLSVEQLTVSEYLRFKELVDG 118
DB 71 AFEDVLEAAQEAIVIPPPVAVAIAPRGWYVYVWVHLSVEQLTVSEYLRFKELVDG 130

QY 119 QHNDPYVLELDFEPFNVSVPNRSSIGNGVQFLNRHLSIMFNDRDCLPLDPLGRH 178
DB 131 GFNNVFLVDLDFEPFNVSVPNRSSIGNGVQFLNRHLSIMFNDRDCLPLDPLGRH 190

QY 179 RHKGHVWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKQEWGLKMGWDTAG 238
DB 191 NYKQWMLNDRIQSLGRQSVLTAKAEHLKSLPADTPYSQFAYKQEWGLKMGWDTAG 250

QY 239 HVLEMIHLLDITQAPDPSLTLEKFLGRIPIFNVVVVSPHGYFQANVGLPDTGGQIV 298
DB 251 RAQETIHLHLLDLEAPDPSLTLEKFLGRIPIFNVVVVSPHGYFQANVGLPDTGGQIV 310

QY 299 ILDOVRALENEMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRV 358
DB 311 ILDOVRALENEMVLRLKQGLDVSPPKILIVTRLLPDAKGTSCNORLERISGTQTYILRV 370

QY 359 PFRNENGILKXWISRFDPVWPVYLETFAEDAAGEIAELQGTDPDTIGNYSDGNLVASLLSY 418
DB 371 PFRNENGILKXWISRFDPVWPVYLETFAEDAAGEIAELQGTDPDTIGNYSDGNLVASLLSY 430

QY 419 KMGITQCNIAHALEKTYKYPDSIDFWKFNDEKHYHSCFQADIIAMNADFIITSTYQI 478
DB 431 KMGVTHCTIAHALEKTYKYPDSIDFWKFNDEKHYHSCFQADIIAMNADFIITSTYQI 490

QY 479 GSKNTVQYESHTAFTPLGLYRVVGHIDVDPKFNIVSPGADMSIYPHTEKAKRLTSLH 538
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Db 491 GSKTGVQVESHMAFTMPGLGVVWVGIDVDFPKFNVSPGADLSIYFPPTESHKRLTSLH 550
QY 539 GSIEINLYDPEONDESHIGHLDORSKPLFSMARLDKVNKNTGLVNEAFACAKRLRLNVLV 598
Db 551 PRIBELLYSQTEHKKFVLDNRKPLIFSMARLDKVNKNTGLVLYGNKRLQELNVLV 610
QY 599 VVAGYNDVNVKSDBEEIABIEKHELIKTHNIFGQFRWISAOQNRARNGELYRYIADTHG 658
Db 611 VVCG-DHGNFSKDBEQAEBKMFOLIEQYNLNGHIRWISAOQNRVRNGELYRYICDTKG 669
QY 659 AFVQALYAFAGLTVEAMTCGLPFAHLHGGPAEIIHGVSGFHDVPHQPAQVNLMD 718
Db 670 AFVQAFYAFAGLTVEAMTCGLPFAHTAYGPAEIIHGVSGFHDVPHQPAQVNLMD 729
QY 719 FEDRCQDQDHHWNISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYYSKLERLETRY 778
Db 730 FDKQCAEHSWSKISQSGLRLEBKTYWKLYSERLMTLAGVVGFWKYYSKLERLETRY 789
QY 779 LEMFYIKFRELAKTVPLAID 799
Db 790 LEMLYAKYRTMASTVPLAVE 810

RESULT 7
SUSY PHAAU
ID SUSY PHAAU STANDARD; PRT; 805 AA.
AC Q01390;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase).
GN SS1.
OS Phaseolus aureus (mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 517-537.
RA Arai M., Mori H., Imaseki H.;
RT "Expression of the gene for sucrose synthase during growth of mung
RL bean seedlings."
RL Plant Cell Physiol. 33:503-506 (1992).
CC -!- FUNCTION: Sucrose-cleaving enzyme that provides UDP-glucose and
CC fructose for various metabolic pathways.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose = UDP + sucrose.
CC -!- SIMILARITY: Belongs to the glucosyltransferase family 1. Plant
CC sucrose synthase subfamily.
CC -----
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CC -----
CC EMBL; D10266; BAA01108.1; -
CC InterPro: IPR001296; Glyco trans 1.
CC InterPro: IPR000368; Sucrose synth.
CC Pfam; PF00534; Glycos_transf_1; 1.
CC Pfam; PF00862; Sucrose_synth; 1.
CC Transferrase; Glycosyltransferase.
SQ SEQUENCE 805 AA; 92092 MW; A39683CPDF54EF4A CRC64;

Query Match 70.7%; Score 2983.5; DB 1; Length 805;
Best Local Similarity 69.9%; Pred.No. 4.5e-191;
Matches 557; Conservative 112; Mismatches 127; Indels 1; Gaps 1;

QY 3 HASGDRVEDTLHAHRNELVALLSKYNGKGLQPHILDALDEVQSGGRLAEGPFLD 62
Db 10 HSLRLRLDTLSANREILLALSRIEKGKGLQHQHVIAEFEEIPEESQKLTGDAFGE 69

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QY 63 VLRSQAQEAIVLPFPFAVAIVRPRGVMVYRVNVHLSVQLTVSEYLRFKBELVDGQND 122
Db 70 VLRSQEAIVLPFPFAVAIVRPRGVMVYRVNVHLSVQLTVSEYLRFKBELVDGSSNG 129
QY 123 PTVLELDFPFPNVSPRPNRSSISGNGVQFLNPHLSLIMPRNEDCLEPLDLGLRGRHK 182
Db 130 NFVLELDFPFPNTASFPPTLANKSIGNGVQFLNPHLSLIMPRNEDCLEPLDLGLRGRHK 189
QY 183 HVMMNLNDRIQSLGRQLSVLTQAEHLKSLPADTPYSPQAYKFOEWGLKKGWGTAGHVLE 242
Db 190 KILMNLNDRQLNDALQHLVLRKAEELVGTVPETPYSAFHKFOEIGLGRGWDNAERVLE 249
QY 243 MIHLLDITIQADPSTLEKPLGRPMIFNVVVSPHGVQGANVLGPDTPGQGVIVLDQ 302
Db 250 SIQLLDLLEAPDPCLETFLAGRIPMVFNVLSPHGVQGANVLGPDTPGQGVIVLDQ 309
QY 303 VRALENEMVLRLKQGLDVSPKLIIVTRLIPDAKGTSCNORLERISGTQITQITLIRVPPFN 362
Db 310 VRALENEMHLRIKQGLDIVPRILITRLIPDAVGTTCQRLKVKVFTESHLLRVPFRT 369
QY 363 ENGILKKWISRFEDVWPEYLETFAADAGEIAAEILOGTTPDFIIGNYSDGNIVASLLSYOMGI 422
Db 370 ENGIVKWIISRFEDVWPEYLETFAADAGEIAAEILOGTTPDFIIGNYSDGNIVASLLSYOMGI 429
QY 423 TQCNIAHALEKTYSDSDIFWKNFDEKYHFSOFTADITAMNNADFTITSTYQELAGSKN 482
Db 430 TQCNIAHALEKTYSDSDIFWKNFDEKYHFSOFTADITAMNNADFTITSTYQELAGSKN 489
QY 483 TVGOYESHATAFTLPLGLYRVVHGDVDFPKFNVSPGADMSIYFPHTKAKRLTSLHGSIE 542
Db 490 TVGOYESHATAFTLPLGLYRVVHGDVDFPKFNVSPGADMSIYFPHTKAKRLTSLHGSIE 549
QY 543 NLIYDEQNDHEHGHLDLRSKPLFSMARLDKVNITGLVNEAFACAKRLNVLNVLVAVG 602
Db 550 ELLYSVSENEEHICVLKDRSKPIIFTMAKLDKVNITGLVNEAFACAKRLNVLNVLVAVG 609
QY 603 YNDVNSKOREEIAEIEKHELIKTHNIFGQFRWISAOQNRARNGELYRYIADTHGAFVQ 662
Db 610 -DRRKESKDLKEAEKMKYSLIETKYLKQGFNWISSOMNRVNGELYRYIADTHGAFVQ 666
QY 663 PALYEAFTLVVEMTCGLPFAHLHGGPAEIIHGVSGFHDVPHQPAQVNLMDADFDR 722
Db 669 PAVYEAFTLVVEMTCGLPFAHLHGGPAEIIHGVSGFHDVPHQPAQVNLMDADFDR 728
QY 723 CKQDPHWNISGAGLQRIYKTYWKIYSERLMTLAGVVGFWKYYSKLERLETRYLEMF 782
Db 729 VKVDPSSHWDKISQAGLQRIEETWQISQRLTLTGVGVFWKXVSNLDRRERRRYLEMF 789
QY 783 YILKPRELAKTVPLAID 799
Db 789 YALKYKRLAESVPLAVE 805

RESULT 8
SUSY SOYBN
ID SUSY SOYBN STANDARD; PRT; 805 AA.
AC P13708; O22624;
DT 01-JAN-1990 (Rel. 13, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase)
DE (Modulin-100).
DE SS.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Hobbit; TISSUE=Root nodules;
RA Zhang X.-Q., Verma D.P.S., Patil S., Arredondo-Peter R., Miao G.-H.,

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